

```

QY 1 GTTCAGCTTCTTGTCACAAAGTTGG 25
Db 1 GTTCAGCTTCTTGTCACAAAGTTGG 25

RESULT 4
AAAD14444
ID AAD14444 standard; DNA; 25 BP.
XX
AC AAD14444;
XX
DT 01-NOV-2001 (first entry)
XX
DE Recombination site attP2,P3 DNA.
XX
KW Recombination site; copy number; replicon; recombinatorial cloning;
XX attP2,P3; ds.
XX
OS Unidentified.
XX
PN US6270969-B1.
XX
PD 07-AUG-2001.
XX
PF 20-JAN-1999; 99US-0233492.
XX
PR 07-JUN-1996; 96US-0663002.
XX
PR 07-JUN-1995; 95US-0486139.
XX
PA (INVI-) INVITROGEN CORP.
XX
XX Hartley JL, Brasch MA;
XX WPI; 2001-488248/53.
XX
PT Methods for apposing nucleic acids comprising an expression signal and
PT a gene/partial gene, using recombinatorial cloning by incubating the
PT nucleic acids in the presence of a recombination protein under
PT conditions for recombination -
XX
PS Claim 14; Column 18; 76pp; English.
XX
XX The invention relates to a method for apposing an expression signal and
XX a gene or partial gene, using recombinatorial cloning. The method
XX incubates nucleic acids comprising the expression signal and the gene/
XX partial gene in the presence of a recombination protein under conditions
XX sufficient to cause recombination and therefore appose the expression
XX signal and the gene or partial gene. The methods are useful for apposing
XX an expression signal and a gene or partial gene using recombinatorial
XX cloning. The methods are also useful for changing vectors, constructing
XX genes for fusion proteins, changing copy number, changing replicons,
XX cloning into phages, and cloning e.g., PCR products (with an attB site
XX at one end and a loxP site at the other end), genomic DNAs, and cDNAs.
XX The methods are highly specific, rapid, and less labour intensive than
XX prior art methods. The present sequence is a recombination site
XX useful for recombination cloning.
XX
SQ Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;

Query Match 100.0%; Score 25; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTCACAAAGTTGG 25
Db 1 GTTCAGCTTCTTGTCACAAAGTTGG 25

RESULT 5
AAF55745
ID AAF55745 standard; DNA; 25 BP.
XX
AC AAF55745;
XX
DT 12-APR-2001 (first entry)
XX
DE Recombination site attP2,P3.
XX
KW Recombination site; cloning; att; ss.
XX
OS Unidentified.
XX
PN US6171861-B1.
XX
PD 09-JAN-2001.
XX
PF 12-JAN-1999; 98US-0005476.

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XX
DT 12-APR-2001 (first entry)
XX
DE Recombination site attR3.
XX
KW Recombination site; cloning; att; ss.
XX
OS Unidentified.
XX
PN US6171861-B1.
XX
PD 09-JAN-2001.
XX
PF 12-JAN-1998; 98US-0005476.
XX
PR 07-JUN-1996; 96US-0663002.
XX
PR 07-JUN-1995; 95US-0486139.
XX
PA (LIFE-) LIFE TECHNOLOGIES INC.
XX
PI Hartley JL, Brasch MA;
XX WPI; 2001-136877/14.
XX
PT In vitro cloning of nucleic acid involves mixing vectors comprising
PT recombination sites and/or nucleic acid, incubating mixture to produce
PT chimeric molecule, contacting hosts with mixture and selecting host -
XX
PS Claim 25; Column 46; 73pp; English.
XX
XX The present invention relates to a method for in vitro cloning of a
XX nucleic acid of interest. The method involves mixing in vitro two vectors
XX each comprising at least one recombination site and the nucleic acid of
XX interest; incubating the mixture in the presence of at least one
XX recombination protein to result in recombination of the recombination
XX sites, leading to production of a chimeric nucleic acid molecule
XX comprising the nucleic acid of interest; contacting hosts with the
XX mixture; and selecting for a host comprising the chimeric nucleic acid
XX molecule, and selecting against a host comprising the vectors comprising
XX the second vector, to clone the nucleic acid. The present sequence is a
XX recombination site, which may be used in the method of the present
XX invention.
XX
SQ Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;

Query Match 100.0%; Score 25; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTCACAAAGTTGG 25
Db 1 GTTCAGCTTCTTGTCACAAAGTTGG 25

RESULT 6
AAF55750
ID AAF55750 standard; DNA; 25 BP.
XX
AC AAF55750;
XX
DT 12-APR-2001 (first entry)
XX
DE Recombination site attP2,P3.
XX
KW Recombination site; cloning; att; ss.
XX
OS Unidentified.
XX
PN US6171861-B1.
XX
PD 09-JAN-2001.
XX
PF 12-JAN-1999; 98US-0005476.

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XX 07-JUN-1996; 96US-0663002.
 PR 07-JUN-1995; 95US-0486139.
 XX (LIFE-) LIFE TECHNOLOGIES INC.
 XX Hartley JL, Brasch MA;
 PI WPI; 2001-136877/14.
 DR
 XX In vitro cloning of nucleic acid involves mixing vectors comprising
 PT recombination sites and/or nucleic acid, incubating mixture to produce
 PT chimeric molecule, contacting hosts with mixture and selecting host
 XX
 PS Claim 25; Column 46; 73pp; English.
 XX The present invention relates to a method for in vitro cloning of a
 CC nucleic acid of interest. The method involves mixing in vitro two vectors
 CC each comprising at least one recombination site and the nucleic acid of
 CC interest; incubating the mixture in the presence of at least one
 CC recombination protein to result in recombination of the recombination
 CC sites, leading to production of a chimeric nucleic acid molecule
 CC comprising the nucleic acid of interest; contacting hosts with the
 CC mixture; and selecting for a host comprising the chimeric nucleic acid
 CC molecule, and selecting against a host comprising the vectors comprising
 CC the second vector, to clone the nucleic acid. The present sequence is a
 CC recombination site, which may be used in the method of the present
 CC invention.
 XX
 XX Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;
 SQ
 Query Match 100.0%; Score 25; DB 22; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.11; Indels 0; Gaps 0;
 Matches 25; Conservative 0; Mismatches 0;
 QY 1 GTTCAGCTTCTTGTTACAAAGTTGG 25
 Db 1 GTTCAGCTTCTTGTTACAAAGTTGG 25
 RESULT 7
 AAC87876
 ID AAC87876 standard; DNA; 25 BP.
 XX
 AC AAC87876;
 XX
 DT 02-MAR-2001 (first entry)
 XX
 DE Escherichia coli core region recombinant site attr3 SEQ ID NO:11.
 KW Core region; recombination site; cloning; chimeric DNA;
 KW characteristic; mutation; att site; lox site; ss.
 XX
 OS Escherichia coli.
 XX
 XX US6143557-A.
 XX
 PD 07-NOV-2000.
 XX
 XX 20-JAN-1999; 99US-0233493.
 PF
 XX 07-JUN-1996; 96US-0663002.
 PR 12-JAN-1998; 98US-0005476.
 PR 07-JUN-1995; 95US-0486139.
 XX
 XX (LIFE-) LIFE TECHNOLOGIES INC.
 XX
 XX Brasch MA, Hartley JL;
 PI WPI; 2001-049004/06.
 DR
 XX Isolated nucleic acid molecules comprising a DNA segment having two
 PT engineered recombination sites, derived from att or lox, which flank a
 PT selectable marker and comprise a core region having an engineered
 PT mutation -
 XX
 PS Claim 1; Column 18; 73pp; English.
 XX The present invention describes an isolated nucleic acid molecule (I)

PT selectable marker and comprise a core region having an engineered
 PT mutation -
 XX
 PS Claim 1; Column 18; 73pp; English.
 XX The present invention describes an isolated nucleic acid molecule (I)
 CC comprising a first nucleic acid sequence having a defined sequence
 CC (AAC87866 to AAC87881), sequences complementary to AAC87866 to AAC87881,
 CC or an RNA sequence corresponding to AAC87866 to AAC87881. Also described
 CC are: (1) an isolated nucleic acid molecule (II) comprising a first
 CC mutated recombination site that removes one or more stop codons from the
 CC recombination site or avoids hairpin formation, the recombination site
 CC being an att or lox site; (2) an isolated nucleic acid molecule (III)
 CC comprising a first att recombination site comprising a mutation that
 CC enhances recombination specificity; (3) vectors (IV) comprising the above
 CC mentioned nucleic acids; and (4) cells comprising the above
 CC mentioned nucleic acids or (IV). The nucleic acids are used in
 CC engineering a core region of a given recombination site to provide
 CC mutative sites suitable for subcloning reactions. The use of nucleic
 CC acids for obtaining engineered recombination in vitro or in vivo makes
 CC the methods for DNA or RNA subcloning, highly specific, rapid, and
 CC less labour intensive.
 XX
 XX Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;
 SQ
 Query Match 100.0%; Score 25; DB 22; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.11; Indels 0; Gaps 0;
 Matches 25; Conservative 0; Mismatches 0;
 QY 1 GTTCAGCTTCTTGTTACAAAGTTGG 25
 Db 1 GTTCAGCTTCTTGTTACAAAGTTGG 25
 RESULT 8
 AAC87881
 ID AAC87881 standard; DNA; 25 BP.
 XX
 AC AAC87881;
 XX
 DT 02-MAR-2001 (first entry)
 XX
 DE Escherichia coli core region recombinant site attP2,P3 SEQ ID NO:16.
 KW Core region; recombination site; cloning; chimeric DNA;
 KW characteristic; mutation; att site; lox site; ss.
 XX
 OS Escherichia coli.
 XX
 XX US6143557-A.
 XX
 PD 07-NOV-2000.
 XX
 XX 20-JAN-1999; 99US-0233493.
 PF
 XX 07-JUN-1996; 96US-0663002.
 PR 12-JAN-1998; 98US-0005476.
 PR 07-JUN-1995; 95US-0486139.
 XX
 XX (LIFE-) LIFE TECHNOLOGIES INC.
 XX
 XX Brasch MA, Hartley JL;
 PI WPI; 2001-049004/06.
 DR
 XX Isolated nucleic acid molecules comprising a DNA segment having two
 PT engineered recombination sites, derived from att or lox, which flank a
 PT selectable marker and comprise a core region having an engineered
 PT mutation -
 XX
 PS Claim 1; Column 18; 73pp; English.
 XX The present invention describes an isolated nucleic acid molecule (I)

comprising a first nucleic acid sequence having a defined sequence (AAC87866 to AAC87881), sequences complementary to AAC87866 to AAC87881, or an RNA sequence corresponding to AAC87866 to AAC87881. Also described are: (1) an isolated nucleic acid molecule (II) comprising a first mutated recombination site that removes one or more stop codons from the recombination site or avoids hairpin formation, the recombination site being an att or lox site; (2) an isolated nucleic acid molecule (III) comprising a first att recombination site comprising a mutation that enhances recombination specificity; (3) vectors (IV) comprising the above mentioned nucleic acids; and (4) cells comprising the above mentioned nucleic acids or (IV). The nucleic acids are used in engineering a core region of a given recombination site to provide mutative sites suitable for subcloning reactions. The use of nucleic acids for obtaining engineered recombination in vitro or in vivo makes the methods for DNA or RNA subcloning, highly specific, rapid, and less labour intensive.

Query Match 100.0%; Score 25; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. NO. 0.11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTACAAAGTTGG 25
|||||
Db 1 GTTCAGCTTCTTGTACAAAGTTGG 25

RESULT 9
AAS14786
ID AAS14786 standard; DNA; 25 BP.

AC AAS14786;

DT 27-FEB-2002 (first entry)

DE Lambda phage Int recombinase site core region DNA sequence attR3.

Recombinant nucleic acid vector; carcinoembryonic antigen; CEA; cytokine; syncytium-inducing polypeptide; fusogenic membrane glycoprotein; tumour; recombinase; tumour-specific promoter; hypoxic response element; HRE; ss; tyrosinase promoter; Cre; FLP; retroviral vector; malignant cell; cancer; cytostatic; gene therapy; Int recombinase site core region; attR3; exsive recombination.

OS Bacteriophage lambda.

PN WO200174861-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US10250.

PR 31-MAR-2000; 2000US-193977P.

PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.

PI Vile RG, Harrington K, Murphy S, Bateman A;

DR WPI; 2001-656985/75.

Recombinant nucleic acid vector for reducing tumour size, has expression cassette comprises a promoter linked to nucleic acid sequence encoding a syncytium-inducing polypeptide and flanked on either side by recombination -

PS Disclosure; Page 42; 84pp; English.

The invention relates to a recombinant nucleic acid vector comprising a first expression cassette, comprising a first promoter operably linked to a nucleic acid sequence encoding a syncytium-inducing polypeptide (such as a fusogenic membrane glycoprotein) and flanked on either side by a sequence recognised by a recombinase, and/or a second expression cassette

comprising a tumour-specific promoter operably linked to a nucleic acid sequence encoding a recombination. The nucleic acid of the first expression cassette may be linked to a hypoxic response element (HRE), the second expression cassette may contain a promoter linked to a nucleic acid encoding a cytokine, and a third cassette may contain a tumour specific promoter linked to the nucleic acid encoding the recombination. The tumour specific promoter is, for example, a carcinoembryonic antigen (CEA) promoter or a tyrosinase promoter and the recombination is, for example, Cre recombinase or FLP recombinase. The invention is useful for reducing tumour size by administering the compositions as retroviral vectors, or in a cell containing the vector, to an individual in need of treatment for a disease caused by malignant cells. This sequence represents an Int recombinase site core region attR3, required for exsive recombination.

XX Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;

Query Match 100.0%; Score 25; DB 23; Length 25;
Best Local Similarity 100.0%; Pred. NO. 0.11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTACAAAGTTGG 25
|||||
Db 1 GTTCAGCTTCTTGTACAAAGTTGG 25

RESULT 10
ABQ82123
ID ABQ82123 standard; DNA; 25 BP.

AC ABQ82123;

DT 11-DEC-2002 (first entry)

DE Core sequence of recombination site attR3 SEQ ID NO:6.

Chimeric nucleic acid construct; recombinational cloning; silencing; recombination site; double stranded RNA; plant; ss.

OS Synthetic.

PN WO200259294-A1.

PD 01-AUG-2002.

PF 24-JAN-2002; 2002WO-AU00073.

PR 26-JAN-2001; 2001US-264067P.

PR 29-NOV-2001; 2001US-333743P.

PA (CSIR) COMMONWEALTH SCI & IND RES ORG.

PI Wesley S, Waterhouse P, Helliwell C;

DR WPI; 2002-692669/73.

New vectors comprising operably linked DNA fragments having an origin of replication, a selectable marker and a chimeric DNA construct, useful for silencing target nucleic acids and for producing large amounts of double-stranded RNA -

PS Disclosure; Page 15; 104pp; English.

The present invention describes a vector (i) comprising operably linked DNA fragments having: (a) origin of replication allowing replication in a recipient cell, preferably in bacteria such as Escherichia coli; (b) selectable marker region capable of being expressed in the recipient cell; and (c) a chimeric DNA construct comprising: (i) promoter or promoter region capable of being recognized by RNA polymerases of a eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second, third and fourth recombination sites; (iii) 3' transcription terminating and polyadenylation region functional in the eukaryotic cell. The first and fourth recombination sites, or the second and third recombination sites are capable of reacting with a same recombination site, and

CC preferably are identical. The first and second recombination sites, or
CC the third and fourth recombination sites, do not recombine with each
CC other or with a same recombination site. The vector is useful for
CC producing large amounts of double-stranded RNA which can be used for
CC silencing target nucleic acid sequences. The vectors can also be used to
CC convert a DNA fragment into an inverted repeat structure. Plants
CC transformed with a vector from the present invention can be used in a
CC conventional breeding scheme to produce more plants with the same
CC characteristics or to introduce a chimeric gene for reduction of the
CC phenotypic expression of nucleic acids. The present sequence represents
CC the core sequence of recombination site attB1 which is given in the
CC exemplification of the present invention.
XX
XX Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;

Query Match 100.0%; Score 25; DB 24; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGACAAAGTTGG 25
|||||
Db 1 GTTCAGCTTCTTGACAAAGTTGG 25

RESULT 11
ABQ82128
ID ABQ82128 standard; DNA; 25 BP.
XX
AC ABQ82128;
XX
DT 11-DEC-2002 (first entry)
XX
DE Core sequence of recombination site attP2,P3 SEQ ID NO:11.

XX Chimeric nucleic acid construct; recombinational cloning; silencing;
KW recombination site; double stranded RNA; plant; ss.
XX
OS Synthetic.

XX WO200259294-A1.
XX 01-AUG-2002.
XX 24-JAN-2002; 2002WO-AU00073.
XX 26-JAN-2001; 2001US-264067P.
XX 29-NOV-2001; 2001US-333743P.
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX
XX Wesley S, Waterhouse P, Helliwell C;
XX WPI; 2002-682669/73.

XX New vectors comprising operably linked DNA fragments having an origin
PT of replication, a selectable marker and a chimeric DNA construct,
PT useful for silencing target nucleic acids and for producing large
PT amounts of double-stranded RNA
XX
XX Claim 12; Page 15; 104pp; English.

XX The present invention describes a vector (I) comprising operably linked
CC DNA fragments having: (a) origin of replication allowing replication in a
CC recipient cell, preferably in bacteria such as Escherichia coli;
CC (b) selectable marker region capable of being expressed in the recipient
CC cell; and (c) a chimeric DNA construct comprising: (i) promoter or
CC promoter region capable of being recognized by RNA polymerases of a
CC eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second,
CC third and fourth recombination sites; (iii) 3' transcription terminating
CC and polyadenylation region functional in the eukaryotic cell. The first
CC and fourth recombination sites, or the second and third recombination
CC sites are capable of reacting with a same recombination site, and
CC preferably are identical. The first and second recombination sites, or

CC the third and fourth recombination sites, do not recombine with each
CC other or with a same recombination site. The vector is useful for
CC producing large amounts of double-stranded RNA which can be used for
CC silencing target nucleic acid sequences. The vectors can also be used to
CC convert a DNA fragment into an inverted repeat structure. Plants
CC transformed with a vector from the present invention can be used in a
CC conventional breeding scheme to produce more plants with the same
CC characteristics or to introduce a chimeric gene for reduction of the
CC phenotypic expression of nucleic acids. The present sequence represents
CC the core sequence of recombination site attB1 which is given in the
CC exemplification of the present invention.
XX
XX Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;

Query Match 100.0%; Score 25; DB 24; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGACAAAGTTGG 25
|||||
Db 1 GTTCAGCTTCTTGACAAAGTTGG 25

RESULT 12
ACC44660
ID ACC44660 standard; DNA; 25 BP.
XX
AC ACC44660;
XX
DT 29-MAY-2003 (first entry)
XX
DE Recombination site related oligonucleotide SEQ ID NO:51.

XX Chromosome-based platform; artificial chromosome; eukaryotic chromosome;
KW att site; integrase; recombinase; ACes; gene therapy; transgenic animal;
KW platform artificial chromosome expression system; PCR primer; ss.
XX
OS Synthetic.

XX WO200297059-A2.
XX 05-DEC-2002.
XX 30-MAY-2002; 2002WO-US17452.
XX 30-MAY-2001; 2001US-294758P.
XX 21-MAR-2002; 2002US-366891P.
XX (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
XX
XX Perkins E, Perez C, Lindenbaum M, Greene A, Leung J, Fleming E;
XX Stewart S, Shellard J;
XX WPI; 2003-140461/13.

XX Novel eukaryotic chromosome comprising one or many att sites which
PT permits site-directed integration in the presence of lambda-integrase,
PT useful for site-specific recombination-directed integration of DNA of
PT interest
XX
XX Claim 43; Page 143; 272pp; English.

XX The present invention describes a eukaryotic chromosome (I) comprising
CC one or several att sites, where an att site is heterologous to the
CC chromosome, and permits site-directed integration in the presence of
CC lambda-integrase. Also described: (i) a platform artificial chromosome
CC expression system (ACes) (ii) comprising several sites that participate
CC in recombinase catalysed recombination; and (2) a method (M1) for
CC introducing a heterologous nucleic acid into a platform artificial
CC chromosome. (I) can be used in gene therapy. (M1) is useful for
CC introducing a heterologous nucleic acid molecule into a platform
CC artificial chromosome, preferably an ACes. (II) is useful for producing a
CC transgenic animal (e.g. a fish, insect, reptile, amphibian, arachnid, or

CC mammal) by introducing (II) by cell fusion, lipid-mediated transfection
 CC by a carrier system, microinjection, microcell fusion, electroporation,
 CC microprojectile bombardment or direct DNA transfer into an embryonic
 CC cell, preferably a stem cell or an embryo. (II) comprises a heterologous
 CC nucleic acid that encodes a therapeutic product which is useful for
 CC making a library of ACes comprising random portions of a genome. ACC44612
 CC to ACC44732 and ABP96650 to ABP96657 represent sequences used in the
 CC exemplification of the present invention.

XX Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;
 SQ Query Match 100.0%; Score 25; DB 25; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTTACAAAGTTGG 25
 |||||
 DB 1 GTTCAGCTTCTTGTTACAAAGTTGG 25

RESULT 13
 ACC44665
 ID ACC44665 standard; DNA; 25 BP.

XX AC ACC44665;

XX DT 29-MAY-2003 (first entry)

XX DE Recombination site related oligonucleotide SEQ ID NO:56.

XX KW Chromosome-based platform; artificial chromosome; eukaryotic chromosome;
 KW art site; integrase; recombinase; ACes; gene therapy; transgenic animal;
 KW platform artificial chromosome expression system; PCR primer; ss.

XX OS Synthetic.

XX PN WO200297059-A2.

XX PD 05-DEC-2002.

XX PF 30-MAY-2002; 2002WO-US17452.

XX PR 30-MAY-2001; 2001US-294759P.

XX PR 21-MAR-2002; 2002US-366891P.

XX PA (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.

XX PI Perkins E, Perez C, Lindenbaum M, Greene A, Leung J, Fleming E;

XX PI Stewart S, Shellard J;

XX DR WPI; 2003-140461/13.

XX PT Novel eukaryotic chromosome comprising one or many att sites which
 PT permits site-directed integration in the presence of lambda-integrase,
 PT useful for site-specific recombination-directed integration of DNA of
 PT interest

XX PS Claim 43; Page 143; 272pp; English.

XX CC The present invention describes a eukaryotic chromosome (I) comprising
 CC one or several att sites, where an att site is heterologous to the
 CC chromosome, and permits site-directed integration in the presence of
 CC lambda-integrase. Also described: (1) a platform artificial chromosome
 CC expression system (ACes) (II) comprising several sites that participate
 CC in recombinase catalysed recombination; and (2) a method (M1) for
 CC introducing a heterologous nucleic acid into a platform artificial
 CC chromosome. (I) can be used in gene therapy. (M1) is useful for
 CC introducing a heterologous nucleic acid molecule into a platform
 CC artificial animal (e.g. a fish, insect, reptile, amphibian, arachnid, or
 CC transgenic animal) by introducing (II) by cell fusion, lipid-mediated transfection
 CC mammal) by introducing (II) by cell fusion, lipid-mediated transfection
 CC by a carrier system, microinjection, microcell fusion, electroporation,
 CC microprojectile bombardment or direct DNA transfer into an embryonic

CC cell, preferably a stem cell or an embryo. (II) comprises a heterologous
 CC nucleic acid that encodes a therapeutic product which is useful for
 CC making a library of ACes comprising random portions of a genome. ACC44612
 CC to ACC44732 and ABP96650 to ABP96657 represent sequences used in the
 CC exemplification of the present invention.

XX Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;

XX Query Match 100.0%; Score 25; DB 25; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTTACAAAGTTGG 25
 |||||
 DB 1 GTTCAGCTTCTTGTTACAAAGTTGG 25

RESULT 14
 ABT16630

ID ABT16630 standard; DNA; 25 BP.

XX AC ABT16630;

XX DT 03-APR-2003 (first entry)

XX DE Artificial plant chromosome related oligo SEQ ID No 42.

XX KW Plant artificial chromosome; PAC; transgenic plant; vaccine;

XX KW blood factor; herbicide; stress; agronomical; nutrient quality;

XX KW bacterial artificial chromosome; BAC; yeast artificial chromosome; YAC;

XX KW ds.

XX OS Unidentified.

XX PN WO200296923-A1.

XX PD 05-DEC-2002.

XX PF 30-MAY-2002; 2002WO-US17451.

XX PR 30-MAY-2001; 2001US-294687P.

XX PR 04-JUN-2001; 2001US-296329P.

XX PA (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.

XX PA (AGRI-) AGRISOMA INC.

XX PI Perez C, Fabijanski SF, Perkins E;

XX PI WPI; 2003-140436/13.

XX DR WPI; 2003-140436/13.

XX PS Disclosure; Page 263; 269pp; English.

XX CC The invention relates to a novel method for producing plant artificial
 CC chromosomes. The invention also relates to methods for targeting
 CC insertion of heterologous DNA into plant artificial chromosomes, methods
 CC for delivery of plant chromosomes to selected cells and tissues. The
 CC isolated plant artificial chromosome (PAC) is useful for producing a
 CC transgenic plant, which involves introducing the PAC into a plant cell.
 CC The PAC comprises a heterologous nucleic acid encoding a gene product
 CC such as enzymes, antisense RNA, rRNA, xDNA, structural proteins, marker
 CC proteins, ligands, receptors, ribozymes, therapeutic proteins, and
 CC biopharmaceutical proteins, vaccines, blood factors, antigens, hormones,
 CC cytokines, growth factors, antibodies, or a product that provides for
 CC resistance to diseases, insects, herbicides, or stress in a plant. The
 CC heterologous nucleic acid optionally encodes a product that provides an
 CC agronomically important trait in the plant, e.g. a product that alters
 CC nutrient use and/or improves the nutrient quality of the plant. The
 CC heterologous nucleic acid is contained within a bacterial artificial

CC chromosome (BAC) or a yeast artificial chromosome (YAC). This
 CC polynucleotide sequence represents an oligo relating to the method for
 CC producing plant artificial chromosomes of the invention.
 XX
 SQ Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;
 Query Match 100.0%; Score 25; DB 25; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTTCAGCTTCTGTACAAAGTTGG 25
 |||||
 DB 1 GTTCAGCTTCTGTACAAAGTTGG 25
 |||||
 RESULT 15
 ABT16635
 ID ABT16635 standard; DNA; 25 BP.
 XX
 AC ABT16635;
 XX
 DT 03-APR-2003 (first entry)
 XX
 DE Artificial plant chromosome related oligo SEQ ID No 47.
 XX
 KW Plant artificial chromosome; PAC; transgenic plant; vaccine;
 KW blood factor; herbicide; stress; agronomical; nutrient quality;
 KW bacterial artificial chromosome; BAC; yeast artificial chromosome; YAC;
 KW ds.
 XX
 OS Unidentified.
 XX
 PN WO200296923-A1.
 XX
 PD 05-DEC-2002.
 XX
 PF 30-MAY-2002; 2002WO-US17451.
 XX
 PR 30-MAY-2001; 2001US-294687P.
 PR 04-JUN-2001; 2001US-296329P.
 XX
 PA (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
 PA (AGRI-) AGRISOMA INC.
 XX
 PI Perez C, Fabijanski SF, Perkins E;
 XX
 DR WPI; 2003-140436/13.
 XX
 PT Producing artificial chromosome by introducing a nucleic acid into
 PT plant cell, selecting artificial chromosome that has one or more repeat
 PT regions with equivalent amounts of euchromatic and heterochromatic
 PT nucleic acids -
 XX
 PS Disclosure; Page 263; 269pp; English.
 XX
 CC The invention relates to a novel method for producing plant artificial
 CC chromosomes. The invention also relates to methods for targeting
 CC insertion of heterologous DNA into plant artificial chromosomes, methods
 CC for delivery of plant chromosomes to selected cells and tissues. The
 CC isolated plant artificial chromosome (PAC) is useful for producing a
 CC transgenic plant, which involves introducing the PAC into a plant cell.
 CC The PAC comprises a heterologous nucleic acid encoding a gene product
 CC such as enzymes, antisense RNA, tRNA, rDNA, structural proteins, marker
 CC proteins, ligands, receptors, ribozymes, therapeutic proteins, and
 CC pharmaceutical proteins, vaccines, blood factors, antigens, hormones,
 CC cytokines, growth factors, antibodies, or a product that provides for
 CC resistance to diseases, insects, herbicides, or stress in a plant. The
 CC heterologous nucleic acid optionally encodes a product that provides an
 CC agronomically important trait in the plant, e.g. a product that alters
 CC nutrient use and/or improves the nutrient quality of the plant. The
 CC heterologous nucleic acid is contained within a bacterial artificial
 CC chromosome (BAC) or a yeast artificial chromosome (YAC). This
 CC polynucleotide sequence represents an oligo relating to the method for

CC producing plant artificial chromosomes of the invention.
 XX
 SQ Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;
 Query Match 100.0%; Score 25; DB 25; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTTCAGCTTCTGTACAAAGTTGG 25
 |||||
 DB 1 GTTCAGCTTCTGTACAAAGTTGG 25
 |||||
 RESULT 16
 AAS06183
 ID AAS06183 standard; DNA; 27 BP.
 XX
 AC AAS06183;
 XX
 DT 12-SEP-2001 (first entry)
 XX
 DE Phage-lambda recombination site attP2.
 XX
 KW Bacteriophage lambda; recombination; att site; PCR primer; lambda Int;
 KW lambda integrase; therapeutic; ss.
 XX
 OS Bacteriophage lambda.
 XX
 PN WO200142509-A1.
 XX
 PD 14-JUN-2001.
 XX
 PF 11-DEC-2000; 2000WO-US33546.
 XX
 PR 10-DEC-1999; 99US-0169983.
 PR 09-MAR-2000; 2000US-0188020.
 XX
 PA (CHRO/) CHEO D.
 PA (BRAS/) BRASCH M A.
 PA (TEMP/) TEMPLE G F.
 PA (HART/) HARTLEY J L.
 PA (BYRD/) BYRD D R N.
 XX
 PI Cheo D, Brasch MA, Temple GF, Hartley JL, Byrd DRN;
 XX
 DR WPI; 2001-356174/37.
 XX
 PT Producing hybrid nucleic acids, useful for expressing novel therapeutic
 PT polypeptides, by mixing the same or different nucleic acids having one
 PT or more recombination sites in the presence of recombination proteins,
 PT e.g. Cre -
 XX
 PS Disclosure; Fig 24A; 357pp; English.
 XX
 CC AAS06174-AAS06322 represent Bacteriophage lambda att recombination
 CC site nucleic acid sequences, and PCR primers of the invention. The
 CC att sequences are recognised by the recombination protein lambda
 CC integrase (Int). The invention is a new method of producing a population
 CC of hybrid nucleic acids comprising mixing at least a first population of
 CC nucleic acids comprising one or more recombination sites with at least
 CC one target nucleic acid comprising one or more recombination sites and
 CC causing some or all of the nucleic acids to recombine with all or some of
 CC the target nucleic acids. The method is useful for producing a population
 CC of hybrid nucleic acids which may be the same or different. The nucleic
 CC acids may be used to express therapeutic proteins or peptides and they
 CC may also be used to create novel fusion proteins by expressing different
 CC sequences linked to each other. The method allows simultaneous cloning of
 CC two or more different nucleic acids.
 XX
 SQ Sequence 27 BP; 6 A; 5 C; 6 G; 10 T; 0 other;
 Query Match 100.0%; Score 25; DB 22; Length 27;
 Best Local Similarity 100.0%; Pred. No. 0.11;

```
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTCTGTACAAAGTTGG 25
    |||||
Db 1 GTTCAGCTTCTCTGTACAAAGTTGG 25

RESULT 17
ABZ58736
ID ABZ58736 standard; DNA; 27 BP.
XX
AC ABZ58736;
XX
DT 01-MAY-2003 (first entry)
XX
DE Att site nucleotide sequence attP2.
XX
KW Nucleic acid insertion; recombination; nucleic acid selection;
KW nucleic acid isolation; att; ds.
XX
OS Synthetic.
XX
XX WO200295055-A2.
XX
XX 28-NOV-2002.
XX
XX 21-MAY-2002; 2002WO-US15947.
XX
XX 21-MAY-2001; 2001US-291973P.
XX
PA (INVT-) INVITROGEN CORP.
XX
XX Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN;
XX
XX WPI; 2003-129436/12.
XX
PT Inserting a population of nucleic acids into a second target molecule
PT for selecting and isolating nucleic acid molecules by mixing the second
PT population of nucleic acid with a second target nucleic acid -
XX
PS Disclosure; Fig 13A; 273pp; English.
XX
CC The invention relates to inserting a population of nucleic acids into a
CC second target molecule. The method involves (a) mixing a first population
CC of nucleic acid comprising one or more recombination sites with a target
CC nucleic acid; (b) causing some or all of the nucleic acid molecules of
CC the first population to recombine with the first target nucleic acid
CC molecules to form a second population; (c) mixing the second population
CC of nucleic acid with a second target nucleic acid; and (d) causing some
CC or all of the nucleic acid molecules of the second population to
CC recombine with some or all of the second target nucleic acid molecules to
CC form a third population of nucleic acid. The method is useful for
CC selecting and isolating nucleic acid molecules. Sequences ABZ58727-762
CC represent att recombination site sequences used in the method of the
CC invention.
XX
XX Sequence 27 BP; 6 A; 5 C; 6 G; 10 T; 0 other;
SQ

Query Match 100.0%; Score 25; DB 25; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTCTGTACAAAGTTGG 25
    |||||
Db 1 GTTCAGCTTCTCTGTACAAAGTTGG 25

RESULT 18
AAC55383/c
ID AAC55383 standard; DNA; 233 BP.
XX
AC AAC55383;
XX
XX 11-JAN-2001 (first entry)
DT
```

```
DT 11-JAN-2001 (first entry)
XX
DE Recombination site nucleotide sequence attP2.
XX
KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
KW mutant; recombinational cloning; entry vector; destination vector;
KW gene product targeting; fusion tag cleavage; ds.
XX
XX Bacteriophage lambda.
OS
XX WO2000052027-A1.
XX
XX 08-SEP-2000.
XX
XX 02-MAR-2000; 2000WO-US05432.
XX
XX 02-MAR-1999; 99US-0122389.
XX
XX 23-MAR-1999; 99US-0126049.
XX
XX 28-MAY-1999; 99US-0136744.
XX
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX
XX Hartley JL, Brasch MA, Temple GF, Cheo D;
XX
XX WPI; 2000-543948/49.
XX
XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
XX attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
XX recombinational cloning of polypeptides -
XX
XX Claim 1; Fig 9; 459pp; English.
XX
CC The present invention describes isolated nucleic acid molecules (I)
CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
CC molecule (II) comprising one or more att recombination sites comprising
CC at least one mutation in its core region that increases the specificity
CC of interaction between the recombination site and a second att
CC recombination site; and (2) an isolated nucleic acid molecule (III)
CC comprising one or more mutated att recombination sites comprising at
CC least one mutation in its core region that enhances the efficiency of
CC recombination between a first nucleic acid molecule comprising the
CC mutated att recombination site and a second nucleic acid molecule
CC comprising a second recombination site that interacts with the mutated
CC att recombination site. (I), (II), (III), primers, vectors and methods
CC from the present invention are used for the recombinational cloning of
CC nucleic acid molecules. They can be used for changing vectors, targeting
CC gene products to intracellular locations, cleaving fusion tags from
CC desired proteins, operably linking nucleic acid molecules of interest to
CC regulatory genetic sequences, constructing genes for fusion proteins,
CC changing copy number, changing replicons, cloning into phages and
CC cloning. (I), (II), (III), host cells and vectors can be used in the
CC production of polypeptides and antibodies. The present sequence is
CC used in the exemplification of the present invention.
XX
XX Sequence 233 BP; 94 A; 35 C; 32 G; 72 T; 0 other;
SQ

Query Match 100.0%; Score 25; DB 21; Length 233;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTCTGTACAAAGTTGG 25
    |||||
Db 100 GTTCAGCTTCTCTGTACAAAGTTGG 76

RESULT 19
AAC55524/c
ID AAC55524 standard; DNA; 4165 BP.
XX
AC AAC55524;
XX
XX 11-JAN-2001 (first entry)
DT
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```
XX DE Donor plasmid pDONR204 nucleotide sequence.
XX KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
XX KW mutant; recombinational cloning; entry vector; destination vector;
XX KW gene product targeting; fusion tag cleavage; ds.
XX OS Bacteriophage lambda.
XX OS Synthetic.
XX PN WO200052027-A1.
XX PD 08-SEP-2000.
XX PF 02-MAR-2000; 2000WO-US05432.
XX PR 02-MAR-1999; 99US-0122389.
XX PR 23-MAR-1999; 99US-0126049.
XX PR 28-MAY-1999; 99US-0136744.
XX PA (LIFE-) LIFE TECHNOLOGIES INC.
XX PI Hartley JL, Brasch MA, Temple GF, Chao D;
XX PI WPI; 2000-543948/49.
XX DR
XX PT Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
XX PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
XX PT recombinational cloning of polypeptides -
XX PS Example 9; Fig 52; 459pp; English.
XX CC The present invention describes isolated nucleic acid molecules (I)
XX CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
XX CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
XX CC molecule (II) comprising one or more att recombination sites comprising
XX CC at least one mutation in its core region that increases the specificity
XX CC of interaction between the recombination site and a second att
XX CC recombination site; and (2) an isolated nucleic acid molecule (III)
XX CC comprising one or more mutated att recombination sites comprising at
XX CC least one mutation in its core region that enhances the efficiency of
XX CC recombination between a first nucleic acid molecule comprising the
XX CC mutated att recombination site and a second nucleic acid molecule
XX CC comprising a second recombination site that interacts with the mutated
XX CC att recombination site. (I), (II), (III), primers, vectors and methods
XX CC from the present invention are used for the recombinational cloning of
XX CC nucleic acid molecules. They can be used for changing vectors, targeting
XX CC gene products to intracellular locations, cleaving fusion tags from
XX CC desired proteins, operably linking nucleic acid molecules of interest to
XX CC regulatory genetic sequences, constructing genes for fusion proteins,
XX CC changing copy number, changing replicons, cloning into phages and
XX CC cloning. (I), (II), (III), host cells and vectors can be used in the
XX CC production of polypeptides and antibodies. The present sequence is
XX CC used in the exemplification of the present invention.
XX SQ Sequence 4165 BP; 1117 A; 926 C; 925 G; 1196 T; 1 other;

Query Match 100.0%; Score 25; DB 21; Length 4165;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTCACAAAGTTGG 25
Db 2209 GTTCAGCTTCTTGTCACAAAGTTGG 2185

RESULT 20
AAC55522/c
ID AAC55522 standard; DNA; 4204 BP.
XX AC AAC55522;
XX DT 11-JAN-2001 (first entry)
```

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XX DE Donor plasmid pDONR202 nucleotide sequence.
XX KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
XX KW mutant; recombinational cloning; entry vector; destination vector;
XX KW gene product targeting; fusion tag cleavage; ds.
XX OS Bacteriophage lambda.
XX OS Synthetic.
XX PN WO200052027-A1.
XX PD 08-SEP-2000.
XX PF 02-MAR-2000; 2000WO-US05432.
XX PR 02-MAR-1999; 99US-0122389.
XX PR 23-MAR-1999; 99US-0126049.
XX PR 28-MAY-1999; 99US-0136744.
XX PA (LIFE-) LIFE TECHNOLOGIES INC.
XX PI Hartley JL, Brasch MA, Temple GF, Chao D;
XX PI WPI; 2000-543948/49.
XX DR
XX PT Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
XX PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
XX PT recombinational cloning of polypeptides -
XX PS Example 9; Fig 50; 459pp; English.
XX CC The present invention describes isolated nucleic acid molecules (I)
XX CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
XX CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
XX CC molecule (II) comprising one or more att recombination sites comprising
XX CC at least one mutation in its core region that increases the specificity
XX CC of interaction between the recombination site and a second att
XX CC recombination site; and (2) an isolated nucleic acid molecule (III)
XX CC comprising one or more mutated att recombination sites comprising at
XX CC least one mutation in its core region that enhances the efficiency of
XX CC recombination between a first nucleic acid molecule comprising the
XX CC mutated att recombination site and a second nucleic acid molecule
XX CC comprising a second recombination site that interacts with the mutated
XX CC att recombination site. (I), (II), (III), primers, vectors and methods
XX CC from the present invention are used for the recombinational cloning of
XX CC nucleic acid molecules. They can be used for changing vectors, targeting
XX CC gene products to intracellular locations, cleaving fusion tags from
XX CC desired proteins, operably linking nucleic acid molecules of interest to
XX CC regulatory genetic sequences, constructing genes for fusion proteins,
XX CC changing copy number, changing replicons, cloning into phages and
XX CC cloning. (I), (II), (III), host cells and vectors can be used in the
XX CC production of polypeptides and antibodies. The present sequence is
XX CC used in the exemplification of the present invention.
XX SQ Sequence 4204 BP; 1198 A; 912 C; 959 G; 1135 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 4204;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTCACAAAGTTGG 25
Db 2248 GTTCAGCTTCTTGTCACAAAGTTGG 2224

RESULT 21
AAC55523
ID AAC55523 standard; DNA; 4208 BP.
XX AC AAC55523;
XX DT 11-JAN-2001 (first entry)
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XX DE Donor plasmid pDONR203 nucleotide sequence.
XX DE
XX KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
XX KW mutant; recombinational cloning; entry vector; destination vector;
XX KW gene product targeting; fusion tag cleavage; ds.
XX OS Bacteriophage lambda.
XX OS Synthetic.
XX PN WO200052027-A1.
XX PD 08-SEP-2000.
XX XX
XX PF 02-MAR-2000; 2000WO-US05432.
XX XX
XX PR 02-MAR-1999; 99US-0122389.
XX PR 23-MAR-1999; 99US-0126049.
XX PR 28-MAY-1999; 99US-0136744.
XX XX
XX PA (LIFE-) LIFE TECHNOLOGIES INC.
XX XX
XX PI Hartley JL, Brasch MA, Temple GF, Cheo D;
XX WPI; 2000-543948/49.
XX XX
XX PT Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
XX PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
XX PT recombinational cloning of polypeptides -
XX PS Example 9; Fig 51; 459pp; English.
XX XX
XX CC The present invention describes isolated nucleic acid molecules (I)
XX CC encoding an attB1, attB2, attP1, attL1, attL2, attR1, and attR2
XX CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
XX CC molecule (II) comprising one or more att recombination sites comprising
XX CC at least one mutation in its core region that increases the specificity
XX CC of interaction between the recombination site and a second att
XX CC recombination site; and (2) an isolated nucleic acid molecule (III)
XX CC comprising one or more mutated att recombination sites comprising at
XX CC least one mutation in its core region that enhances the efficiency of
XX CC recombination between a first nucleic acid molecule comprising the
XX CC mutated att recombination site and a second nucleic acid molecule
XX CC comprising a second recombination site that interacts with the mutated
XX CC att recombination site. (I), (II), (III), primers, vectors and methods
XX CC from the present invention are used for the recombinational cloning of
XX CC nucleic acid molecules. They can be used for changing vectors, targeting
XX CC gene products to intracellular locations, cleaving fusion tags from
XX CC desired proteins, operably linking nucleic acid molecules of interest to
XX CC regulatory genetic sequences, constructing genes for fusion proteins,
XX CC changing copy number, changing replicons, cloning into phages and
XX CC cloning. (I), (II), (III), host cells and vectors can be used in the
XX CC production of polypeptides and antibodies. The present sequence is
XX CC used in the exemplification of the present invention.
XX SQ Sequence 4208 BP; 1172 A; 997 C; 875 G; 1164 T; 0 other;

  Query Match      100.0%; Score 25; DB 21; Length 4208;
  Best Local Similarity 100.0%; Pred. No. 0.18;
  Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAAGTTGG 25
Db 1291 GTTCAGCTTTCTGTACAAAGTTGG 1315

RESULT 22
ID ABZ58768
XX ABZ58768 standard; DNA; 4428 BP.
XX AC
XX ABZ58768;
XX 01-MAY-2003 (first entry)
DT

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XX DE Destination plasmid pDONR212 nucleotide sequence.
XX DE
XX KW Nucleic acid insertion; recombination; nucleic acid selection;
XX KW nucleic acid isolation; ds.
XX OS Synthetic.
XX PN WO200295055-A2.
XX PD 28-NOV-2002.
XX XX
XX PF 21-MAY-2002; 2002WO-US15947.
XX XX
XX PR 21-MAY-2001; 2001US-291973P.
XX XX
XX PA (INVI-) INVITROGEN CORP.
XX PI Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN;
XX WPI; 2003-129436/12.
XX XX
XX PT Inserting a population of nucleic acids into a second target molecule
XX PT for selecting and isolating nucleic acid molecules by mixing the second
XX PT population of nucleic acid with a second target nucleic acid -
XX PS Disclosure; Fig 27B-C; 273pp; English.
XX XX
XX CC The invention relates to inserting a population of nucleic acids into a
XX CC second target molecule. The method involves (a) mixing a first population
XX CC of nucleic acid comprising one or more recombination sites with a target
XX CC nucleic acid; (b) causing some or all of the nucleic acid molecules of
XX CC the first population to recombine with the first target nucleic acid
XX CC molecules to form a second population; (c) mixing the second population
XX CC of nucleic acid with a second target nucleic acid; and (d) causing some
XX CC or all of the nucleic acid molecules of the second population to
XX CC recombine with some or all of the second target nucleic acid molecules to
XX CC form a third population of nucleic acid. The method is useful for
XX CC selecting and isolating nucleic acid molecules. The present sequence
XX CC represents the destination plasmid pDONR212 nucleotide sequence.
XX SQ Sequence 4428 BP; 1214 A; 1064 C; 929 G; 1221 T; 0 other;

  Query Match      100.0%; Score 25; DB 25; Length 4428;
  Best Local Similarity 100.0%; Pred. No. 0.18;
  Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAAGTTGG 25
Db 3180 GTTCAGCTTTCTGTACAAAGTTGG 3204

RESULT 23
AAC55521
ID AAC55521 standard; DNA; 4470 BP.
XX AC
XX AAC55521;
XX 11-JAN-2001 (first entry)
XX DE
XX DE Donor plasmid pDONR201 nucleotide sequence.
XX KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
XX KW mutant; recombinational cloning; entry vector; destination vector;
XX KW gene product targeting; fusion tag cleavage; ds.
XX OS Bacteriophage lambda.
XX OS Synthetic.
XX PN WO200052027-A1.
XX PD 08-SEP-2000.
XX XX

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PF 02-MAR-2000; 2000WO-US05432.
XX
XX
PR 02-MAR-1999; 99US-0122389.
PR 23-MAR-1999; 99US-0126049.
PR 28-MAY-1999; 99US-0136744.
XX
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX
XX Hartley JL, Brasch MA, Temple GF, Cheo D;
XX WPI; 2000-543948/49.
XX
XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
XX attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
XX recombinational cloning of polypeptides -
XX Example 9; Fig 49; 459pp; English.
XX
XX The present invention describes isolated nucleic acid molecules (I)
XX encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
XX nucleotide sequence. Also described are: (1) an isolated nucleic acid
XX molecule (II) comprising one or more att recombination sites comprising
XX at least one mutation in its core region that increases the specificity
XX of interaction between the recombination site and a second att
XX recombination site; and (2) an isolated nucleic acid molecule (III)
XX comprising one or more mutated att recombination sites comprising at
XX least one mutation in its core region that enhances the efficiency of
XX recombination between a first nucleic acid molecule comprising the
XX mutated att recombination site and a second nucleic acid molecule
XX comprising a second recombination site that interacts with the mutated
XX att recombination site. (I), (II), (III) primers, vectors and methods
XX from the present invention are used for the recombinational cloning of
XX nucleic acid molecules. They can be used for changing vectors, targeting
XX gene products to intracellular locations, cleaving fusion tags from
XX desired proteins, operably linking nucleic acid molecules of interest to
XX regulatory genetic sequences, constructing genes for fusion proteins,
XX changing copy number, changing replicons, cloning into phages and
XX cloning. (I), (II), (III), host cells and vectors can be used in the
XX production of polypeptides and antibodies. The present sequence is
XX used in the exemplification of the present invention.
XX
XX Sequence 4470 BP; 1193 A; 1037 C; 977 G; 1263 T; 0 other;
Query Match 100.0%; Score 25; DB 21; Length 4470;
Best Local Similarity 100.0%; Pred. No. 0.18; Mismatches 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCAGCTTCTTGTTACAAAGTTGG 25
DB 2343 GTTCAGCTTCTTGTTACAAAGTTGG 2367
RESULT 24
ABZ58767
ID ABZ58767 standard; DNA; 4470 BP.
XX
XX
AC ABZ58767;
XX
XX
DT 01-MAY-2003 (first entry)
XX
XX Destination plasmid pDONR201 nucleotide sequence.
XX
XX Nucleic acid insertion; recombination; nucleic acid selection;
XX nucleic acid isolation; ds.
XX
XX Synthetic.
XX
XX WO200295055-A2.
XX
XX 28-NOV-2002.
XX
XX 21-MAY-2002; 2002WO-US15947.
XX
XX 21-MAY-2001; 2001US-291973P.
XX
XX (INVI-) INVITROGEN CORP.
XX
XX Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN;
XX WPI; 2003-129436/12.
XX
XX Inserting a population of nucleic acids into a second target molecule
XX for selecting and isolating nucleic acid molecules by mixing the second
XX population of nucleic acid with a second target nucleic acid -
XX Disclosure; Fig 28B-C; 273pp; English.

PR 21-MAY-2001; 2001US-291973P.
XX
XX (INVI-) INVITROGEN CORP.
XX
XX Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN;
XX WPI; 2003-129436/12.
XX
XX Inserting a population of nucleic acids into a second target molecule
XX for selecting and isolating nucleic acid molecules by mixing the second
XX population of nucleic acid with a second target nucleic acid -
XX Disclosure; Fig 26B-C; 273pp; English.
XX
XX The invention relates to inserting a population of nucleic acids into a
XX second target molecule. The method involves (a) mixing a first population
XX of nucleic acid comprising one or more recombination sites with a target
XX nucleic acid; (b) causing some or all of the nucleic acid molecules of
XX the first population to recombine with the first target nucleic acid
XX molecules to form a second population; (c) mixing the second population
XX of nucleic acid with a second target nucleic acid; and (d) causing some
XX or all of the nucleic acid molecules of the second population to
XX recombine with some or all of the second target nucleic acid molecules to
XX form a third population of nucleic acid. The method is useful for
XX selecting and isolating nucleic acid molecules. The present sequence
XX represents the destination plasmid pDONR201 nucleotide sequence.
XX
XX Sequence 4470 BP; 1193 A; 1037 C; 977 G; 1263 T; 0 other;
Query Match 100.0%; Score 25; DB 25; Length 4470;
Best Local Similarity 100.0%; Pred. No. 0.18; Mismatches 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCAGCTTCTTGTTACAAAGTTGG 25
DB 2343 GTTCAGCTTCTTGTTACAAAGTTGG 2367
RESULT 25
ABZ58769
ID ABZ58769 standard; DNA; 4627 BP.
XX
XX
AC ABZ58769;
XX
XX
DT 01-MAY-2003 (first entry)
XX
XX Destination plasmid pDONR212(F) nucleotide sequence.
XX
XX Nucleic acid insertion; recombination; nucleic acid selection;
XX nucleic acid isolation; ds.
XX
XX Synthetic.
XX
XX WO200295055-A2.
XX
XX 28-NOV-2002.
XX
XX 21-MAY-2002; 2002WO-US15947.
XX
XX 21-MAY-2001; 2001US-291973P.
XX
XX (INVI-) INVITROGEN CORP.
XX
XX Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN;
XX WPI; 2003-129436/12.
XX
XX Inserting a population of nucleic acids into a second target molecule
XX for selecting and isolating nucleic acid molecules by mixing the second
XX population of nucleic acid with a second target nucleic acid -
XX Disclosure; Fig 28B-C; 273pp; English.

CC The invention relates to inserting a population of nucleic acids into a
CC second target molecule. The method involves (a) mixing a first population
CC of nucleic acid comprising one or more recombination sites with a target
CC nucleic acid; (b) causing some or all of the nucleic acid molecules of
CC the first population to recombine with the first target nucleic acid
CC molecules to form a second population; (c) mixing the second population
CC of nucleic acid with a second target nucleic acid; and (d) causing some
CC or all of the nucleic acid molecules of the second population to
CC recombine with some or all of the second target nucleic acid molecules to
CC form a third population of nucleic acid. The method is useful for
CC selecting and isolating nucleic acid molecules. The present sequence
CC represents the destination plasmid pDONR212(F) nucleotide sequence.

XX SQ Sequence 4627 BP; 1262 A; 1126 C; 990 G; 1249 T; 0 other;

Query Match 100.0%; Score 25; DB 25; Length 4627;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTTACAAAGTTGG 25
|||
Db 2331 GTTCAGCTTCTTGTTACAAAGTTGG 2355

RESULT 26
ABZ58770
ID ABZ58770 standard; DNA; 4627 BP.
XX AC ABZ58770;
XX DT 01-MAY-2003 (first entry)
XX DE Destination plasmid pDONR212(R) nucleotide sequence.
XX KW Nucleic acid insertion; recombination; nucleic acid selection;
XX KW nucleic acid isolation; ds.
XX OS Synthetic.
XX XX WO200295055-A2.
XX PD 28-NOV-2002.
XX PF 21-MAY-2002; 2002WO-US15947.
XX PR 21-MAY-2001; 2001US-291973P.
XX PA (INVI-) INVITROGEN CORP.

XX PI Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN;
XX WPI; 2003-129436/12.
XX XX Inserting a population of nucleic acids into a second target molecule
XX for selecting and isolating nucleic acid molecules by mixing the second
XX PT population of nucleic acid with a second target nucleic acid -
XX PS Disclosure; Fig 29B-C; 273pp; English.

XX CC The invention relates to inserting a population of nucleic acids into a
XX second target molecule. The method involves (a) mixing a first population
XX of nucleic acid comprising one or more recombination sites with a target
XX nucleic acid; (b) causing some or all of the nucleic acid molecules of
XX the first population to recombine with the first target nucleic acid
XX molecules to form a second population; (c) mixing the second population
XX of nucleic acid with a second target nucleic acid; and (d) causing some
XX or all of the nucleic acid molecules of the second population to
XX recombine with some or all of the second target nucleic acid molecules to
XX form a third population of nucleic acid. The method is useful for
XX selecting and isolating nucleic acid molecules. The present sequence
XX CC represents the destination plasmid pDONR212(R) nucleotide sequence.

XX SQ Sequence 4627 BP; 1262 A; 1126 C; 990 G; 1249 T; 0 other;

Query Match 100.0%; Score 25; DB 25; Length 4627;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTTACAAAGTTGG 25
|||
Db 2331 GTTCAGCTTCTTGTTACAAAGTTGG 2355

RESULT 27
AAC55525
ID AAC55525 standard; DNA; 4939 BP.
XX AC AAC55525;
XX DT 11-JAN-2001 (first entry)
XX DE Donor plasmid pDONR205 nucleotide sequence.

XX KW Bacteriophage lambda; att; recombination site; attB; attP; attL; attR;
XX KW mutant; recombinational cloning; entry vector; destination vector;
XX KW gene product targeting; fusion tag cleavage; ds.

XX OS Bacteriophage lambda.
XX OS Synthetic.

XX PN WO200052027-A1.
XX PD 08-SEP-2000.
XX PF 02-MAR-2000; 2000WO-US05432.
XX PR 02-MAR-1999; 99US-0122389.
XX PR 23-MAR-1999; 99US-0126049.
XX PR 28-MAY-1999; 99US-0136744.
XX PA (LIFE-) LIFE TECHNOLOGIES INC.

XX PI Hartley JL, Brasch MA, Temple GF, Cheo D;
XX WPI; 2000-543948/49.

XX PT Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
XX attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
XX PT recombinational cloning of polypeptides -

XX XX Example 10; Fig 53; 459pp; English.

XX CC The present invention describes isolated nucleic acid molecules (I)
XX encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
XX nucleotide sequence. Also described are: (1) an isolated nucleic acid
XX molecule (II) comprising one or more att recombination sites comprising
XX at least one mutation in its core region that increases the specificity
XX of interaction between the recombination site and a second att
XX recombination site; and (2) an isolated nucleic acid molecule (III)
XX comprising one or more mutated att recombination sites comprising at
XX least one mutation in its core region that enhances the efficiency of
XX recombination between a first nucleic acid molecule comprising the
XX mutated att recombination site and a second nucleic acid molecule
XX comprising a second recombination site that interacts with the mutated
XX att recombination site. (I), (II), (III), primers, vectors and methods
XX from the present invention are used for the recombinational cloning of
XX nucleic acid molecules. They can be used for changing vectors, targeting
XX gene products to intracellular locations, cleaving fusion tags from
XX desired proteins, operably linking nucleic acid molecules of interest to
XX regulatory genetic sequences, constructing genes for fusion proteins,
XX changing copy number, changing replicons, cloning into phages and
XX cloning (I), (II), (III), host cells and vectors can be used in the
XX production of polypeptides and antibodies. The present sequence is
XX used in the exemplification of the present invention.

XX SQ Sequence 4939 BP; 1193 A; 1285 C; 1152 G; 1309 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 4939;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTCACAAAGTTGG 25
|||||
Db 938 GTTCAGCTTCTTGTCACAAAGTTGG 962

RESULT 28
AAC5525/c
ID AAC55256 standard; DNA; 5156 BP.

XX AC AAC5526;

DT 11-JAN-2001 (first entry)

XX DE Donor plasmid pDONR206 nucleotide sequence.

XX KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
KW mutant; recombinational cloning; entry vector; destination vector;
KW gene product targeting; fusion tag cleavage; ds.

XX OS Bacteriophage lambda.
OS Synthetic.

XX PN WO200052027-A1.

XX PD 08-SEP-2000.

XX PF 02-MAR-2000; 2000WO-US05432.

XX PR 02-MAR-1999; 99US-0122389.

XX PR 23-MAR-1999; 99US-0126049.

XX PR 28-MAY-1999; 99US-0136744.

XX PA (LIFE-) LIFE TECHNOLOGIES INC.

XX PI Hartley JL, Brasch MA, Temple GF, Cheo D;

XX DR WPI; 2000-543948/49.

XX PT Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
attL1, attL2, attR1, and attR2 nucleotide sequence useful for the

XX PT recombinational cloning of polypeptides -

XX PS Example 9; Fig 54; 459pp; English.

XX CC The present invention describes isolated nucleic acid molecules (I)
CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
CC molecule (II) comprising one or more att recombination sites comprising
CC at least one mutation in its core region that increases the specificity
CC of interaction between the recombination site and a second att
CC recombination site; and (2) an isolated nucleic acid molecule (III)
CC comprising one or more mutated att recombination sites comprising at
CC least one mutation in its core region that enhances the efficiency of
CC recombination between a first nucleic acid molecule comprising the
CC mutated att recombination site and a second nucleic acid molecule
CC comprising a second recombination site that interacts with the mutated
CC att recombination site. (I), (II), (III), primers, vectors and methods
CC from the present invention are used for the recombinational cloning of
CC nucleic acid molecules. They can be used for changing vectors, targeting
CC gene products to intracellular locations, cleaving fusion tags from
CC desired proteins, operably linking nucleic acid molecules of interest to
CC regulatory genetic sequences, constructing genes for fusion proteins,
CC changing copy number, changing replicons, cloning into phages and
CC cloning. (I), (II), (III), host cells and vectors can be used in the
CC production of polypeptides and antibodies. The present sequence is
CC used in the exemplification of the present invention.

XX SQ Sequence 5156 BP; 1413 A; 1183 C; 1216 G; 1342 T; 2 other;

Query Match 100.0%; Score 25; DB 21; Length 5156;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTCACAAAGTTGG 25
|||||
Db 3200 GTTCAGCTTCTTGTCACAAAGTTGG 3176

RESULT 29

AAC55632/c

ID AAC55632 standard; DNA; 5584 BP.

XX AC AAC55632;

DT 11-JAN-2001 (first entry)

XX DE Donor plasmid pDONR207 nucleotide sequence.

XX KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
KW mutant; recombinational cloning; entry vector; destination vector;
KW gene product targeting; fusion tag cleavage; ds.

XX OS Bacteriophage lambda.
OS Synthetic.

XX PN WO200052027-A1.

XX PD 08-SEP-2000.

XX PF 02-MAR-2000; 2000WO-US05432.

XX PR 02-MAR-1999; 99US-0122389.

XX PR 23-MAR-1999; 99US-0126049.

XX PR 28-MAY-1999; 99US-0136744.

XX PA (LIFE-) LIFE TECHNOLOGIES INC.

XX PI Hartley JL, Brasch MA, Temple GF, Cheo D;

XX DR WPI; 2000-543948/49.

XX PT Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
attL1, attL2, attR1, and attR2 nucleotide sequence useful for the

XX PT recombinational cloning of polypeptides -

XX PS Disclosure; Fig 97; 459pp; English.

XX CC The present invention describes isolated nucleic acid molecules (I)
CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
CC molecule (II) comprising one or more att recombination sites comprising
CC at least one mutation in its core region that increases the specificity
CC of interaction between the recombination site and a second att
CC recombination site; and (2) an isolated nucleic acid molecule (III)
CC comprising one or more mutated att recombination sites comprising at
CC least one mutation in its core region that enhances the efficiency of
CC recombination between a first nucleic acid molecule comprising the
CC mutated att recombination site and a second nucleic acid molecule
CC comprising a second recombination site that interacts with the mutated
CC att recombination site. (I), (II), (III), primers, vectors and methods
CC from the present invention are used for the recombinational cloning of
CC nucleic acid molecules. They can be used for changing vectors, targeting
CC gene products to intracellular locations, cleaving fusion tags from
CC desired proteins, operably linking nucleic acid molecules of interest to
CC regulatory genetic sequences, constructing genes for fusion proteins,
CC changing copy number, changing replicons, cloning into phages and
CC cloning. (I), (II), (III), host cells and vectors can be used in the
CC production of polypeptides and antibodies. The present sequence is
CC used in the exemplification of the present invention.

XX SQ Sequence 5584 BP; 1521 A; 1294 C; 1341 G; 1428 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 5584;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGTTACAAAGTTGG 25
|||||
Db 3243 GTTCAGCTTTCTTGTTACAAAGTTGG 3219

RESULT 30
ABZ58766/C
ID ABZ58766 standard; DNA; 5584 BP.
XX
AC ABZ58766;
XX
DT 01-MAY-2003 (first entry)
XX
DE Donor plasmid pDONR207 nucleotide sequence.

XX Nucleic acid insertion; recombination; nucleic acid selection;
KW nucleic acid isolation; ds.
KW
XX
OS Synthetic.

XX WO200295055-A2.
XX
XX 28-NOV-2002.
PD
XX
XX 21-MAY-2002; 2002WO-US15947.
PF
XX
XX 21-MAY-2001; 2001US-291973P.
PR

XX (INVI-) INVITROGEN CORP.
XX
XX Bransch MA, Cheo D, Li X, Esposito D, Byrd DRN;
PI
XX WPI; 2003-129436/12.
DR

XX Inserting a population of nucleic acids into a second target molecule
PT for selecting and isolating nucleic acid molecules by mixing the second
PT population of nucleic acid with a second target nucleic acid -

XX Disclosure; Fig 18B-C; 273pp; English.

XX The invention relates to inserting a population of nucleic acids into a
CC second target molecule. The method involves (a) mixing a first population
CC of nucleic acid comprising one or more recombination sites with a target
CC nucleic acid; (b) causing some or all of the nucleic acid molecules of
CC the first population to recombine with the first target nucleic acid
CC molecules to form a second population; (c) mixing the second population
CC of nucleic acid with a second target nucleic acid; and (d) causing some
CC or all of the nucleic acid molecules of the second population to
CC recombine with some or all of the second target nucleic acid molecules to
CC form a third population of nucleic acid. The method is useful for
CC selecting and isolating nucleic acid molecules. The present sequence
CC represents the donor plasmid pDONR207 nucleotide sequence.

XX SQ Sequence 5584 BP; 1521 A; 1294 C; 1341 G; 1428 T; 0 other;

Query Match 100.0%; Score 25; DB 25; Length 5584;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGTTACAAAGTTGG 25
|||||
Db 3243 GTTCAGCTTTCTTGTTACAAAGTTGG 3219

RESULT 31
ABQ82130
ID ABQ82130 standard; DNA; 18691 BP.
XX
XX

AC ABQ82130;
XX
XX 11-DEC-2002 (first entry)
DT
XX
XX Acceptor vector pHELLSGATE nucleotide sequence SEQ ID NO:13.
DE
XX
XX Chimeric nucleic acid construct; recombinational cloning; silencing;
KW recombination site; double stranded RNA; plant; ds.
KW
XX
XX Synthetic.

XX WO200259294-A1.

XX 01-AUG-2002.

XX 24-JAN-2002; 2002WO-AU00073.

XX 26-JAN-2001; 2001US-264067P.

XX 29-NOV-2001; 2001US-333743P.

XX (CSIR) COMMONWEALTH SCI & IND RES ORG.

XX Wesley S, Waterhouse P, Helliwell C;

XX WPI; 2002-682669/73.

XX New vectors comprising operably linked DNA fragments having an origin
XX of replication, a selectable marker and a chimeric DNA construct,
XX useful for silencing target nucleic acids and for producing large
XX amounts of double-stranded RNA -

XX Claim 13; Page 62-72; 104pp; English.

XX The present invention describes a vector (I) comprising operably linked
XX DNA fragments having: (a) origin of replication allowing replication in a
XX recipient cell, preferably in bacteria such as Escherichia coli;
XX (b) selectable marker region capable of being expressed in the recipient
XX cell; and (c) a chimeric DNA construct comprising: (i) promoter or
XX promoter region capable of being recognized by RNA polymerases of a
XX eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second,
XX third and fourth recombination sites; (iii) 3' transcription terminating
XX and polyadenylation region functional in the eukaryotic cell. The first
XX and fourth recombination sites, or the second and third recombination
XX sites are capable of reacting with a same recombination site, and
XX preferably are identical. The first and second recombination sites, or
XX the third and fourth recombination sites, do not recombine with each
XX other or with a same recombination site. The vector is useful for
XX producing large amounts of double-stranded RNA which can be used for
XX silencing target nucleic acid sequences. The vectors can also be used to
XX convert a DNA fragment into an inverted repeat structure. Plants
XX transformed with a vector from the present invention can be used in a
XX conventional breeding scheme to produce more plants with the same
XX characteristics or to introduce a chimeric gene for reduction of the
XX phenotypic expression of nucleic acids. The present sequence represents
XX an acceptor vector nucleotide sequence from the present invention.

XX SQ Sequence 18691 BP; 4837 A; 4621 C; 4607 G; 4626 T; 0 other;

Query Match 100.0%; Score 25; DB 24; Length 18691;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGTTACAAAGTTGG 25
|||||
Db 14520 GTTCAGCTTTCTTGTTACAAAGTTGG 14544

RESULT 32
ABQ82130/C
ID ABQ82130 standard; DNA; 18691 BP.
XX
XX ABQ82130;
XX
XX

DT 11-DEC-2002 (first entry)
XX Acceptor vector PHELLSGATE nucleotide sequence SEQ ID NO:13.
XX Chimeric nucleic acid construct; recombinational cloning; silencing;
KW recombination site; double stranded RNA; plant; ds.
XX Synthetic.
OS WO200259294-A1.
FN 01-AUG-2002.
XX 24-JAN-2002; 2002WO-AU000073.
XX 26-JAN-2001; 2001US-264067P.
XX 29-NOV-2001; 2001US-333743P.
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX Wesley S, Waterhouse P, Helliwell C;
PI WPI; 2002-682669/73.
XX New vectors comprising operably linked DNA fragments having an origin
PT of replication, a selectable marker and a chimeric DNA construct,
PT useful for silencing target nucleic acids and for producing large
PT amounts of double-stranded RNA -
XX Claim 13; Page 62-72; 104pp; English.
XX The present invention describes a vector (I) comprising operably linked
CC DNA fragments having: (a) origin of replication allowing replication in a
CC recipient cell, preferably in bacteria such as *Escherichia coli*;
CC (b) selectable marker region capable of being expressed in the recipient
CC cell; and (c) a chimeric DNA construct comprising: (i) promoter or
CC promoter region capable of being recognized by RNA polymerases of a
CC eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second,
CC third and fourth recombination sites; (iii) 3' transcription terminating
CC and polyadenylation region functional in the eukaryotic cell. The first
CC and fourth recombination sites, or the second and third recombination
CC sites are capable of reacting with a same recombination site, and
CC preferably are identical. The first and second recombination sites, or
CC the third and fourth recombination sites, do not recombine with each
CC other or with a same recombination site. The vector is useful for
CC producing large amounts of double-stranded RNA which can be used for
CC silencing target nucleic acid sequences. The vectors can also be used to
CC convert a DNA fragment into an inverted repeat structure. Plants
CC transformed with a vector from the present invention can be used in a
CC conventional breeding scheme to produce more plants with the same
CC characteristics or to introduce a chimeric gene for reduction of the
CC phenotypic expression of nucleic acids. The present sequence represents
XX an acceptor vector nucleotide sequence from the present invention.
XX Sequence 18691 BP; 4837 A; 4621 C; 4607 G; 4626 T; 0 other;
Query Match 100.0%; Score 25; DB 24; Length 18691;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCAGCTTCTTGACAAAGTTGG 25
Db 16418 GTTCAGCTTCTTGACAAAGTTGG 16394
RESULT 33
AAAX78977
ID AAX78977 standard; DNA; 25 BP.
XX AAX78977;
AC AAX78977;
XX 17-AUG-1999 (first entry)
DT 17-AUG-1999 (first entry)
XX

DE Oligonucleotide #43 for recombination and cloning method.
XX Cloning; donor; recombination site; vector; chimeric; ss.
XX Synthetic.
XX WO9921977-A1.
XX 06-MAY-1999.
XX 26-OCT-1998; 98WO-US22589.
XX 23-OCT-1998; 98US-0177387.
XX 24-OCT-1997; 97US-0065930.
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX Brasch MA, Fox DK, Hartley JL, Temple GF;
PI WPI; 1999-303011/25.
XX New nucleic acid cloning methods
XX Disclosure; Page 171; 185pp; English.
XX The invention relates to novel methods for cloning or subcloning one or
CC more nucleic acid molecules (NMs) comprising: (a) combining in vitro or
CC in vivo: (i) at least one insert donor molecules (IDMs) comprising one
CC or more desired nucleic acid segments flanked by at least 2
CC recombination sites which do not recombine with each other; (2) one or
CC more vector donor molecules (VDMs) comprising at least 2 recombination
CC sites which do not recombine with each other; and (3) one or more
CC site-specific recombination proteins; (b) incubating the combination to
CC transfer one or more of the desired segments into one or more of the
CC VDMs, thereby producing one or more desired product molecules (PMs). The
CC methods can be used for the efficient and specific recombination of NAM
CC segments. They can be used to generate chimeric DNA or RNA molecules that
CC have the desired characteristics and/or nucleic acid segments. The
CC methods can also be used for changing vectors. The oligonucleotides
CC AAX78935-X78994 are used in the method of the invention.
XX Sequence 25 BP; 4 A; 3 C; 5 G; 10 T; 3 other;
SQ Query Match 95.2%; Score 23.8; DB 20; Length 25;
Best Local Similarity 88.0%; Pred. No. 0.37;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCAGCTTCTTGACAAAGTTGG 25
Db 1 GTTCAGCTTCTTGACAAAGTTGG 25
RESULT 34
AAT48224
ID AAT48224 standard; DNA; 25 BP.
XX AAT48224;
AC AAT48224;
XX 20-OCT-1997 (first entry)
DT 20-OCT-1997 (first entry)
XX attP1 core region.
DE attP1 core region.
XX att recombination site; core region; mutation; enhance; recombination;
KW vector; subcloning; regulation; exchange; ss.
XX Synthetic.
XX WO9640724-A1.
XX 19-DEC-1996.
XX 07-JUN-1996; 96WO-US10082.
XX

PR 07-JUN-1995; 95US-0486139.
 XX (LIFE-) LIFE TECHNOLOGIES INC.
 XX
 XX Brasch MA, Hartley JL;
 XX WPI; 1997-065168/06.
 DR
 XX Nucleic acids, vectors and methods to obtain chimeric nucleic acid -
 PT using recombinant proteins and engineered recombination sites in
 PT vitro or in vivo
 XX
 XX Claim 14; Page 56; 106pp; English.
 XX
 XX AAT48210-25 are att recombination site core region DNA sequences. The
 CC core region has at least one engineered mutation that enhances
 CC recombination in vitro in the formation of a Cointegrate or Product DNA.
 CC These core regions can be incorporated into novel vector donor DNA
 CC molecules. The nucleic acids, vectors and methods of the invention are
 CC used to obtain chimeric nucleic acid using recombination proteins and
 CC engineered recombination sites in vitro or in vivo. The improved
 CC specificity, speed and yields of the invention facilitates DNA or RNA
 CC subcloning, regulation or exchange useful for any related purpose, e.g.
 CC in vitro recombination of DNA segments, and in vitro or in vivo insertion
 CC or modification of transcribed, replicated, isolated or genomic DNA or
 CC RNA.
 XX
 XX Sequence 25 BP; 5 A; 3 C; 6 G; 11 T; 0 other;
 SQ
 Query Match 93.6%; Score 23.4; DB 18; Length 25;
 Best Local Similarity 96.0%; Pred. No. 0.56;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GTTCAGCTTCTTGTACAAAGTTGG 25
 Db 1 GTTCAGCTTTTGTACAAAGTTGG 25
 XX
 RESULT 35
 AAX78949
 ID AAX78949 standard; DNA; 25 BP.
 XX
 XX AAX78949;
 AC
 XX 17-AUG-1999 (first entry)
 DT
 XX Oligonucleotide #15 for recombination and cloning method.
 DE
 XX Cloning; donor; recombination site; vector; chimeric; ss.
 KW
 XX Synthetic.
 OS
 XX WO9921977-A1.
 PN
 XX 06-MAY-1999.
 PD
 XX 26-OCT-1998; 98WO-US22589.
 PF
 XX 23-OCT-1998; 98US-0177387.
 PR
 XX 24-OCT-1997; 97US-0065930.
 PR
 XX (LIFE-) LIFE TECHNOLOGIES INC.
 PA
 XX Brasch MA, Fox DK, Hartley JL, Temple GF;
 PI
 XX WPI; 1999-303011/25.
 DR
 XX New nucleic acid cloning methods
 PT
 XX Disclosure; Page 162; 185pp; English.
 PS
 XX The invention relates to novel methods for cloning or subcloning one or
 CC more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or

CC in vivo: (1) at least one insert donor molecules (IDMs) comprising one
 CC or more desired nucleic acid segments flanked by at least 2
 CC recombination sites which do not recombine with each other; (2) one or
 CC more vector donor molecules (VDMs) comprising at least 2 recombination
 CC sites which do not recombine with each other; and (3) one or more
 CC site-specific recombination proteins; (b) incubating the combination to
 CC transfer one or more of the desired segments into one or more of the
 CC VDMs, thereby producing one or more desired product molecules (PMs). The
 CC methods can be used for the efficient and specific recombination of NAM
 CC segments. They can be used to generate chimeric DNA or RNA molecules that
 CC have the desired characteristics and/or nucleic acid segments. The
 CC methods can also be used for changing vectors. The oligonucleotides
 CC AAX78935-X78994 are used in the method of the invention.
 XX
 XX Sequence 25 BP; 5 A; 3 C; 6 G; 11 T; 0 other;
 SQ
 Query Match 93.6%; Score 23.4; DB 20; Length 25;
 Best Local Similarity 96.0%; Pred. No. 0.56;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GTTCAGCTTCTTGTACAAAGTTGG 25
 Db 1 GTTCAGCTTTTGTACAAAGTTGG 25
 XX
 RESULT 36
 AAD14443
 ID AAD14443 standard; DNA; 25 BP.
 XX
 XX AAD14443;
 AC
 XX 01-NOV-2001 (first entry)
 DT
 XX Recombination site attP1 DNA.
 DE
 XX Recombination site; copy number; replicon; recombinatorial cloning;
 KW attP1; ds.
 XX
 XX Unidentified.
 OS
 XX US6270969-B1.
 PN
 XX 07-AUG-2001.
 PD
 XX 20-JAN-1999; 99US-0233492.
 PF
 XX 07-JUN-1996; 96US-0663002.
 PR
 XX 07-JUN-1995; 95US-0486139.
 PR
 XX (INVI-) INVITROGEN CORP.
 PA
 XX Hartley JL, Brasch MA;
 PI
 XX WPI; 2001-488248/53.
 DR
 XX
 XX Methods for apposing nucleic acids comprising an expression signal and
 PT a gene/partial gene, using recombinatorial cloning by incubating the
 PT nucleic acids in the presence of a recombination protein under
 PT conditions for recombination -
 XX
 XX Claim 14; Column 18; 76pp; English.
 PS
 XX The invention relates to a method for apposing an expression signal and
 CC a gene or partial gene, using recombinatorial cloning. The method
 CC incubates nucleic acids comprising the expression signal and the gene/
 CC partial gene in the presence of a recombination protein under conditions
 CC sufficient to cause recombination and therefore appose the expression
 CC signal and the gene or partial gene. The methods are useful for apposing
 CC an expression signal and a gene or partial gene using recombinatorial
 CC cloning. The methods are also useful for changing vectors, constructing
 CC genes for fusion proteins, changing copy number, changing replicons,
 CC cloning into phages, and cloning e.g., PCR products (with an attB site
 CC at one end and a loxP site at the other end), genomic DNAs, and cDNAs.

CC The methods are highly specific, rapid, and less labour intensive than
CC prior art methods. The present sequence is a recombination site
CC useful for recombination cloning.

XX SQ Sequence 25 BP; 5 A; 3 C; 6 G; 11 T; 0 other;
Query Match 93.6%; Score 23.4; DB 22; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.56;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGACAAAGTTGG 25
Db 1 GTTCAGCTTCTTGACAAAGTTGG 25

RESULT 37
AAF55749
ID AAF55749 standard; DNA; 25 BP.

XX AC AAF55749;
XX DT 12-APR-2001 (first entry)
XX DE Recombination site attP1.
XX KW Recombination site; cloning; att; ss.

XX OS Unidentified.
XX PN US6171861-B1.
XX PD 09-JAN-2001.

XX PF 12-JAN-1998; 98US-0005476.
XX PR 07-JUN-1996; 96US-0663002.
XX PR 07-JUN-1995; 95US-0486139.
XX PA (LIFE-) LIFE TECHNOLOGIES INC.

XX PI Hartley JL, Brasch MA;
XX DR MPI; 2001-136877/14.

XX PT In vitro cloning of nucleic acid involves mixing vectors comprising
PT recombination sites and/or nucleic acid, incubating mixture to produce
PT chimeric molecule, contacting hosts with mixture and selecting host -
PS Claim 25; Column 46; 73pp; English.

XX CC The present invention relates to a method for in vitro cloning of a
CC nucleic acid of interest. The method involves mixing in vitro two vectors
CC each comprising at least one recombination site and the nucleic acid of
CC interest; incubating the mixture in the presence of at least one
CC recombination protein to result in recombination of the recombination
CC sites, leading to production of a chimeric nucleic acid molecule
CC comprising the nucleic acid of interest; contacting hosts with the
CC mixture; and selecting for a host comprising the chimeric nucleic acid
CC molecule, and selecting against a host comprising the vectors comprising
CC the second vector, to clone the nucleic acid. The present sequence is a
CC recombination site, which may be used in the method of the present
CC invention.

XX SQ Sequence 25 BP; 5 A; 3 C; 6 G; 11 T; 0 other;
Query Match 93.6%; Score 23.4; DB 22; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.56;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGACAAAGTTGG 25
Db 1 GTTCAGCTTCTTGACAAAGTTGG 25

RESULT 38
AAC87880

ID AAC87880 standard; DNA; 25 BP.

XX AC AAC87880;

XX DT 02-MAR-2001 (first entry)

XX DE Escherichia coli core region recombinant site attP1 SEQ ID NO.15.

XX KW Core region; recombination site; cloning; chimeric DNA;
XX characterisitic; mutation; att site; lox site; ss.

XX OS Escherichia coli.

XX PN US6143557-A.

XX PD 07-NOV-2000.

XX PF 20-JAN-1999; 99US-0233493.

XX PR 07-JUN-1996; 96US-0663002.

XX PR 12-JAN-1998; 98US-0005476.

XX PR 07-JUN-1995; 95US-0486139.

XX PA (LIFE-) LIFE TECHNOLOGIES INC.

XX PI Brasch MA, Hartley JL;

XX DR MPI; 2001-049004/06.

XX PT Isolated nucleic acid molecules comprising a DNA segment having two
PT engineered recombination sites, derived from att or lox, which flank a
PT selectable marker and comprise a core region having an engineered
PT mutation -

XX PS Claim 1; Column 18; 73pp; English.

XX CC The present invention describes an isolated nucleic acid molecule (I)
CC comprising a first nucleic acid sequence having a defined sequence
CC (AAC87866 to AAC87881), sequences complementary to AAC87866 to AAC87881,
CC or an RNA sequence corresponding to AAC87866 to AAC87881. Also described
CC are: (1) an isolated nucleic acid molecule (II) comprising a first
CC mutated recombination site that removes one or more stop codons from the
CC recombination site or avoids hairpin formation, the recombination site
CC being an att or lox site; (2) an isolated nucleic acid molecule (III)
CC comprising a first att recombination site comprising a mutation that
CC enhances recombination specificity; (3) vectors (IV) comprising the
CC above mentioned nucleic acids; and (4) cells comprising the above
CC mentioned nucleic acids or (IV). The nucleic acids are used in
CC engineering a core region of a given recombination site to provide
CC mutative sites suitable for subcloning reactions. The use of nucleic
CC acids for obtaining engineered recombination in vitro or in vivo makes
CC the methods for DNA or RNA subcloning, highly specific, rapid, and
CC less labour intensive.

XX SQ Sequence 25 BP; 5 A; 3 C; 6 G; 11 T; 0 other;

Query Match 93.6%; Score 23.4; DB 22; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.56;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGACAAAGTTGG 25
Db 1 GTTCAGCTTCTTGACAAAGTTGG 25

RESULT 39

ABQ82127
ID ABQ82127 standard; DNA; 25 BP.

XX ABQ82127;
AC ABQ82127;

XX 11-DEC-2002 (first entry)
 XX Core sequence of recombination site attP1 SEQ ID NO:10.
 DE Chimeric nucleic acid construct; recombinational cloning; silencing;
 XX recombination site; double stranded RNA; plasmid; ss.
 KW Synthetic.
 OS WO200259294-A1.
 XX 01-AUG-2002.
 XX 24-JAN-2002; 2002WO-AU00073.
 XX 26-JAN-2001; 2001US-264067P.
 PR 29-NOV-2001; 2001US-333743P.
 XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
 XX Wesley S, Waterhouse P, Helliwell C;
 XX WPI; 2002-682669/73.
 XX New vectors comprising operably linked DNA fragments having an origin
 PT of replication, a selectable marker and a chimeric DNA construct,
 PT useful for silencing target nucleic acids and for producing large
 PT amounts of double-stranded RNA -
 XX Claim 12; Page 15; 104pp; English.
 XX The present invention describes a vector (I) comprising operably linked
 CC DNA fragments having: (a) origin of replication allowing replication in a
 CC recipient cell, preferably in bacteria such as *Escherichia coli*;
 CC (b) selectable marker region capable of being expressed in the recipient
 CC cell; and (c) a chimeric DNA construct comprising: (i) promoter or
 CC promoter region capable of being recognized by RNA polymerases of a
 CC eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second,
 CC third and fourth recombination sites; (iii) 3' transcription terminating
 CC and polyadenylation region functional in the eukaryotic cell. The first
 CC and fourth recombination sites, or the second and third recombination
 CC sites are capable of reacting with a same recombination site, and
 CC preferably are identical. The first and second recombination sites, or
 CC the third and fourth recombination sites, do not recombine with each
 CC other or with a same recombination site. The vector is useful for
 CC producing large amounts of double-stranded RNA which can be used for
 CC silencing target nucleic acid sequences. The vectors can also be used to
 CC convert a DNA fragment into an inverted repeat structure. Plants
 CC transformed with a vector from the present invention can be used in a
 CC conventional breeding scheme to produce more plants with the same
 CC characteristics or to introduce a chimeric gene for reduction of the
 CC phenotypic expression of nucleic acids. The present sequence represents
 CC the core sequence of recombination site attB1 which is given in the
 CC exemplification of the present invention.
 XX SQ Sequence 25 BP; 5 A; 3 C; 6 G; 11 T; 0 other;
 Query Match 93.6%; Score 23.4; DB 24; Length 25;
 Best Local Similarity 96.0%; Pred. No. 0.56;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GTTCAGCTTTCTTGTACAAAGTTGG 25
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 Db 1 GTTCAGCTTTTGTGTACAAAGTTGG 25
 |||||
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 ACC44664
 ID ACC44664 standard; DNA; 25 BP.
 XX
 AC ACC44664;
 XX

DT 29-MAY-2003 (first entry)
 XX Recombination site related oligonucleotide SEQ ID NO:55.
 DE Chromosome-based platform; artificial chromosome; eukaryotic chromosome;
 XX att site; integrase; recombinase; ACes; gene therapy; transgenic animal;
 KW platform artificial chromosome expression system; PCR primer; ss.
 XX Synthetic.
 OS WO200297059-A2.
 XX 05-DEC-2002.
 XX 30-MAY-2002; 2002WO-US17452.
 XX 30-MAY-2001; 2001US-294758P.
 PR 21-MAR-2002; 2002US-366891P.
 XX (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
 XX Perkins E, Perez C, Lindenbaum M, Greene A, Leung J, Fleming E;
 PI Stewart S, Shellard J;
 XX WPI; 2003-140461/13.
 XX Novel eukaryotic chromosome comprising one or many att sites which
 PT permits site-directed integration in the presence of lambda-integrase,
 PT useful for site-specific recombination-directed integration of DNA of
 PT interest -
 XX Claim 43; Page 143; 272pp; English.
 XX The present invention describes a eukaryotic chromosome (I) comprising
 CC one or several att sites, where an att site is heterologous to the
 CC chromosome, and permits site-directed integration in the presence of
 CC lambda-integrase. Also described: (1) a platform artificial chromosome
 CC expression system (ACes) (II) comprising several sites that participate
 CC in recombinase catalyzed recombination; and (2) a method (M1) for
 CC introducing a heterologous nucleic acid into a platform artificial
 CC chromosome. (I) can be used in gene therapy. (M1) is useful for
 CC introducing a heterologous nucleic acid molecule into a platform
 CC artificial chromosome, preferably an ACes. (II) is useful for producing a
 CC transgenic animal (e.g. a fish, insect, reptile, amphibian, arachnid, or
 CC mammal) by introducing (II) by cell fusion, lipid-mediated transfection,
 CC by a carrier system, microinjection, microcell fusion, electroporation,
 CC microprojectile bombardment or direct DNA transfer into an embryonic
 CC cell, preferably a stem cell or an embryo. (II) comprises a heterologous
 CC nucleic acid that encodes a therapeutic product which is useful for
 CC making a library of ACes comprising random portions of a genome. ACC44612
 CC to ACC44732 and ABP96650 to ABP96657 represent sequences used in the
 CC exemplification of the present invention.
 XX SQ Sequence 25 BP; 5 A; 3 C; 6 G; 11 T; 0 other;
 Query Match 93.6%; Score 23.4; DB 25; Length 25;
 Best Local Similarity 96.0%; Pred. No. 0.56;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GTTCAGCTTTCTTGTACAAAGTTGG 25
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 Db 1 GTTCAGCTTTTGTGTACAAAGTTGG 25
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 Search completed: November 6, 2003, 22:26:30
 Job time : 112.5 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 6, 2003, 23:06:49 ; Search time 102.25 Seconds
(without alignments)
780.185 Million cell updates/sec

Title: US-10-055-001A-11

Perfect score: 25
Sequence: 1 gttcagctttctgtacaaagtgg 25

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2141354 seqs, 1595478879 residues

Total number of hits satisfying chosen parameters: 4282708

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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- 3: /cgn2_6/prodata/1/pubpna/US06_NEW_PUB.seq:*
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- 11: /cgn2_6/prodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/prodata/1/pubpna/US09_NEW_PUB.seq:*
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- 14: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/prodata/1/pubpna/US10_NEW_PUB.seq:*
- 16: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq:*
- 17: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	25	9	US-09-855-797A-16
2	25	100.0	25	10	US-09-822-634-8
3	25	100.0	25	10	US-09-907-900-16
4	25	100.0	25	10	US-09-907-719-16
5	25	100.0	25	11	US-09-432-085-11
6	25	100.0	25	11	US-09-432-085-11
7	25	100.0	25	12	US-09-985-448-16
8	25	100.0	25	12	US-10-300-892-16
9	25	100.0	25	14	US-10-055-001A-11
10	25	100.0	25	14	US-10-055-001A-11
11	25	100.0	25	14	US-10-058-292-11
12	25	100.0	25	14	US-10-058-292-16
13	25	100.0	25	14	US-10-162-879-11
14	25	100.0	25	14	US-10-162-879-16
15	25	100.0	25	14	US-10-161-403-51
16	25	100.0	25	14	US-10-161-403-56

17	25	100.0	27	9	US-09-732-914-10
18	25	100.0	27	14	US-10-151-690-34
19	25	100.0	4428	14	US-10-151-690-62
20	25	100.0	4470	14	US-10-151-690-21
21	25	100.0	4627	14	US-10-151-690-63
22	25	100.0	4627	14	US-10-151-690-64
23	25	100.0	5584	14	US-10-151-690-61
24	25	100.0	17862	14	US-10-055-001A-23
25	25	100.0	17862	14	US-10-055-001A-23
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28	23.8	95.2	25	9	US-09-855-797A-43
29	23.8	95.2	25	10	US-09-907-900-43
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31	23.8	95.2	25	12	US-09-985-448-43
32	23.8	95.2	25	12	US-10-300-892-43
33	23.4	93.6	25	9	US-09-855-797A-15
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35	23.4	93.6	25	10	US-09-907-719-15
36	23.4	93.6	25	11	US-09-432-085-15
37	23.4	93.6	25	12	US-09-985-448-15
38	23.4	93.6	25	12	US-10-300-892-15
39	23.4	93.6	25	14	US-10-055-001A-10
40	23.4	93.6	25	14	US-10-058-292-15
41	23.4	93.6	25	14	US-10-162-879-15
42	23.4	93.6	25	14	US-10-161-403-55
43	23.4	93.6	27	9	US-09-732-914-6
44	23.4	93.6	27	14	US-10-151-690-30
45	23.4	93.6	4470	14	US-10-151-690-21

ALIGNMENTS

RESULT 1
US-09-855-797A-16
; Sequence 16, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855,797A
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 16
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-855-797A-16

Query Match 100.0%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.05; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0

Qy 1 GTTCAGCTTTCTTGTACAAAGTTGG 25
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Db 1 GTTCAGCTTTCTTGTACAAAGTTGG 25
|||||

RESULT 2

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US-09-822-634-8
; Sequence 8, Application US/09822634
; Patent No. US2002015056A1
; GENERAL INFORMATION:
; APPLICANT: Vile, Richard G.
; APPLICANT: Harrington, Kevin
; APPLICANT: Bateman, Andrew
; APPLICANT: Murphy, Steven
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TISSUE
; TITLE OF INVENTION: SPECIFIC GENE REGULATION THERAPY
; FILE REFERENCE: 07039-289001
; CURRENT APPLICATION NUMBER: US/09/822,634
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 60/193,977
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated vector sequence
US-09-822-634-8
Query Match 100.0%; Score 25; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCAGCTTCTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTCTTGTACAAAGTTGG 25
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US-09-907-900-16
; Sequence 16, Application US/09907900
; Patent No. US2002017297A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,900
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-900-16
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Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCAGCTTCTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTCTTGTACAAAGTTGG 25
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US-09-907-719-16
; Sequence 16, Application US/09907719
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; Publication No. US20020192819A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,719
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 25
; TYPE: DNA
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; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-719-16
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Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 GTTCAGCTTCTTGTACAAAGTTGG 25
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US-09-432-085-11
; Sequence 11, Application US/09432085
; Publication No. US20030100110A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; FILING DATE: (Herewith)
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; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
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; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-432-085-16

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Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GTTCAGCTTCTCTGTACAAAGTTGG 25

RESULT 7
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; Sequence 16, Application US/09985448
; Publication No. US20030157716A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/985,448
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
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; SEQ ID NO 16
; LENGTH: 25
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; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-985-448-16

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Best Local Similarity 100.0%; Pred. No. 0.05;
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DB 1 GTTCAGCTTCTCTGTACAAAGTTGG 25

RESULT 8
US-10-300-892-16
; Sequence 16, Application US/10300892
; Publication No. US20030175970A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/10/300,892
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/907,719
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
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; TYPE: DNA
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; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: Products
US-10-300-892-16

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Best Local Similarity 100.0%; Pred. No. 0.05;
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DB 1 GTTCAGCTTTCTTGTCACAAAGTTGG 25

RESULT 9
US-10-055-001A-6
; Sequence 6, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: core sequence of recombination site attR3
US-10-055-001A-6

Query Match 100.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGTCACAAAGTTGG 25
| | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1 GTTCAGCTTTCTTGTCACAAAGTTGG 25

RESULT 10
US-10-055-001A-11
; Sequence 11, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: core sequence of recombination site attP2,P3
US-10-055-001A-11

Query Match 100.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.05;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTCTTGTCACAAAGTTGG 25
| | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1 GTTCAGCTTTCTTGTCACAAAGTTGG 25

RESULT 11
US-10-058-292-11
; Sequence 11, Application US/10058292
; Publication No. US20030054552A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; Recombination Sites

NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/058,292
FILING DATE: 30-Jan-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/432,085
FILING DATE: 1999-11-02
APPLICATION NUMBER: 09/233,493
FILING DATE: 20-JAN-1999
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-058-292-11

Query Match 100.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGTCACAAAGTTGG 25
| | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1 GTTCAGCTTTCTTGTCACAAAGTTGG 25

RESULT 12
US-10-058-292-16
; Sequence 16, Application US/10058292
; Publication No. US20030054552A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.

;;
;; TITLE OF INVENTION: Recombinational Cloning Using Engineered
;; Recombination Sites
;;
;; NUMBER OF SEQUENCES: 35
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
;; STREET: 1100 New York Ave., N. W. Suite 600
;; CITY: Washington
;; STATE: DC
;; COUNTRY: USA
;; ZIP: 20005-3934
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/058,292
;; FILING DATE: 30-Jan-2002
;; CLASSIFICATION: <Unknown>
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 09/432,085
;; FILING DATE: 1999-11-02
;; APPLICATION NUMBER: 09/233,493
;; FILING DATE: 20-JAN-1999
;; APPLICATION NUMBER: 09/005,476
;; FILING DATE: 12-JAN-1998
;; APPLICATION NUMBER: 08/663,002
;; FILING DATE: 07-JUN-1996
;; APPLICATION NUMBER: 08/486,139
;; FILING DATE: 07-JUN-1995
;;
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-2600
;; TELEFAX: 202-371-2540
;;
;; INFORMATION FOR SEQ ID NO: 16:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 25 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: both
;; TOPOLOGY: both
;; MOLECULE TYPE: cdna
;; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-058-292-16
Query Match 100.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCAGCTTCTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTCTTGTACAAAGTTGG 25
RESULT 13
US-10-162-879-11
Sequence 11, Application US/10162879
Publication No. US20030068799A1
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

;;
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/162,879
;; FILING DATE: 06-Jun-2002
;; CLASSIFICATION: <Unknown>
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/09/432,085
;; FILING DATE: <Unknown>
;; APPLICATION NUMBER: 09/233,493
;; FILING DATE: 20-JAN-1999
;; APPLICATION NUMBER: 09/005,476
;; FILING DATE: 12-JAN-1998
;; APPLICATION NUMBER: 08/663,002
;; FILING DATE: 07-JUN-1996
;; APPLICATION NUMBER: 08/486,139
;; FILING DATE: 07-JUN-1995
;;
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-2600
;; TELEFAX: 202-371-2540
;;
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 25 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: both
;; TOPOLOGY: both
;; MOLECULE TYPE: cdna
;; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-162-879-11
Query Match 100.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCAGCTTCTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTCTTGTACAAAGTTGG 25
RESULT 14
US-10-162-879-16
Sequence 16, Application US/10162879
Publication No. US20030068799A1
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/162,879
FILING DATE: 06-Jun-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/432,085
FILING DATE: <Unknown>
APPLICATION NUMBER: 09/233,493
FILING DATE: 20-JAN-1999
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995

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; APPLICATION NUMBER: 08/496,139
; FILING DATE: 07-JUN-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-162-879-16

Query Match      100.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTCTTGTACAAAGTTGG 25

RESULT 15
US-10-161-403-51
; Sequence 51, Application US/10161403
; Publication No. US20030119104A1
; GENERAL INFORMATION:
; APPLICANT: Perkins, Edward
; APPLICANT: Perez, Carl
; APPLICANT: Lindenbaum, Michael
; APPLICANT: Greene, Amy
; APPLICANT: Leung, Josephine
; APPLICANT: Fleming, Elena
; APPLICANT: Stewart, Sandra
; APPLICANT: Shellard, Joan
; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
; FILE REFERENCE: 24601-420
; CURRENT APPLICATION NUMBER: US/10/161,403
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/294,758
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 60/366,891
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: attR3
US-10-161-403-51

Query Match      100.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTCTTGTACAAAGTTGG 25

RESULT 16
US-10-161-403-56
; Sequence 56, Application US/10161403
; Publication No. US20030119104A1
; GENERAL INFORMATION:
; APPLICANT: Perkins, Edward
; APPLICANT: Perez, Carl
; APPLICANT: Lindenbaum, Michael
; APPLICANT: Greene, Amy
; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
; FILE REFERENCE: 24601-420
; CURRENT APPLICATION NUMBER: US/10/161,403
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/294,758
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 60/366,891
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: attR3
US-10-161-403-51

Query Match      100.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTCTTGTACAAAGTTGG 25

RESULT 17
US-09-732-914-10
; Sequence 10, Application US/09732914
; Patent No. US20020007051A1
; GENERAL INFORMATION:
; APPLICANT: Cheo, David
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Hartley, James L.
; APPLICANT: Byrd, Devon R.N.
; TITLE OF INVENTION: Use of Multiple Recombination Sites with Unique Specificity in
; FILE REFERENCE: 0942.5010002
; CURRENT APPLICATION NUMBER: US/09/732,914
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/169,983
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 60/188,020
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 27
; TYPE: DNA
; ORGANISM: attP2
US-09-732-914-10

Query Match      100.0%; Score 25; DB 9; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTCTTGTACAAAGTTGG 25

RESULT 18
US-10-151-690-34
; Sequence 34, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: Brasch, Michael A.
```

```
; APPLICANT: Leung, Josephine
; APPLICANT: Fleming, Elena
; APPLICANT: Stewart, Sandra
; APPLICANT: Shellard, Joan
; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
; FILE REFERENCE: 24601-420
; CURRENT APPLICATION NUMBER: US/10/161,403
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/294,758
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 60/366,891
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: attP2,P3
US-10-161-403-56

Query Match      100.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTCTTGTACAAAGTTGG 25

RESULT 17
US-09-732-914-10
; Sequence 10, Application US/09732914
; Patent No. US20020007051A1
; GENERAL INFORMATION:
; APPLICANT: Cheo, David
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Hartley, James L.
; APPLICANT: Byrd, Devon R.N.
; TITLE OF INVENTION: Use of Multiple Recombination Sites with Unique Specificity in
; FILE REFERENCE: 0942.5010002
; CURRENT APPLICATION NUMBER: US/09/732,914
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/169,983
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 60/188,020
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 27
; TYPE: DNA
; ORGANISM: attP2
US-09-732-914-10

Query Match      100.0%; Score 25; DB 9; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTCTTGTACAAAGTTGG 25

RESULT 18
US-10-151-690-34
; Sequence 34, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
```

```

; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MOI
; FILE REFERENCE: 0942.5120001
; CURRENT APPLICATION NUMBER: US/10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 27
; TYPE: DNA
; ORGANISM: attp2
US-10-151-690-34

Query Match      100.0%; Score 25; DB 14; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTCTTGTACAAAGTTGG 25

RESULT 19
US-10-151-690-62
; Sequence 62, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MOI
; FILE REFERENCE: 0942.5120001
; CURRENT APPLICATION NUMBER: US/10/151,690
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
; LENGTH: 4428
; TYPE: DNA
; ORGANISM: Artificial sequence
; OTHER INFORMATION: plasmid pDONR212
US-10-151-690-62

Query Match      100.0%; Score 25; DB 14; Length 4428;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTTGTACAAAGTTGG 25
Db 3180 GTTCAGCTTCTTGTACAAAGTTGG 3204

RESULT 20
US-10-151-690-21
; Sequence 21, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID

```

```

; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MOI
; FILE REFERENCE: 0942.5120001
; CURRENT APPLICATION NUMBER: US/10/151,690
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 4470
; TYPE: DNA
; ORGANISM: Artificial sequence
; OTHER INFORMATION: plasmid pDONR201
US-10-151-690-21

Query Match      100.0%; Score 25; DB 14; Length 4470;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTTGTACAAAGTTGG 25
Db 2343 GTTCAGCTTCTTGTACAAAGTTGG 2367

RESULT 21
US-10-151-690-63
; Sequence 63, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MOI
; FILE REFERENCE: 0942.5120001
; CURRENT APPLICATION NUMBER: US/10/151,690
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/151,690

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; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 4627
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: plasmid pDONR212
US-10-151-690-63

Query Match 100.0%; Score 25; DB 14; Length 4627;
Best Local Similarity 100.0%; Pred. No. 0.13; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY 1 GTTCAGCTTCTCTGTACAAAGTTGG 25
|||||
Db 2331 GTTCAGCTTCTCTGTACAAAGTTGG 2355

RESULT 22
US-10-151-690-64
; Sequence 64, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MO
; FILE REFERENCE: 0942.5120001
; CURRENT APPLICATION NUMBER: US/10/151,690
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 4627
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: plasmid pDONR212
US-10-151-690-64

Query Match 100.0%; Score 25; DB 14; Length 4627;
Best Local Similarity 100.0%; Pred. No. 0.13; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY 1 GTTCAGCTTCTCTGTACAAAGTTGG 25
|||||
Db 2331 GTTCAGCTTCTCTGTACAAAGTTGG 2355

RESULT 23
US-10-151-690-61/c
; Sequence 61, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MO
; FILE REFERENCE: 0942.5120001
; CURRENT APPLICATION NUMBER: US/10/151,690
; CURRENT FILING DATE: 2002-05-21

; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
; LENGTH: 5584
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: plasmid pDONR207
US-10-151-690-61

Query Match 100.0%; Score 25; DB 14; Length 5584;
Best Local Similarity 100.0%; Pred. No. 0.13; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY 1 GTTCAGCTTCTCTGTACAAAGTTGG 25
|||||
Db 3243 GTTCAGCTTCTCTGTACAAAGTTGG 3219

RESULT 24
US-10-055-001A-23
; Sequence 23, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 17862
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE4
US-10-055-001A-23

Query Match 100.0%; Score 25; DB 14; Length 17862;
Best Local Similarity 100.0%; Pred. No. 0.16; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY 1 GTTCAGCTTCTCTGTACAAAGTTGG 25
|||||
Db 14520 GTTCAGCTTCTCTGTACAAAGTTGG 14544

RESULT 25
US-10-055-001A-23/c
; Sequence 23, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 17862
; TYPE: DNA

```

; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE4
US-10-055-001A-23

Query Match      100.0%; Score 25; DB 14; Length 17862;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGTCACAAAGTTGG 25
    |||||
Db 15589 GTTCAGCTTTCTTGTCACAAAGTTGG 15565

RESULT 26
US-10-055-001A-13
; Sequence 13, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCES: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 18691
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE

; NAME/KEY: misc feature
; LOCATION: (7922)..(9985)
; OTHER INFORMATION: spectinomycin resistance
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (10706)..(11324)
; OTHER INFORMATION: right T-DNA border fragment
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (11674)..(13019)
; OTHER INFORMATION: CamV35S promoter fragment
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (17890)..(17659)
; OTHER INFORMATION: attP1 recombination site (complement)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (17610)..(16855)
; OTHER INFORMATION: ccdB selection marker (complement)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (16551)..(16319)
; OTHER INFORMATION: attP2 recombination site (complement)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (14660)..(16258)
; OTHER INFORMATION: pdk2 intron 2
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15002)..(15661)
; OTHER INFORMATION: chloramphenicol resistance gene
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (14387)..(14619)
; OTHER INFORMATION: attP2 recombination site
; FEATURE:
; NAME/KEY: misc feature

```

```

; LOCATION: (13675)..(13980)
; OTHER INFORMATION: ccdB selection marker (complement)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (13049)..(13279)
; OTHER INFORMATION: attP1 recombination site
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (17922)..(18687)
; OTHER INFORMATION: octopine synthase gene terminator region
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (264)..(496)
; OTHER INFORMATION: nopaline synthase gene promoter
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (497)..(1442)
; OTHER INFORMATION: nptII coding region
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1443)..(2146)
; OTHER INFORMATION: nopaline synthase gene terminator
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2149)..(2706)
; OTHER INFORMATION: a left T-DNA border region
; US-10-055-001A-13

Query Match      100.0%; Score 25; DB 14; Length 18691;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGTCACAAAGTTGG 25
    |||||
Db 14520 GTTCAGCTTTCTTGTCACAAAGTTGG 14544

RESULT 27
US-10-055-001A-13/c
; Sequence 13, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCES: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 18691
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (7922)..(9985)
; OTHER INFORMATION: spectinomycin resistance
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (10706)..(11324)
; OTHER INFORMATION: right T-DNA border fragment
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (11674)..(13019)
; OTHER INFORMATION: CamV35S promoter fragment
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (17890)..(17659)

```

```
; OTHER INFORMATION: attP1 recombination site (complement)
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (17610)..(16855)
; OTHER INFORMATION: ccdB selection marker (complement)
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (16551)..(16319)
; OTHER INFORMATION: attP2 recombination site (complement)
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (14660)..(16258)
; OTHER INFORMATION: pdk2 intron 2
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (15002)..(15661)
; OTHER INFORMATION: chloramphenicol resistance gene
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (14387)..(14619)
; OTHER INFORMATION: attP2 recombination site
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (13675)..(13980)
; OTHER INFORMATION: ccdB selection marker (complement)
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (13048)..(13279)
; OTHER INFORMATION: attP1 recombination site
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (17922)..(18687)
; OTHER INFORMATION: octopine synthase gene terminator region
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (264)..(496)
; OTHER INFORMATION: nopaline synthase gene promoter
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (497)..(1442)
; OTHER INFORMATION: nptII coding region
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1443)..(2148)
; OTHER INFORMATION: nopaline synthase gene terminator
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (2149)..(2706)
; OTHER INFORMATION: a left T-DNA border region
; US-10-055-001A-13
```

```
Query Match          100.0%; Score 25; DB 14; Length 18691;
Best Local Similarity 100.0%; Pred. No. 0.17; Mismatches 0; Indels 0; Gaps 0;
Matches 25; Conservative 0;
```

```
QY 1 GTTCAGCTTTCTGTACAAAGTTGG 25
    |||||
Db 16418 GTTCAGCTTTCTGTACAAAGTTGG 16394
```

RESULT 28

```
US-09-855-797A-43
; Sequence 43, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855,797A
```

```
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
; US-09-855-797A-43
```

```
Query Match          95.2%; Score 23.8; DB 9; Length 25;
Best Local Similarity 88.0%; Pred. No. 0.18;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GTTCAGCTTTCTGTACAAAGTTGG 25
    |||||
Db 1 GTTCAGCTTTCTGTACAAAGTTGG 25
```

RESULT 29

```
US-09-907-900-43
; Sequence 43, Application US/09907900
; Patent No. US20020172997A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,900
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
; US-09-907-900-43
```

```
Query Match          95.2%; Score 23.8; DB 10; Length 25;
Best Local Similarity 88.0%; Pred. No. 0.18;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GTTCAGCTTTCTGTACAAAGTTGG 25
    |||||
Db 1 GTTCAGCTTTCTGTACAAAGTTGG 25
```

RESULT 30

```
US-09-907-719-43
; Sequence 43, Application US/09907719
; Publication No. US20020192819A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
```

; CURRENT APPLICATION NUMBER: US/09/907,719
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 43
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-719-43

Query Match 95.2%; Score 23.8; DB 10; Length 25;
Best Local Similarity 88.0%; Pred. No. 0.18;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAAGTTGG 25
|||||:|||||:|||||:|||||
Db 1 GTTCAGCTTTTTRTACWAAGTTGG 25

RESULT 31
US-09-985-448-43
; Sequence 43, Application US/09985448
; Publication No. US20030157716A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.285004
; CURRENT APPLICATION NUMBER: US/09/985,448
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 43
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-985-448-43

Query Match 95.2%; Score 23.8; DB 12; Length 25;
Best Local Similarity 88.0%; Pred. No. 0.18;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAAGTTGG 25
|||||:|||||:|||||:|||||
Db 1 GTTCAGCTTTTTRTACWAAGTTGG 25

RESULT 32
US-10-300-892-43
; Sequence 43, Application US/10300892
; Publication No. US20030175970A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites

; FILE REFERENCE: 0942.285004
; CURRENT APPLICATION NUMBER: US/10/300,892
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/907,719
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 43
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-10-300-892-43

Query Match 95.2%; Score 23.8; DB 12; Length 25;
Best Local Similarity 88.0%; Pred. No. 0.18;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAAGTTGG 25
|||||:|||||:|||||:|||||
Db 1 GTTCAGCTTTTTRTACWAAGTTGG 25

RESULT 33
US-09-855-797A-15
; Sequence 15, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.285008
; CURRENT APPLICATION NUMBER: US/09/855,797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 15
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-855-797A-15

Query Match 93.6%; Score 23.4; DB 9; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.28;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAAGTTGG 25
|||||:|||||:|||||:|||||
Db 1 GTTCAGCTTTTTRTACWAAGTTGG 25

RESULT 34
US-09-907-900-15
; Sequence 15, Application US/09907900
; Patent No. US20020172997A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.


```
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,900
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-900-15

Query Match          93.6%; Score 23.4; DB 10; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.28;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTCTTGTCACAAAGTTGG 25
Db 1 GTTCAGCTTTTGTGTCACAAAGTTGG 25

RESULT 35
US-09-907-719-15
; Sequence 15, Application US/09907719
; Publication No. US20020192819A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,719
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-719-15

Query Match          93.6%; Score 23.4; DB 10; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.28;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTCTTGTCACAAAGTTGG 25
Db 1 GTTCAGCTTTTGTGTCACAAAGTTGG 25

RESULT 36
US-09-432-085-15
; Sequence 15, Application US/09432085
; Publication No. US20030100110A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
```

```
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/432,085
; APPLICATION NUMBER: US/09/432,085
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-432-085-15

Query Match          93.6%; Score 23.4; DB 11; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.28;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTCTTGTCACAAAGTTGG 25
Db 1 GTTCAGCTTTTGTGTCACAAAGTTGG 25

RESULT 37
US-09-985-448-15
; Sequence 15, Application US/09985448
; Publication No. US20030157716A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/985,448
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
```

```
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 15
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Unknown
/ FEATURE:
/ OTHER INFORMATION: Description of Unknown Organism: recombination
/ OTHER INFORMATION: products
US-09-985-448-15
```

```
Query Match          93.6%; Score 23.4; DB 12; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.28;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 GTTCAGCTTTCTTGTACAAAGTTGG 25
|||||
DB 1 GTTCAGCTTTTGTACAAAGTTGG 25
```

```
RESULT 38
US-10-300-892-15
/ Sequence 15, Application US/10300892
/ Publication No. US20030175970A1
/ GENERAL INFORMATION:
/ APPLICANT: Hartley, James L.
/ APPLICANT: Brasch, Michael A.
/ APPLICANT: Temple, Gary F.
/ APPLICANT: Fox, Donna K.
/ TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
/ FILE REFERENCE: 0942.285004
/ CURRENT APPLICATION NUMBER: US/10/300,892
/ CURRENT FILING DATE: 2002-11-21
/ PRIOR APPLICATION NUMBER: US/09/907,719
/ PRIOR FILING DATE: 2001-07-19
/ PRIOR APPLICATION NUMBER: US/09/177,387
/ PRIOR FILING DATE: 1998-10-23
/ NUMBER OF SEQ ID NOS: 60
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 15
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Unknown
/ FEATURE:
/ OTHER INFORMATION: Description of Unknown Organism: recombination
/ OTHER INFORMATION: products
US-10-300-892-15
```

```
Query Match          93.6%; Score 23.4; DB 12; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.28;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 GTTCAGCTTTCTTGTACAAAGTTGG 25
|||||
DB 1 GTTCAGCTTTTGTACAAAGTTGG 25
```

```
RESULT 39
US-10-055-001a-10
/ Sequence 10, Application US/10055001A
/ Publication No. US20030049835A1
/ GENERAL INFORMATION:
/ APPLICANT: Wesley, Susan V.
/ APPLICANT: Waterhouse, Peter
/ APPLICANT: Helliwell, Christopher A.
/ TITLE OF INVENTION: Method and means for producing efficient silencing constructs
/ TITLE OF INVENTION: using recombinational cloning
/ FILE REFERENCE: HELIGA
/ CURRENT APPLICATION NUMBER: US/10/055,001A
/ CURRENT FILING DATE: 2002-06-11
/ NUMBER OF SEQ ID NOS: 26
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 10
```

```
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: core sequence of recombination site attP1
US-10-055-001A-10
```

```
Query Match          93.6%; Score 23.4; DB 14; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.28;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 GTTCAGCTTTCTTGTACAAAGTTGG 25
|||||
DB 1 GTTCAGCTTTTGTACAAAGTTGG 25
```

```
RESULT 40
US-10-058-292-15
/ Sequence 15, Application US/10058292
/ Publication No. US20030054552A1
/ GENERAL INFORMATION:
/ APPLICANT: Hartley, James L.
/ APPLICANT: Brasch, Michael A.
/ TITLE OF INVENTION: Recombinational Cloning Using Engineered
/ RECOMBINATION SITES
/ NUMBER OF SEQUENCES: 35
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C
/ STREET: 1100 New York Ave., N. W. Suite 600
/ CITY: Washington
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20005-3934
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/058,292
/ FILING DATE: 30-Jan-2002
/ CLASSIFICATION: <unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/432,085
/ FILING DATE: 1999-11-02
/ APPLICATION NUMBER: 09/233,493
/ FILING DATE: 20-JAN-1999
/ APPLICATION NUMBER: 09/005,476
/ FILING DATE: 12-JAN-1998
/ APPLICATION NUMBER: 08/663,002
/ FILING DATE: 07-JUN-1996
/ APPLICATION NUMBER: 08/486,139
/ FILING DATE: 07-JUN-1995
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-371-2600
/ TELEFAX: 202-371-2540
/ INFORMATION FOR SEQ ID NO: 15:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 25 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: both
/ TOPOLOGY: both
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Fri Nov 7 08:08:38 2003

us-10-055-001a-11.rnpb

Page 14

Search completed: November 7, 2003, 02:22:27
Job time : 103.25 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 6, 2003, 22:08:13 ; Search time 1093.75 Seconds
(without alignments)
555.531 Million cell updates/sec

Title: US-10-055-001A-11
Perfect score: 25
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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2: em_esthum:*
3: em_estin:*
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6: em_estpl:*
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8: em_htc:*
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29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 2	22	88.0	90	14	CB392047
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c 4	22	88.0	94	14	CB402408

c 5	22	88.0	95	14	CB400591
c 6	22	88.0	95	14	CB401751
c 7	22	88.0	97	14	CB401179
c 8	22	88.0	98	14	CB402581
c 9	22	88.0	100	14	CB392051
c 10	22	88.0	100	14	CB400512
c 11	22	88.0	102	14	CB392040
c 12	22	88.0	103	14	CB401874
c 13	22	88.0	107	14	CB388456
c 14	22	88.0	111	14	CB394444
c 15	22	88.0	114	14	CB402012
c 16	22	88.0	120	14	CB392055
c 17	22	88.0	120	14	CB400382
c 18	22	88.0	124	14	CB399813
c 19	22	88.0	126	14	CB400130
c 20	22	88.0	128	14	CB400226
c 21	22	88.0	128	14	CB401884
c 22	22	88.0	129	14	CB401218
c 23	22	88.0	227	14	CB398923
c 24	22	88.0	247	14	CB401020
c 25	22	88.0	262	14	CB395877
c 26	22	88.0	263	14	CB395890
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c 28	22	88.0	435	12	BI174871
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c 30	22	88.0	467	12	BI174361
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c 37	22	88.0	613	12	BI174910
c 38	22	88.0	1388	14	CB960041
c 39	21	84.0	559	9	AL515389
c 40	21	84.0	982	14	CD048261
c 41	21	84.0	1097	9	AL515449
c 42	20.8	83.2	1048	29	CC260943
c 43	20.6	82.4	959	9	AL514767
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ALIGNMENTS

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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

87 bp mRNA linear EST 15-MAY-2003
OSTF167D8_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
CB400039_1 GI:30741766
EST.
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Pelodierinae; Caenorhabditis.
1 (bases 1 to 87)

Reboul,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M., Armstrong
, C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T., Hudson
, J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.,
Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V., Tolias,P.P.,
Pracek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,
Doucette-Stamm,L., Hill,D.E. and Vidal,M.
C. elegans ORFome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
expression
Nat. Genet. (2003) In press
Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180

Fax: 617 632 5739
 Email: Marc.Vidal@dfci.harvard.edu
 Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project : Contact david_hill@dfci.harvard.edu or marc_vidal@dfci.harvard.edu
 POLYA=No.

FEATURES

Location/Qualifiers

1. .87
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/note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

BASE COUNT

26 a 16 c 21 g 24 t

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OSTF163A10_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.

ACCESSION

CB392047.1 GI:30733757

VERSION

EST.

SOURCE

ORGANISM

Caenorhabditis elegans

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea

; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 90)

Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong

, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson

, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,

Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolia, P.P.

, Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,

Doucette-Stamm, L., Hill, D.E. and Vidal, M.

C. elegans ORFeome version 1.1: experimental verification of the

genome annotation and resource for proteome-scale protein

expression

Nat. Genet., (2003) In press

Contact: Vidal M

Marc Vidal Laboratory

1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA

Tel: 617 632 5180

Fax: 617 632 5739

Email: Marc.Vidal@dfci.harvard.edu

Sequence tag of Gateway entry clones. The primers used were

designed on the predicted protein encoding ORF. C. elegans ORFeome

cloning project : Contact david_hill@dfci.harvard.edu or

marc_vidal@dfci.harvard.edu

POLYA=No.

FEATURES

Location/Qualifiers

1. .90
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 /dev_stage="mixed stage"
 /clone_lib="AD-wrmcDNA"

/note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

27 a 18 c 17 g 28 t

BASE COUNT

ORIGIN

Query Match 88.0%; Score 22; DB 14; Length 90;
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LOCUS

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OSTF214C1_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.

ACCESSION

CB402537.1 GI:30744264

VERSION

EST.

KEYWORDS

SOURCE

ORGANISM

Caenorhabditis elegans

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea

; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 92)

Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong

, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson

, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,

Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolia, P.P.

, Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,

Doucette-Stamm, L., Hill, D.E. and Vidal, M.

C. elegans ORFeome version 1.1: experimental verification of the

genome annotation and resource for proteome-scale protein

expression

Nat. Genet., (2003) In press

Contact: Vidal M

Marc Vidal Laboratory

1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA

Tel: 617 632 5180

Fax: 617 632 5739

Email: Marc.Vidal@dfci.harvard.edu

Sequence tag of Gateway entry clones. The primers used were

designed on the predicted protein encoding ORF. C. elegans ORFeome

cloning project : Contact david_hill@dfci.harvard.edu or

marc_vidal@dfci.harvard.edu

POLYA=No.

FEATURES

Location/Qualifiers

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25 a 13 c 26 g 28 t

BASE COUNT

ORIGIN

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DEFINITION OSTF1286_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION  CB402408
VERSION     CB402408.1 GI:30744135
KEYWORDS   EST.
SOURCE     Caenorhabditis elegans
ORGANISM   Caenorhabditis elegans
REFERENCE  1 (bases 1 to 94)
AUTHORS    Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong,
; Rhabditidae; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
; C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson
; J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,
; Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, P.P.,
; Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,
; Doucette-Stamm, L., Hill, D.E. and Vidal, M.
; C. elegans ORFeome version 1.1: experimental verification of the
; genome annotation and resource for proteome-scale protein
; expression
JOURNAL    Nat. Genet. (2003) In press
COMMENT    Contact: Vidal M
            Dana Farber Cancer Institute
            1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
            Tel: 617 632 5180
            Fax: 617 632 5739
            Email: Marc.Vidal@dfci.harvard.edu
            Sequence tag of Gateway entry clones. The primers used were
            designed on the predicted protein encoding ORF. C. elegans ORFeome
            cloning project : Contact david_hill@dfci.harvard.edu or
            marc_vidal@dfci.harvard.edu
POLYA-No.
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            RNA isolated from both hermaphrodite and male N2 worms of
            all larval stages, embryos, adults and dauers and the
            subsequent generation of cDNAs by poly(A) priming. The
            cDNAs were cloned into pPC86"
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ACCESSION  CB401751
VERSION     CB401751.1 GI:30743478
KEYWORDS   EST.
SOURCE     Caenorhabditis elegans
ORGANISM   Caenorhabditis elegans
REFERENCE  1 (bases 1 to 95)
AUTHORS    Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong,
; Rhabditidae; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
; C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson

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CB400591
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CB400591
VERSION  CB400591.1 GI:30742318
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ORGANISM Caenorhabditis elegans
REFERENCE 1 (bases 1 to 95)
AUTHORS   Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong,
; Rhabditidae; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
; C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson
; J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,
; Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, P.P.,
; Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,
; Doucette-Stamm, L., Hill, D.E. and Vidal, M.
; C. elegans ORFeome version 1.1: experimental verification of the
; genome annotation and resource for proteome-scale protein
; expression
JOURNAL    Nat. Genet. (2003) In press
COMMENT    Contact: Vidal M
            Dana Farber Cancer Institute
            1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
            Tel: 617 632 5180
            Fax: 617 632 5739
            Email: Marc.Vidal@dfci.harvard.edu
            Sequence tag of Gateway entry clones. The primers used were
            designed on the predicted protein encoding ORF. C. elegans ORFeome
            cloning project : Contact david_hill@dfci.harvard.edu or
            marc_vidal@dfci.harvard.edu
POLYA-No.
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Db 29 CAGCTTTCTTGTTACAAAGTTGG 8

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ACCESSION  CB401751
VERSION     CB401751.1 GI:30743478
KEYWORDS   EST.
SOURCE     Caenorhabditis elegans
ORGANISM   Caenorhabditis elegans
REFERENCE  1 (bases 1 to 95)
AUTHORS    Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong,
; Rhabditidae; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
; C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson

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J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolia, P.P., Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H., Doucette-Stamm, L., Hill, D.E. and Vidal, M.

C. elegans ORFeome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein expression

Nat. Genet., (2003) In press

Contact: Vidal M

Marc Vidal Laboratory

Dana Farber Cancer Institute

1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA

Tel: 617 632 5180

Fax: 617 632 5739

Email: Marc.Vidal@fci.harvard.edu

Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project : Contact david_hill@fci.harvard.edu or marc_vidal@fci.harvard.edu

POLYA-No.

Location/Qualifiers

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BASE COUNT
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Query Match 88.0%; Score 22; DB 14; Length 95;

Best Local Similarity 100.0%; Pred. No. 24;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CAGCTTTCTTGTCACAAAGTTGG 25

Db 29 CAGCTTTCTTGTCACAAAGTTGG 8

RESULT 7
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LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea

; Rhabditidae; Peloderinae; Caenorhabditis.

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Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong

, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson

, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,

Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolia, P.P.

, Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,

Doucette-Stamm, L., Hill, D.E. and Vidal, M.

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genome annotation and resource for proteome-scale protein

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Nat. Genet., (2003) In press

Contact: Vidal M

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Dana Farber Cancer Institute

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Tel: 617 632 5180

Fax: 617 632 5739

Email: Marc.Vidal@fci.harvard.edu

Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project : Contact david_hill@fci.harvard.edu or marc_vidal@fci.harvard.edu

POLYA-No.

Location/Qualifiers

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Best Local Similarity 100.0%; Pred. No. 25;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 32 CAGCTTTCTTGTCACAAAGTTGG 11

RESULT 8
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LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea

; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 98)

Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong

, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson

, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,

Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolia, P.P.

, Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,

Doucette-Stamm, L., Hill, D.E. and Vidal, M.

C. elegans ORFeome version 1.1: experimental verification of the

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expression

Nat. Genet., (2003) In press

Contact: Vidal M

Marc Vidal Laboratory

Dana Farber Cancer Institute

1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA

Tel: 617 632 5180

Fax: 617 632 5739

Email: Marc.Vidal@fci.harvard.edu

Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project : Contact david_hill@fci.harvard.edu or marc_vidal@fci.harvard.edu

POLYA-No.

Location/Qualifiers

1. .98

/organism="Caenorhabditis elegans"

/mol_type="mRNA"

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/strain="N2"
/db_xref="taxon:6239"
/sex="Hermaphrodite and male"
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/clone_lib="AD-wrmcDNA"
/notes="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
24 a 22 c 20 g 32 t
BASE COUNT
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 25;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTCTTGTACAAAGTTGG 25
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Db 32 CAGCTTCTTGTACAAAGTTGG 11

RESULT 9
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LOCUS 100 bp mRNA linear EST 15-MAY-2003
DEFINITION OSTF163A3_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION CB392051
VERSION CB392051.1 GI:30733761
KEYWORDS EST.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
REFERENCE 1 (bases 1 to 100)
AUTHORS Reboul,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M., Armstrong
,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T., Hudson
,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.,
Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V., Toliaas,P.P.,
Ptacek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,
Doucette-Stamm,L., Hill,D.E. and Vidal,M.
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Tel: 617 632 5180
Fax: 617 632 5739
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designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david_hill@fci.harvard.edu or
marc_vidal@fci.harvard.edu
POLYA-No. Location/Qualifiers
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/mol_type="mRNA"
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/notes="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
32 a 24 c 18 g 26 t
BASE COUNT
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 25;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTCTTGTACAAAGTTGG 25
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Db 30 CAGCTTCTTGTACAAAGTTGG 9

RESULT 11

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ORIGIN

Query Match 88.0%; Score 22; DB 14; Length 100;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTCTTGTACAAAGTTGG 25
|||||
Db 32 CAGCTTCTTGTACAAAGTTGG 11

RESULT 10
CB400512/c
LOCUS 100 bp mRNA linear EST 15-MAY-2003
DEFINITION OSTF17G3_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION CB400512
VERSION CB400512.1 GI:30742239
KEYWORDS EST.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
REFERENCE 1 (bases 1 to 100)
AUTHORS Reboul,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M., Armstrong
,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T., Hudson
,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.,
Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V., Toliaas,P.P.,
Ptacek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,
Doucette-Stamm,L., Hill,D.E. and Vidal,M.
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Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc_vidal@fci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david_hill@fci.harvard.edu or
marc_vidal@fci.harvard.edu
POLYA-No. Location/Qualifiers
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/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
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RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
31 a 22 c 14 g 33 t
BASE COUNT
ORIGIN

Query Match 88.0%; Score 22; DB 14; Length 100;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTCTTGTACAAAGTTGG 25
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Db 30 CAGCTTCTTGTACAAAGTTGG 9

RESULT 11

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CB392040/c
 LOCUS CB392040 102 bp mRNA linear EST 15-MAY-2003
 DEFINITION OSTF162H10_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
 ACCESSION CB392040
 VERSION CB392040.1 GI:30733750
 KEYWORDS EST.
 SOURCE Caenorhabditis elegans
 ORGANISM Caenorhabditis elegans
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
 ; Rhabditidae; Peloderinae; Caenorhabditis.
 REFERENCE 1 (bases 1 to 102)
 AUTHORS Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong
 , C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson
 , J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,
 Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolia, P.P.,
 Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,
 Doucette-Stamm, L., Hill, D.E. and Vidal, M.
 TITLE C. elegans ORFeome version 1.1: experimental verification of the
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 JOURNAL Nat. Genet., (2003) In press
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 Dana Farber Cancer Institute
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 Tel: 617 632 5180
 Fax: 617 632 5739
 Email: Marc.Vidal@dfci.harvard.edu
 Sequence tag of Gateway entry clones. The primers used were
 designed on the predicted protein encoding ORF. C. elegans ORFeome
 cloning project : Contact david_hill@dfci.harvard.edu or
 marc_vidal@dfci.harvard.edu
 POLYA=No.
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 1..102
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 subsequent generation of cDNAs by poly(A) priming. The
 cDNAs were cloned into pC86"
 BASE COUNT 31 a 14 c 22 g 35 t
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 Query Match 88.0%; Score 22; DB 14; Length 102;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 CAGCTTCTCTGTACAAAGTTGG 25
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 Db 35 CAGCTTCTCTGTACAAAGTTGG 14
 |||||||
 RESULT 12
 LOCUS CB401874/c 103 bp mRNA linear EST 15-MAY-2003
 DEFINITION OSTF202B11_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
 ACCESSION CB401874
 VERSION CB401874.1 GI:30743601
 KEYWORDS EST.
 SOURCE Caenorhabditis elegans
 ORGANISM Caenorhabditis elegans
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
 ; Rhabditidae; Peloderinae; Caenorhabditis.
 REFERENCE 1 (bases 1 to 103)
 AUTHORS Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong

, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson
 , J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,
 Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolia, P.P.,
 Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,
 Doucette-Stamm, L., Hill, D.E. and Vidal, M.
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 Tel: 617 632 5180
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 Email: Marc.Vidal@dfci.harvard.edu
 Sequence tag of Gateway entry clones. The primers used were
 designed on the predicted protein encoding ORF. C. elegans ORFeome
 cloning project : Contact david_hill@dfci.harvard.edu or
 marc_vidal@dfci.harvard.edu
 POLYA=No.
 FEATURES Location/Qualifiers
 1..103
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 /strain="N2"
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 /tissue_type="whole animal"
 /dev_stage="mixed stage"
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 /note="The AD-wrmcDNA library was generated with poly(A)+
 RNA isolated from both hermaphrodite and male N2 worms of
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 subsequent generation of cDNAs by poly(A) priming. The
 cDNAs were cloned into pPC96"
 BASE COUNT 21 a 18 c 21 g 43 t
 ORIGIN
 Query Match 88.0%; Score 22; DB 14; Length 103;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 CAGCTTCTCTGTACAAAGTTGG 25
 |||||||
 Db 36 CAGCTTCTCTGTACAAAGTTGG 15
 |||||||
 RESULT 13
 LOCUS CB388456/c 107 bp mRNA linear EST 15-MAY-2003
 DEFINITION OSTF099E7_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
 ACCESSION CB388456
 VERSION CB388456.1 GI:30730166
 KEYWORDS EST.
 SOURCE Caenorhabditis elegans
 ORGANISM Caenorhabditis elegans
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
 ; Rhabditidae; Peloderinae; Caenorhabditis.
 REFERENCE 1 (bases 1 to 107)
 AUTHORS Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong
 , C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson
 , J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,
 Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolia, P.P.,
 Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,
 Doucette-Stamm, L., Hill, D.E. and Vidal, M.
 TITLE C. elegans ORFeome version 1.1: experimental verification of the
 genome annotation and resource for proteome-scale protein
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 JOURNAL Nat. Genet., (2003) In press
 COMMENT Contact: Vidal M
 Marc Vidal Laboratory
 Dana Farber Cancer Institute

1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739

Email: Marc.Vidal@fci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project : Contact david_hill@fci.harvard.edu or marc_vidal@fci.harvard.edu

POLYA-No. Location/Qualifiers

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BASE COUNT 34 a 18 c 16 g 39 t

ORIGIN

Query Match 88.0%; Score 22; DB 14; Length 107;

Best Local Similarity 100.0%; Pred. No. 25;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTCTTGTACAAAGTTGG 25

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Db 29 CAGCTTCTTGTACAAAGTTGG 8

RESULT 14

CB394444

LOCUS

OSTR137H4_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence. EST 15-MAY-2003

ACCESSION

CB394444

VERSION

CB394444.1 GI:30736155

KEYWORDS

EST.

SOURCE

ORGANISM

Caenorhabditis elegans

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea

; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 111)

Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong

, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson

, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,

Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, P.P.

, Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,

Doucette-Stamm, L., Hill, D.E. and Vidal, M.

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Marc Vidal Laboratory

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cloning project : Contact david_hill@fci.harvard.edu or

marc_vidal@fci.harvard.edu

POLYA-No. Location/Qualifiers

1..111

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RNA isolated from both hermaphrodite and male N2 worms of

all larval stages, embryos, adults and dauers and the

subsequent generation of cDNAs by poly(A) priming. The

cDNAs were cloned into pPC86"

BASE COUNT 32 a 18 c 22 g 39 t

ORIGIN

Query Match 88.0%; Score 22; DB 14; Length 111;

Best Local Similarity 100.0%; Pred. No. 26;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTCTTGTACAAAGTTGG 25

|||||

Db 71 CAGCTTCTTGTACAAAGTTGG 92

RESULT 15

CB402012/c

LOCUS

OSTF205B3_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence. EST 15-MAY-2003

ACCESSION

CB402012

VERSION

CB402012.1 GI:30743739

KEYWORDS

EST.

SOURCE

ORGANISM

Caenorhabditis elegans

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea

; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 114)

Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong

, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson

, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,

Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, P.P.

, Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,

Doucette-Stamm, L., Hill, D.E. and Vidal, M.

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Email: Marc.Vidal@fci.harvard.edu

Sequence tag of Gateway entry clones. The primers used were

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cloning project : Contact david_hill@fci.harvard.edu or

marc_vidal@fci.harvard.edu

POLYA-No. Location/Qualifiers

1..114

/organism="Caenorhabditis elegans"

/mol_type="mRNA"

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RNA isolated from both hermaphrodite and male N2 worms of

all larval stages, embryos, adults and dauers and the

subsequent generation of cDNAs by poly(A) priming. The

cDNAs were cloned into pPC86"

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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CAGCTTTCTTGTACAAAGTTGG 25
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Db 34 CAGCTTTCTTGTACAAAGTTGG 13

RESULT 16
CB392055/c
LOCUS      120 bp      mRNA      linear      EST 15-MAY-2003
DEFINITION OSTF163B1_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION  CB392055
VERSION     CB392055.1 GI:30733765
KEYWORDS   EST.
SOURCE     Caenorhabditis elegans
ORGANISM   Caenorhabditis elegans
REFERENCE  1 (bases 1 to 120)
AUTHORS    ,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T., Hudson
            ,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.,
            Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V., Toliaas,P.P.
            , Ptacek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,
            Doucette-Stamm,L., Hill,D.E. and Vidal,M.
            C. elegans ORFeome version 1.1: experimental verification of the
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            expression
            Nat. Genet., (2003) In press
            Contact: Vidal M
            Marc Vidal Laboratory
            Dana Farber Cancer Institute
            1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
            Tel: 617 632 5180
            Fax: 617 632 5739
            Email: Marc.Vidal@dfci.harvard.edu
            Sequence tag of Gateway entry clones. The primers used were
            designed on the predicted protein encoding ORF. C. elegans ORFeome
            cloning project : Contact david_hill@dfci.harvard.edu or
            marc_vidal@dfci.harvard.edu
            POLYA=No.

JOURNAL
COMMENT

FEATURES
source
1..120
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
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/note="The AD-wrmcDNA library was generated with poly(A) +
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
BASE COUNT      36 a      27 c      22 g      35 t
ORIGIN
Query Match      88.0%; Score 22; DB 14; Length 120;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CAGCTTTCTTGTACAAAGTTGG 25
    |||||
Db 56 CAGCTTTCTTGTACAAAGTTGG 35

RESULT 17
CB400382/c
LOCUS      120 bp      mRNA      linear      EST 15-MAY-2003
DEFINITION OSTF175B7_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION  CB400382
VERSION     CB400382.1 GI:30742109
KEYWORDS   EST.
SOURCE     Caenorhabditis elegans
ORGANISM   Caenorhabditis elegans
REFERENCE  1 (bases 1 to 120)
AUTHORS    ,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T., Hudson
            ,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.,
            Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V., Toliaas,P.P.
            , Ptacek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,
            Doucette-Stamm,L., Hill,D.E. and Vidal,M.
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            Dana Farber Cancer Institute
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            Fax: 617 632 5739
            Email: Marc.Vidal@dfci.harvard.edu
            Sequence tag of Gateway entry clones. The primers used were
            designed on the predicted protein encoding ORF. C. elegans ORFeome
            cloning project : Contact david_hill@dfci.harvard.edu or
            marc_vidal@dfci.harvard.edu
            POLYA=No.

JOURNAL
COMMENT

FEATURES
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1..120
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
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RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
BASE COUNT      42 a      22 c      19 g      37 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 26;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CAGCTTTCTTGTACAAAGTTGG 25
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Db 61 CAGCTTTCTTGTACAAAGTTGG 40

RESULT 18
CB399813/c
LOCUS      124 bp      mRNA      linear      EST 15-MAY-2003
DEFINITION OSTF163C2_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION  CB399813
VERSION     CB399813.1 GI:30741540
KEYWORDS   EST.
SOURCE     Caenorhabditis elegans
ORGANISM   Caenorhabditis elegans
REFERENCE  1 (bases 1 to 124)

```

AUTHORS Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolia, P.P., Placsek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H., Doucette-Stamm, L., Hill, D.E. and Vidal, M.

TITLE C. elegans ORFeome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein expression

JOURNAL Nat. Genet., (2003) In press

COMMENT Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739

Email: Marc.Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project : Contact david_hill@dfci.harvard.edu or marc_vidal@dfci.harvard.edu

POLYA=No.

FEATURES Location/Qualifiers

1..124

/organism="Caenorhabditis elegans"

/mol_type="mRNA"

/strain="N2"

/db_xref="taxon:6239"

/sex="Hermaphrodite and male"

/tissue_type="whole animal"

/dev_stage="mixed stage"

/clone_lib="AD-wrmcDNA"

/note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

BASE COUNT 36 a 31 c 22 g 35 t

ORIGIN

Query Match 88.0%; Score 22; DB 14; Length 124;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTCTCTGTACAAAGTTGG 25
|||||

Db 61 CAGCTTCTCTGTACAAAGTTGG 40

RESULT 19

CB400130/c

LOCUS CB400130 126 bp mRNA linear EST 15-MAY-2003

DEFINITION OSTF169C5_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.

ACCESSION CB400130

VERSION CB400130.1 GI:30741857

KEYWORDS EST.

SOURCE Caenorhabditis elegans

ORGANISM Caenorhabditis elegans

REFERENCE 1 (bases 1 to 126)

AUTHORS Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolia, P.P., Placsek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H., Doucette-Stamm, L., Hill, D.E. and Vidal, M.

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Fax: 617 632 5739

Email: Marc.Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project : Contact david_hill@dfci.harvard.edu or marc_vidal@dfci.harvard.edu

POLYA=No.

FEATURES Location/Qualifiers

1..126

/organism="Caenorhabditis elegans"

/mol_type="mRNA"

/strain="N2"

/db_xref="taxon:6239"

/sex="Hermaphrodite and male"

/tissue_type="whole animal"

/dev_stage="mixed stage"

/clone_lib="AD-wrmcDNA"

/note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

BASE COUNT 38 a 27 c 23 g 38 t

ORIGIN

Query Match 88.0%; Score 22; DB 14; Length 126;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTCTCTGTACAAAGTTGG 25
|||||

Db 61 CAGCTTCTCTGTACAAAGTTGG 40

RESULT 20

CB400226/c

LOCUS CB400226 128 bp mRNA linear EST 15-MAY-2003

DEFINITION OSTF171D4_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.

ACCESSION CB400226

VERSION CB400226.1 GI:30741953

KEYWORDS EST.

SOURCE Caenorhabditis elegans

ORGANISM Caenorhabditis elegans

REFERENCE 1 (bases 1 to 128)

AUTHORS Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolia, P.P., Placsek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H., Doucette-Stamm, L., Hill, D.E. and Vidal, M.

TITLE C. elegans ORFeome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein expression

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Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739

Email: Marc.Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project : Contact david_hill@dfci.harvard.edu or marc_vidal@dfci.harvard.edu

POLYA=No.

FEATURES Location/Qualifiers

1..128

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/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"
/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
BASE COUNT      41 a      27 c      22 g      38 t
ORIGIN
Query Match      88.0%; Score 22; DB 14; Length 128;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 CAGCTTTCTTGTACAAAGTTGG 25
        |||||||
Db      61 CAGCTTTCTTGTACAAAGTTGG 40

RESULT 21
CB401884/4      128 bp      mRNA      linear      EST 15-MAY-2003
LOCUS
DEFINITION      OSTF202C5_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION      CB401884
VERSION      CB401884.1 GI:30743611
KEYWORDS      EST.
SOURCE      Caenorhabditis elegans
ORGANISM      Caenorhabditis elegans
REFERENCE      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
AUTHORS      1 (bases 1 to 128)
Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong
, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson
, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,
Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolia, P.P.
, Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,
Doucette-Stamm, L., Hill, D.E. and Vidal, M.
C. elegans ORFeome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
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JOURNAL      Nat. Genet., (2003) In press
COMMENT      Contact: Vidal M
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc.Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david_hill@dfci.harvard.edu or
marc_vidal@dfci.harvard.edu
POLYA=No.

FEATURES
source      Location/Qualifiers
1..128
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"
/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
BASE COUNT      41 a      27 c      22 g      38 t
ORIGIN
Query Match      88.0%; Score 22; DB 14; Length 128;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 CAGCTTTCTTGTACAAAGTTGG 25
        |||||||
Db      61 CAGCTTTCTTGTACAAAGTTGG 40

RESULT 22
CB401218/c      129 bp      mRNA      linear      EST 15-MAY-2003
LOCUS
DEFINITION      OSTF191C6_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION      CB401218
VERSION      CB401218.1 GI:30742945
KEYWORDS      EST.
SOURCE      Caenorhabditis elegans
ORGANISM      Caenorhabditis elegans
REFERENCE      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
AUTHORS      1 (bases 1 to 129)
Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong
, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson
, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,
Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolia, P.P.
, Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,
Doucette-Stamm, L., Hill, D.E. and Vidal, M.
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genome annotation and resource for proteome-scale protein
expression
JOURNAL      Nat. Genet., (2003) In press
COMMENT      Contact: Vidal M
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc.Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david_hill@dfci.harvard.edu or
marc_vidal@dfci.harvard.edu
POLYA=No.

FEATURES
source      Location/Qualifiers
1..129
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"
/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
BASE COUNT      37 a      28 c      20 g      44 t
ORIGIN
Query Match      88.0%; Score 22; DB 14; Length 129;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 CAGCTTTCTTGTACAAAGTTGG 25
        |||||||
Db      62 CAGCTTTCTTGTACAAAGTTGG 41

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RESULT 23
CB398923
LOCUS
DEFINITION 227 bp mRNA linear EST 15-MAY-2003
CB398923_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION
CB398923
VERSION
CB398923.1 GI:30740650
KEYWORDS
EST.
SOURCE
Caenorhabditis elegans
ORGANISM
Caenorhabditis elegans
REFERENCE
1 Rhabditidae; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
AUTHORS
Reboul,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M., Armstrong
,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T., Hudson
,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.,
Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V., Toliaas,P.P.
, Placek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,
Doucette-Stamm,L., Hill,D.E. and Vidal,M.
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JOURNAL
Nat. Genet., (2003) In press
COMMENT
Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc.Vidal@fci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david.hill@fci.harvard.edu or
marc.vidal@fci.harvard.edu
POLYA=No.
FEATURES
Location/Qualifiers
1..227
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/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"
/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
BASE COUNT 72 a 47 c 42 g 66 t
ORIGIN
Query Match 88.0%; Score 22; DB 14; Length 227;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 CAGCTTCTTGTACAAAGTTGG 25
|||||
Db 108 CAGCTTCTTGTACAAAGTTGG 129
|||||
RESULT 24
CB401020/c
LOCUS
DEFINITION 247 bp mRNA linear EST 15-MAY-2003
CB401020_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION
CB401020
VERSION
CB401020.1 GI:30742747
KEYWORDS
EST.
SOURCE
Caenorhabditis elegans
ORGANISM
Caenorhabditis elegans
REFERENCE
1 Rhabditidae; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
AUTHORS
Reboul,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M., Armstrong
,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T., Hudson
,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.,
Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V., Toliaas,P.P.
, Placek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,
Doucette-Stamm,L., Hill,D.E. and Vidal,M.
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Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc.Vidal@fci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david.hill@fci.harvard.edu or
marc.vidal@fci.harvard.edu
POLYA=No.
FEATURES
Location/Qualifiers
1..227
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"
/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
BASE COUNT 72 a 47 c 42 g 66 t
ORIGIN
Query Match 88.0%; Score 22; DB 14; Length 227;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 CAGCTTCTTGTACAAAGTTGG 25
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Db 108 CAGCTTCTTGTACAAAGTTGG 129
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```

```

REFERENCE
AUTHORS
1 (bases 1 to 247)
Reboul,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M., Armstrong
,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T., Hudson
,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.,
Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V., Toliaas,P.P.
, Placek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,
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Sequence tag of Gateway entry clones. The primers used were
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cloning project : Contact david.hill@fci.harvard.edu or
marc.vidal@fci.harvard.edu
POLYA=No.
FEATURES
Location/Qualifiers
1..247
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"
/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
BASE COUNT 72 a 44 c 47 g 84 t
ORIGIN
Query Match 88.0%; Score 22; DB 14; Length 247;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 CAGCTTCTTGTACAAAGTTGG 25
|||||
Db 75 CAGCTTCTTGTACAAAGTTGG 54
|||||
RESULT 25
CB395877
LOCUS
DEFINITION 262 bp mRNA linear EST 15-MAY-2003
CB395877_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION
CB395877.1 GI:30737588
VERSION
EST.
KEYWORDS
Caenorhabditis elegans
SOURCE
Caenorhabditis elegans
ORGANISM
Caenorhabditis elegans
REFERENCE
1 Rhabditidae; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
AUTHORS
Reboul,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M., Armstrong
,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T., Hudson
,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.,
Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V., Toliaas,P.P.
, Placek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,
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Nat. Genet., (2003) In press
COMMENT
Contact: Vidal M

```

Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617-632 5180
Fax: 617-632 5739
Email: Marc_Vidal@dfci.harvard.edu

Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFome cloning project : Contact david_hill@dfci.harvard.edu or marc_vidal@dfci.harvard.edu
POLYA=No.

FEATURES

source

Location/Qualifiers

1..262
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"

/note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

77 a 54 c 48 g 83 t

BASE COUNT

ORIGIN

Query Match 88.0%; Score 22; DB 14; Length 262;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTTCTGTACAAAGTTGG 25

|||||

Db 128 CAGCTTTCTGTACAAAGTTGG 149

RESULT 26

CB395890

LOCUS

CB395890 263 bp mRNA linear EST 15-MAY-2003
OSVR163C2_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.

ACCESSION

CB395890

VERSION

CB395890.1 GI:30737601

KEYWORDS

EST.

SOURCE

Caenorhabditis elegans

ORGANISM

Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 263)

REFERENCE

AUTHORS

Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tollas, P.P., Placsek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H., Doucette-Stamm, L., Hill, D.E. and Vidal, M.

TITLE

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JOURNAL

COMMENT

Nat. Genet., (2003) In press

Contact: Vidal M

Marc Vidal Laboratory

Dana Farber Cancer Institute

1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA

Tel: 617 632 5180

Fax: 617 632 5739

Email: Marc_Vidal@dfci.harvard.edu

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POLYA=No.

FEATURES

Location/Qualifiers

source

1..263

/organism="Caenorhabditis elegans"

/mol_type="mRNA"

/strain="N2"

/db_xref="taxon:6239"

/sex="Hermaphrodite and male"

/tissue_type="whole animal"

/dev_stage="mixed stage"

/clone_lib="AD-wrmcDNA"

/note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

78 a 51 c 54 g 80 t

BASE COUNT

ORIGIN

Query Match 88.0%; Score 22; DB 14; Length 263;

Best Local Similarity 100.0%; Pred. No. 33;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTTCTGTACAAAGTTGG 25

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Db 132 CAGCTTTCTGTACAAAGTTGG 153

RESULT 27

BI174869

LOCUS

BI174869 380 bp mRNA linear EST 09-JUL-2001
OSTF061D8_1 AD-wrmcDNA Caenorhabditis elegans cDNA similar to K04A8.3, mRNA sequence.

ACCESSION

BI174869

VERSION

BI174869.1 GI:14640672

KEYWORDS

EST.

SOURCE

ORGANISM

Caenorhabditis elegans

Caenorhabditis elegans

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea

; Rhabditidae; Peloderinae; Caenorhabditis.

REFERENCE

AUTHORS

Reboul, J., Vaglio, P., Tzellas, N., Thierry-Mieg, N., Moore, T., Jackson, C., Shin-i, T., Kohara, Y., Thierry-Mieg, D., Thierry-Mieg, J., Lee, H., Hitti, J., Doucette-Stamm, L., Hartley, J.L., Temple, G.F., Brasch, M.A., Vandenhaute, J., Lamesch, P.E., Hill, D.E. and Vidal, M.

TITLE

Open-reading-frame sequence tags (OSFs) support the existence of at least 17,300 genes in C. elegans

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Reboul J, Vaglio P

Marc Vidal Laboratory

Dana Farber Cancer Institute

44 Binney Street, Boston, MA 02115, USA

Tel: 617 632 5180

Fax: 617 632 2425

Email: Jerome.Reboul@dfci.harvard.edu

Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFome cloning project : Contact Jerome.Reboul@dfci.harvard.edu or philippe.vaglio@dfci.harvard.edu

POLYA=No.

FEATURES

source

Location/Qualifiers

1..380

/organism="Caenorhabditis elegans"

/mol_type="mRNA"

/strain="N2"

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/tissue_type="whole animal"

/dev_stage="mixed stage"

/clone_lib="AD-wrmcDNA"

/note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the

subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

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Db   333 CAGCTTCTTGTACAAAGTTGG 354

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ACCESSION       BII174871
VERSION         BII174871.1 GI:14640674
KEYWORDS
SOURCE
ORGANISM        Caenorhabditis elegans
                Caenorhabditis elegans
                Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
                ; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE
AUTHORS        Reboul,J., Vaglio,P., Tzellas,N., Thierry-Mieg,N., Moore,T.,
                Jackson,C., Shin-I,T., Kohara,Y., Thierry-Mieg,D., Thierry-Mieg,J.,
                Lee,H., Hitti,J., Doucette-Stamm,L., Hartley,J.L., Temple,G.F.,
                Brasch,M.A., Vandenhaute,J., Lamesch,P.E., Hill,D.E. and Vidal,M.
                Open-reading-frame sequence tags (OSTs) support the existence of at
                least 17,300 genes in C. elegans
                Nat. Genet. 27 (3), 332-336 (2001)
                21135099
                PUBMED
                11242119
COMMENT        Contact: Reboul J, Vaglio P
                Marc Vidal Laboratory
                Dana Farber Cancer Institute
                44 Binney Street, Boston, MA 02115, USA
                Tel: 617 632 5180
                Fax: 617 632 2425
                Email: Jerome.Reboul@dfci.harvard.edu
                Sequence tag of Gateway entry clones. The primers used were
                designed on the predicted protein encoding ORF. C. elegans ORFeome
                cloning project : Contact Jerome.reboul@dfci.harvard.edu or
                philippe.vaglio@dfci.harvard.edu
                POLYA=No.

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/clone_lib="AD-wrmcDNA"
/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"

BASE COUNT      142 a   78 c   86 g   129 t
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Best Local Similarity 100.0%; Pred. No. 39;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  4 CAGCTTCTTGTACAAAGTTGG 25
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Db   393 CAGCTTCTTGTACAAAGTTGG 414

RESULT 30
BII174361
LOCUS
DEFINITION      OSTF042B6.1 AD-wrmcDNA Caenorhabditis elegans cDNA similar to
ACCESSION       BII174361
VERSION         BII174361.1 GI:14640164
KEYWORDS
SOURCE
ORGANISM        Caenorhabditis elegans
                Caenorhabditis elegans
                Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
                ; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE
AUTHORS        Reboul,J., Vaglio,P., Tzellas,N., Thierry-Mieg,N., Moore,T.,
                Jackson,C., Shin-I,T., Kohara,Y., Thierry-Mieg,D., Thierry-Mieg,J.,
                Lee,H., Hitti,J., Doucette-Stamm,L., Hartley,J.L., Temple,G.F.,
                Brasch,M.A., Vandenhaute,J., Lamesch,P.E., Hill,D.E. and Vidal,M.
                Open-reading-frame sequence tags (OSTs) support the existence of at
                least 17,300 genes in C. elegans
                Nat. Genet. 27 (3), 332-336 (2001)
                21135099
                PUBMED
                11242119
COMMENT        Contact: Reboul J, Vaglio P
                Marc Vidal Laboratory
                Dana Farber Cancer Institute
                44 Binney Street, Boston, MA 02115, USA
                Tel: 617 632 5180
                Fax: 617 632 2425
                Email: Jerome.Reboul@dfci.harvard.edu
                Sequence tag of Gateway entry clones. The primers used were
                designed on the predicted protein encoding ORF. C. elegans ORFeome
                cloning project : Contact Jerome.reboul@dfci.harvard.edu or
                philippe.vaglio@dfci.harvard.edu
                POLYA=No.

FEATURES
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/clone_lib="AD-wrmcDNA"
/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"

BASE COUNT      121 a   100 c   122 g   117 t
ORIGIN
Query Match      88.0%; Score 22; DB 12; Length 460;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  4 CAGCTTCTTGTACAAAGTTGG 25
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Db   397 CAGCTTCTTGTACAAAGTTGG 418

RESULT 30
BII174361
LOCUS
DEFINITION      OSTF042B6.1 AD-wrmcDNA Caenorhabditis elegans cDNA similar to
ACCESSION       BII174361
VERSION         BII174361.1 GI:14640164
KEYWORDS
SOURCE
ORGANISM        Caenorhabditis elegans
                Caenorhabditis elegans
                Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
                ; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE
AUTHORS        Reboul,J., Vaglio,P., Tzellas,N., Thierry-Mieg,N., Moore,T.,
                Jackson,C., Shin-I,T., Kohara,Y., Thierry-Mieg,D., Thierry-Mieg,J.,
                Lee,H., Hitti,J., Doucette-Stamm,L., Hartley,J.L., Temple,G.F.,
                Brasch,M.A., Vandenhaute,J., Lamesch,P.E., Hill,D.E. and Vidal,M.
                Open-reading-frame sequence tags (OSTs) support the existence of at
                least 17,300 genes in C. elegans
                Nat. Genet. 27 (3), 332-336 (2001)
                21135099
                PUBMED
                11242119
COMMENT        Contact: Reboul J, Vaglio P
                Marc Vidal Laboratory
                Dana Farber Cancer Institute
                44 Binney Street, Boston, MA 02115, USA
                Tel: 617 632 5180
                Fax: 617 632 2425
                Email: Jerome.Reboul@dfci.harvard.edu
                Sequence tag of Gateway entry clones. The primers used were
                designed on the predicted protein encoding ORF. C. elegans ORFeome
                cloning project : Contact Jerome.reboul@dfci.harvard.edu or
                philippe.vaglio@dfci.harvard.edu
                POLYA=No.

FEATURES
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Location/Qualifiers
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/organism="Caenorhabditis elegans"
/mol_type="mRNA"
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/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"
/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"

BASE COUNT      121 a   100 c   122 g   117 t
ORIGIN
Query Match      88.0%; Score 22; DB 12; Length 460;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  4 CAGCTTCTTGTACAAAGTTGG 25
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Db   397 CAGCTTCTTGTACAAAGTTGG 418

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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 467)

REFERENCE
AUTHORS
Reboul, J., Vaglio, P., Tzellas, N., Thierry-Mieg, N., Moore, T.,
Jackson, C., Shin-i, T., Kohara, Y., Thierry-Mieg, D., Thierry-Mieg, J.,
Lee, H., Hitti, J., Doucette-Stamm, L., Hartley, J. L., Temple, G. F.,
Brasch, M. A., Vandenhaute, J., Lamesch, P. E., Hill, D. E. and Vidal, M.
Open-reading-frame sequence tags (OSTs) support the existence of at
least 17,300 genes in C. elegans
Nat. Genet. 27 (3), 332-336 (2001)

21135099
MEDLINE
PUBMED
11242119

COMMENT
Contact: Reboul J, Vaglio P
Marc Vidal Laboratory
Dana Farber Cancer Institute
44 Binney Street, Boston, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 2425
Email: Jerome.Reboul@fci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact jerome.reboul@fci.harvard.edu or
philippe.vaglio@fci.harvard.edu
POLYA=No.

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/dev_stage="mixed stage"
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/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"

BASE COUNT 153 a 87 c 101 g 126 t

ORIGIN
Query Match 88.0%; Score 22; DB 12; Length 467;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTCTTGTACAAAGTTGG 25
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Db 439 CAGCTTCTTGTACAAAGTTGG 460
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RESULT 31
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LOCUS
DEFINITION
OSTP06111.1 AD-wrmcDNA Caenorhabditis elegans cDNA similar to
W02D7.3, mRNA sequence.
ACCESSION
BI174878
VERSION
BI174878.1 GI:14640681
KEYWORDS
EST.
SOURCE
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 480)

REFERENCE
AUTHORS
Reboul, J., Vaglio, P., Tzellas, N., Thierry-Mieg, N., Moore, T.,
Jackson, C., Shin-i, T., Kohara, Y., Thierry-Mieg, D., Thierry-Mieg, J.,
Lee, H., Hitti, J., Doucette-Stamm, L., Hartley, J. L., Temple, G. F.,
Brasch, M. A., Vandenhaute, J., Lamesch, P. E., Hill, D. E. and Vidal, M.
Open-reading-frame sequence tags (OSTs) support the existence of at
least 17,300 genes in C. elegans
Nat. Genet. 27 (3), 332-336 (2001)

21135099
MEDLINE
PUBMED
11242119

COMMENT
Contact: Reboul J, Vaglio P
Marc Vidal Laboratory
Dana Farber Cancer Institute
44 Binney Street, Boston, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 2425
Email: Jerome.Reboul@fci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact jerome.reboul@fci.harvard.edu or
philippe.vaglio@fci.harvard.edu
POLYA=No.

Contact: Reboul J, Vaglio P
Marc Vidal Laboratory
Dana Farber Cancer Institute
44 Binney Street, Boston, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 2425
Email: Jerome.Reboul@fci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact jerome.reboul@fci.harvard.edu or
philippe.vaglio@fci.harvard.edu
POLYA=No.

FEATURES
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/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"

BASE COUNT 140 a 124 c 80 g 136 t

ORIGIN
Query Match 88.0%; Score 22; DB 12; Length 480;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTCTTGTACAAAGTTGG 25
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Db 408 CAGCTTCTTGTACAAAGTTGG 429
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RESULT 32
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DEFINITION
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ACCESSION
BI174375
VERSION
BI174375.1 GI:14640178
KEYWORDS
EST.
SOURCE
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 501)

REFERENCE
AUTHORS
Reboul, J., Vaglio, P., Tzellas, N., Thierry-Mieg, N., Moore, T.,
Jackson, C., Shin-i, T., Kohara, Y., Thierry-Mieg, D., Thierry-Mieg, J.,
Lee, H., Hitti, J., Doucette-Stamm, L., Hartley, J. L., Temple, G. F.,
Brasch, M. A., Vandenhaute, J., Lamesch, P. E., Hill, D. E. and Vidal, M.
Open-reading-frame sequence tags (OSTs) support the existence of at
least 17,300 genes in C. elegans
Nat. Genet. 27 (3), 332-336 (2001)

21135099
MEDLINE
PUBMED
11242119

COMMENT
Contact: Reboul J, Vaglio P
Marc Vidal Laboratory
Dana Farber Cancer Institute
44 Binney Street, Boston, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 2425
Email: Jerome.Reboul@fci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact jerome.reboul@fci.harvard.edu or
philippe.vaglio@fci.harvard.edu
POLYA=No.

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        cDNAs were cloned into pPC86"
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  OSTF061D7.1 AD-wrmcDNA Caenorhabditis elegans cDNA similar to
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ACCESSION
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VERSION
  BI174868.1 GI:14640671
KEYWORDS
  EST.
SOURCE
  Caenorhabditis elegans
  ORGANISM
    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
    ; Rhabditidae; Pelodierinae; Caenorhabditis.
REFERENCE
  1 (bases 1 to 508)
  Rebol, J., Vaglio, P., Tzellas, N., Thierry-Mieg, N., Moore, T.,
  Jackson, C., Shin-i, T., Kohara, Y., Thierry-Mieg, D., Thierry-Mieg, J.,
  Lee, H., Hitti, J., Doucette-Stamm, L., Hartley, J.L., Temple, G.F.,
  Brasch, M.A., Vandenhaute, J., Lamesch, P.E., Hill, D.E. and Vidal, M.
  Open-reading-frame sequence tags (OSTs) support the existence of at
  least 17,300 genes in C. elegans
  Nat. Genet. 27 (3), 332-336 (2001)
JOURNAL
  Nat. Genet. 27 (3), 332-336 (2001)
MEDLINE
  21135099
PUBMED
  11242119
COMMENT
  Contact: Rebol, J, Vaglio P
  Marc Vidal Laboratory
  Dana Farber Cancer Institute
  44 Binney Street, Boston, MA 02115, USA
  Tel: 617 632 5180
  Fax: 617 632 2425
  Email: Jerome_Rebol@dfci.harvard.edu
  Sequence tag of Gateway entry clones. The primers used were
  designed on the predicted protein encoding ORF. C. elegans ORFeome
  cloning project : Contact jerome_rebol@dfci.harvard.edu or
  philippe_vaglio@dfci.harvard.edu
  POLYA=No.
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        RNA isolated from both hermaphrodite and male N2 worms of
        all larval stages, embryos, adults and dauers and the
        subsequent generation of cDNAs by poly(A) priming. The
        cDNAs were cloned into pPC86"
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      ORIGIN

Query Match      88.0%; Score 22; DB 12; Length 549;
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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
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      ORIGIN

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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      436 CAGCTTTCTTGTACAAAGTTGG 457

RESULT 34
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DEFINITION
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  OSTF061G9.1 AD-wrmcDNA Caenorhabditis elegans cDNA similar to
  P32D1.6, mRNA sequence.
ACCESSION
  BI174892
VERSION
  BI174892.1 GI:14640695
KEYWORDS
  EST.
SOURCE
  Caenorhabditis elegans
  ORGANISM
    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
    ; Rhabditidae; Pelodierinae; Caenorhabditis.
REFERENCE
  1 (bases 1 to 549)
  Rebol, J., Vaglio, P., Tzellas, N., Thierry-Mieg, N., Moore, T.,
  Jackson, C., Shin-i, T., Kohara, Y., Thierry-Mieg, D., Thierry-Mieg, J.,
  Lee, H., Hitti, J., Doucette-Stamm, L., Hartley, J.L., Temple, G.F.,
  Brasch, M.A., Vandenhaute, J., Lamesch, P.E., Hill, D.E. and Vidal, M.
  Open-reading-frame sequence tags (OSTs) support the existence of at
  least 17,300 genes in C. elegans
  Nat. Genet. 27 (3), 332-336 (2001)
JOURNAL
  Nat. Genet. 27 (3), 332-336 (2001)
MEDLINE
  21135099
PUBMED
  11242119
COMMENT
  Contact: Rebol, J, Vaglio P
  Marc Vidal Laboratory
  Dana Farber Cancer Institute
  44 Binney Street, Boston, MA 02115, USA
  Tel: 617 632 5180
  Fax: 617 632 2425
  Email: Jerome_Rebol@dfci.harvard.edu
  Sequence tag of Gateway entry clones. The primers used were
  designed on the predicted protein encoding ORF. C. elegans ORFeome
  cloning project : Contact jerome_rebol@dfci.harvard.edu or
  philippe_vaglio@dfci.harvard.edu
  POLYA=No.
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        /sex="Hermaphrodite and male"
        /tissue_type="whole animal"
        /dev_stage="mixed stage"
        /clone_lib="AD-wrmcDNA"
        /note="The AD-wrmcDNA library was generated with poly(A)+
        RNA isolated from both hermaphrodite and male N2 worms of
        all larval stages, embryos, adults and dauers and the
        subsequent generation of cDNAs by poly(A) priming. The
        cDNAs were cloned into pPC86"
      BASE COUNT      169 a      134 c      119 g      127 t
      ORIGIN

Query Match      88.0%; Score 22; DB 12; Length 549;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 CAGCTTTCTTGTACAAAGTTGG 25
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Db      477 CAGCTTCTTGTACAAAGTTGG 498

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DEFINITION OSR163A10_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION CB395875
VERSION CB395875.1 GI:30737586
KEYWORDS EST.
SOURCE
ORGANISM
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
1 (bases 1 to 559)
Reboul,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M., Armstrong
,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T., Hudson
,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.,
Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V., Tolia,P.P.,
Pracek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,
Doucette-Stamm,L., Hill,D.E. and Vidal,M.
C. elegans ORFeome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
expression
JOURNAL Nat. Genet. (2003) In press
COMMENT Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc.Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david_hille@dfci.harvard.edu or
marc_vidal@dfci.harvard.edu
POLYA-No.
FEATURES
source
Location/Qualifiers
1..559
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"
/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
BASE COUNT 163 a 120 c 113 g 163 t
ORIGIN
Query Match 88.0%; Score 22; DB 14; Length 559;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTCTTGTACAAAGTTGG 25
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Db 98 CAGCTTCTTGTACAAAGTTGG 119

RESULT 36
BI174904
LOCUS
DEFINITION OSTF062B11_1 AD-wrmcDNA Caenorhabditis elegans cDNA similar to
T06A4.2, mRNA sequence.
ACCESSION BI174904
VERSION BI174904.1 GI:14640707
KEYWORDS EST.
SOURCE
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
1 (bases 1 to 583)
Reboul,J., Vaglio,P., Tzellas,N., Thierry-Mieg,N., Moore,T.,
Jackson,C., Shin-I.T., Kohara,Y., Thierry-Mieg,D., Thierry-Mieg,J.,
Lee,H., Hitti,J., Doucette-Stamm,L., Hartley,J.L., Temple,G.F.,
Brasch,M.A., Vandenhaute,J., Lamesch,P.E., Hill,D.E. and Vidal,M.
Open-reading-frame sequence tags (OSTs) support the existence of at
least 17,300 genes in C. elegans
JOURNAL Nat. Genet. 27 (3), 332-336 (2001)
MEDLINE 21135099
COMMENT Contact: Reboul J, Vaglio P
Marc Vidal Laboratory
Dana Farber Cancer Institute
44 Binney Street, Boston, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 2425
Email: Jerome_Reboul@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact jerome_reboul@dfci.harvard.edu or
philippe_vaglio@dfci.harvard.edu
POLYA-No.
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/organism="Caenorhabditis elegans"
/mol_type="mRNA"
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/db_xref="taxon:6239"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"
/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
BASE COUNT 192 a 158 c 109 g 124 t
ORIGIN
Query Match 88.0%; Score 22; DB 12; Length 583;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTCTTGTACAAAGTTGG 25
|||||
Db 519 CAGCTTCTTGTACAAAGTTGG 540

RESULT 37
BI174910
LOCUS
DEFINITION OSTF062B7_1 AD-wrmcDNA Caenorhabditis elegans cDNA similar to
C25A1.13, mRNA sequence.
ACCESSION BI174910
VERSION BI174910.1 GI:14640713
KEYWORDS EST.
SOURCE
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
1 (bases 1 to 613)
Reboul,J., Vaglio,P., Tzellas,N., Thierry-Mieg,N., Moore,T.,
Jackson,C., Shin-I.T., Kohara,Y., Thierry-Mieg,D., Thierry-Mieg,J.,
Lee,H., Hitti,J., Doucette-Stamm,L., Hartley,J.L., Temple,G.F.,
Brasch,M.A., Vandenhaute,J., Lamesch,P.E., Hill,D.E. and Vidal,M.
Open-reading-frame sequence tags (OSTs) support the existence of at
least 17,300 genes in C. elegans
JOURNAL Nat. Genet. 27 (3), 332-336 (2001)
MEDLINE 21135099

```

11242119
 PUBMED
 COMMENT
 Contact: Reboul J, Vaglio P
 Marc Vidal Laboratory
 Dana Farber Cancer Institute
 44 Binney Street, Boston, MA 02115, USA
 Tel: 617 632 5180
 Fax: 617 632 2425
 Email: Jerome.Reboul@dfci.harvard.edu
 Sequence tag of Gateway entry clones. The primers used were
 designed on the predicted protein encoding ORF. C. elegans ORFeome
 cloning project : Contact jerome_reboul@dfci.harvard.edu or
 philippe_vaglio@dfci.harvard.edu
 POLYA=No.

FEATURES

source

Location/Qualifiers
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 /strain="N2"
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 /sex="Hermaphrodite and male"
 /tissue_type="whole animal"
 /dev_stage="mixed stage"
 /clone_lib="AD-wrmcDNA"
 /note="The AD-wrmcDNA library was generated with poly(A)+
 RNA isolated from both hermaphrodite and male N2 worms of
 all larval stages, embryos, adults and dauers and the
 subsequent generation of cDNAs by poly(A) priming. The
 cDNAs were cloned into pPCR86"

BASE COUNT 199 a 143 c 121 g 150 t
 ORIGIN
 Query Match 88.0%; Score 22; DB 12; Length 613;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CAGCTTTCTTGTACAAAGTTGG 25
 |||||
 Db 551 CAGCTTTCTTGTACAAAGTTGG 572
 |||||

RESULT 38
 CB960041/c 1388 bp mRNA linear EST 29-APR-2003
 LOCUS
 DEFINITION
 AGENCOURT_13887498 NIH_MGC_147 Homo sapiens cDNA clone
 IMAGE:30340779 5', mRNA sequence.

ACCESSION CB960041
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1388)
 NIH-MGC <http://mgs.nci.nih.gov/>
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Dr. Stefan Hansson
 CDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
 and advice from Piero Carninci (RIKEN)
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: NDAM371 row: d column: 04
 High quality sequence start: 138
 High quality sequence stop: 355.
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 1. 1388
 /organism="Homo sapiens"
 /mol_type="mRNA"

/db_xref="taxon:9606"
 /clone="IMAGE:30340779"
 /tissue_type="Human Placenta"
 /lab_host="DH10B Tona"
 /clone_lib="NIH_MGC_147"
 /note="Organ: placenta; Vector: pBluescriptR; Site:1;
 all-XhoI; Site 2: BamH; Oligo-dr primed using primer
 5'-TTTTTTTTTTTNN-3', size-selected for average
 insert size 2.3 kb and normalized to ROT 5. This is a
 primary library enriched for full-length clones and
 constructed using the Cap-trapper method (Carninci, in
 preparation). Library constructed by M. Brownstein
 (NIH/NHGRI, National Institutes of Health). Note: This is
 a NIH MGC library."

BASE COUNT 429 a 271 c 314 g 361 t 13 others
 ORIGIN
 Query Match 88.0%; Score 22; DB 14; Length 1388;
 Best Local Similarity 100.0%; Pred. No. 55;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CAGCTTTCTTGTACAAAGTTGG 25
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 Db 154 CAGCTTTCTTGTACAAAGTTGG 133
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RESULT 39
 AL515389/c 559 bp mRNA linear EST 08-MAY-2003
 LOCUS
 DEFINITION
 AL515389 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
 CLOBB019ZB04 3-PRIME, mRNA sequence.

ACCESSION AL515389
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 559)
 Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished
 On Feb 13, 2001 this sequence version replaced gi:12778882.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 1606.r For
 more information about this cluster, see
<http://www.genoscope.cns.fr/>
 cgi-bin/cluster.cgi?seq=CLOBB019ZB04FP1&cluster=1606.r. Contact :
 Feng Liang Email : fliang@lifetech.com URL :
<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CLOBB019ZB04FP1.
 Location/Qualifiers

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 /organism="Homo sapiens"
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 /db_xref="taxon:9606"
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 with a NotI-oligo(dT) primer. Five prime end enriched,
 double-strand cDNA was digested with Not I and cloned into
 the Not I and EcoRV sites of the pCMVSPORT 6 vector.
 Library was not normalized."
 BASE COUNT 190 a 78 c 68 g 163 t
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 Query Match 84.0%; Score 21; DB 9; Length 559;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;

FEATURES

source

1. .559
 /organism="Homo sapiens"
 /mol_type="mRNA"
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 /tissue_type="NEUROBLASTOMA"
 /clone_lib="Homo sapiens NEUROBLASTOMA"
 /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
 with a NotI-oligo(dT) primer. Five prime end enriched,
 double-strand cDNA was digested with Not I and cloned into
 the Not I and EcoRV sites of the pCMVSPORT 6 vector.
 Library was not normalized."
 BASE COUNT 190 a 78 c 68 g 163 t
 ORIGIN

source

1. .559
 /organism="Homo sapiens"
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 /clone_lib="Homo sapiens NEUROBLASTOMA"
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 with a NotI-oligo(dT) primer. Five prime end enriched,
 double-strand cDNA was digested with Not I and cloned into
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 Library was not normalized."
 BASE COUNT 190 a 78 c 68 g 163 t
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 Library was not normalized."
 BASE COUNT 190 a 78 c 68 g 163 t
 ORIGIN

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1. .559
 /organism="Homo sapiens"
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 Library was not normalized."
 BASE COUNT 190 a 78 c 68 g 163 t
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1. .559
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 Library was not normalized."
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 /organism="Homo sapiens"
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 /clone_lib="Homo sapiens NEUROBLASTOMA"
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 with a NotI-oligo(dT) primer. Five prime end enriched,
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 Library was not normalized."
 BASE COUNT 190 a 78 c 68 g 163 t
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 Library was not normalized."
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 the Not I and EcoRV sites of the pCMVSPORT 6 vector.
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 BASE COUNT 190 a 78 c 68 g 163 t
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 /organism="Homo sapiens"
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source

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 Library was not normalized."
 BASE COUNT 190 a 78 c 68 g 163 t
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1. .559
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 Library was not normalized."
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1. .559
 /organism="Homo sapiens"
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 /tissue_type="NEUROBLASTOMA"
 /clone_lib="Homo sapiens NEUROBLASTOMA"
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 with a NotI-oligo(dT) primer. Five prime end enriched,
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 Library was not normalized."
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1. .559
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 Library was not normalized."
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1. .559
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 /organism="Homo sapiens"
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 /tissue_type="NEUROBLASTOMA"
 /clone_lib="Homo sapiens NEUROBLASTOMA"
 /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
 with a NotI-oligo(dT) primer. Five prime end enriched,
 double-strand cDNA was digested with Not I and cloned into
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 Library was not normalized."
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 /clone_lib="Homo sapiens NEUROBLASTOMA"
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 with a NotI-oligo(dT) primer. Five prime end enriched,
 double-strand cDNA was digested with Not I and cloned into
 the Not I and EcoRV sites of the pCMVSPORT 6 vector.
 Library was not normalized."
 BASE COUNT 190 a 78 c 68 g 163 t
 ORIGIN

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTCTTGTCACAAAGTTG 24
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 Db 40 CAGCTTCTTGTCACAAAGTTG 20

RESULT 40
 CD048261 982 bp mRNA linear EST 09-MAY-2003
 LOCUS AGENCOURT_13971692 NIH_MGC_172 Homo sapiens cDNA 5', mRNA sequence.
 CD048261
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE

CD048261.1 GI:30483085
 EST.
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 1 (bases 1 to 982)
 NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs@mail.nih.gov
 Tissue Procurement: Dr. Jamie Thompson, University of WI
 CDNA Library Preparation: Gina Zastrow-Hayes
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: NDKM41 row: p column: 19
 High quality sequence start: 11
 High quality sequence stop: 472.
 Location/Qualifiers

FEATURES
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 /clone_lib="NIH MGC 172"
 /notes="Vector: pDONR201; Site 1: attP2; Site 2: attP1;
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 Embryonic Stem Cells HI; LIBR PROVIDER - Bradfield"
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 ORIGIN

Query Match 84.0%; Score 21; DB 14; Length 982;
 Best Local Similarity 95.5%; Pred. No. 1.4e+02;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCTTCTTGTCACAAAGTTG 25
 |||||
 Db 590 CAGCTTCTTGTCACAAAGTTG 611

Search completed: November 7, 2003, 00:21:01
 Job time : 1094.75 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 6, 2003, 22:12:53 ; Search time 28 Seconds
(without alignments)
394.092 Million cell updates/sec

Title: US-10-055-001A-10
Perfect score: 25
Sequence: 1 gtccagctttttgtacaaagtgg 25

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	25	3 US-09-233-493-15	Sequence 15, Appl
2	25	100.0	25	3 US-09-005-476-15	Sequence 15, Appl
3	25	100.0	25	3 US-09-233-492-15	Sequence 15, Appl
4	25	100.0	25	3 US-09-296-280-15	Sequence 15, Appl
5	25	100.0	25	4 US-09-498-074-15	Sequence 15, Appl
6	25	100.0	25	5 PCT-US96-10082A-15	Sequence 15, Appl
7	23.8	95.2	25	3 US-09-296-280-43	Sequence 43, Appl
8	23.4	93.6	25	3 US-09-233-493-11	Sequence 11, Appl
9	23.4	93.6	25	3 US-09-233-493-16	Sequence 16, Appl
10	23.4	93.6	25	3 US-09-005-476-11	Sequence 11, Appl
11	23.4	93.6	25	3 US-09-005-476-16	Sequence 16, Appl
12	23.4	93.6	25	3 US-09-233-492-11	Sequence 11, Appl
13	23.4	93.6	25	3 US-09-233-492-16	Sequence 16, Appl
14	23.4	93.6	25	3 US-09-296-280-16	Sequence 16, Appl
15	23.4	93.6	25	4 US-09-498-074-11	Sequence 11, Appl
16	23.4	93.6	25	4 US-09-498-074-16	Sequence 16, Appl
17	23.4	93.6	25	5 PCT-US96-10082A-11	Sequence 11, Appl
18	23.4	93.6	25	5 PCT-US96-10082A-16	Sequence 16, Appl
19	22.4	89.6	25	3 US-09-233-493-9	Sequence 9, Appl
20	22.4	89.6	25	3 US-09-005-476-9	Sequence 9, Appl
21	22.4	89.6	25	3 US-09-233-492-9	Sequence 9, Appl
22	22.4	89.6	25	3 US-09-296-280-9	Sequence 9, Appl
23	22.4	89.6	25	4 US-09-498-074-9	Sequence 9, Appl
24	22.4	89.6	25	5 PCT-US96-10082A-9	Sequence 9, Appl
25	22	88.0	25	3 US-09-296-280-42	Sequence 42, Appl
26	21.8	87.2	201	1 US-08-021-667A-18	Sequence 18, Appl
27	21.8	87.2	201	1 US-08-410-544-18	Sequence 18, Appl

28	21.8	87.2	201	1 US-08-728-785A-18	Sequence 18, Appl
29	21.8	87.2	4909	3 US-08-556-978B-78	Sequence 78, Appl
30	21.8	87.2	7652	1 US-07-590-988A-1	Sequence 1, Appl
31	20.8	83.2	25	3 US-09-233-493-10	Sequence 10, Appl
32	20.8	83.2	25	3 US-09-005-476-10	Sequence 10, Appl
33	20.8	83.2	25	3 US-09-233-492-10	Sequence 10, Appl
34	20.8	83.2	25	3 US-09-296-280-10	Sequence 10, Appl
35	20.8	83.2	25	3 US-09-296-280-11	Sequence 10, Appl
36	20.8	83.2	25	4 US-09-498-074-10	Sequence 10, Appl
37	20.8	83.2	25	5 PCT-US96-10082A-10	Sequence 10, Appl
38	20.4	81.6	25	3 US-09-233-493-5	Sequence 5, Appl
39	20.4	81.6	25	3 US-09-233-493-12	Sequence 12, Appl
40	20.4	81.6	25	3 US-09-233-493-14	Sequence 14, Appl
41	20.4	81.6	25	3 US-09-005-476-5	Sequence 5, Appl
42	20.4	81.6	25	3 US-09-005-476-12	Sequence 12, Appl
43	20.4	81.6	25	3 US-09-005-476-14	Sequence 14, Appl
44	20.4	81.6	25	3 US-09-233-492-5	Sequence 5, Appl
45	20.4	81.6	25	3 US-09-233-492-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-09-233-493-15
; Sequence 15, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,493
; FILING DATE: 20-JAN-1993
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; US-09-233-493-15

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Query Match      100.0%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.077; 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 2
US-09-005-476-15
; Sequence 15, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2540
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-005-476-15

Query Match      100.0%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.077; 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 3
US-09-233-492-15
; Sequence 15, Application US/09233492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington

Query Match      100.0%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.077; 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

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US-09-296-280-15
; Sequence 15, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850007
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 15
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
; US-09-296-280-15

Query Match      100.0%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.077; 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;
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Best Local Similarity	89.0%	Pred. No.	0.24				
Matches	22	Conservative	3	Mismatches	0	Indels	0
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QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
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Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 8

US-09-233-493-11
; Sequence 11, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-233-493-11

Query Match 93.6%; Score 23.4; DB 3; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.34;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
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Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 9

US-09-233-493-16
; Sequence 16, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered

; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-233-493-16

Query Match 93.6%; Score 23.4; DB 3; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.34;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
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Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 10

US-09-005-476-11
; Sequence 11, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

[illegible]

	Conservative	Mismatches	Indels	Gaps
Matched	24	0	1	0
Mismatched	0	0	1	0
Indel	0	0	1	0
Gap	0	0	0	0

QY	1	G	T	C	A	C	T	T	T	T	T	T	T	G	T	A	C	A	A	G	T	T	G	25
Db	1	G	T	C	A	C	T	T	T	T	T	T	T	G	T	A	C	A	A	G	T	T	G	25

RESULT 15	
US-09-498-074-11	
; Sequence 11, Application US/09498074	
; Patent No. 6534264	
; GENERAL INFORMATION:	
; APPLICANT: Hartley, James L.	
; APPLICANT: Brasch, Michael A.	
; TITLE OF INVENTION: Recombinational Cloning Using Engineered	
; TITLE OF INVENTION: Recombination Sites	

NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,074
FILING DATE: (Herewith)
CLASSIFICATION:

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-498-074-11

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Query Match	93.6%	Score 23.4	DB 4	Length 25
Best Local Similarity	96.0%	Pred. No. 0.34		
Matches	24	Conservative	0	Mismatches 1; Indels
QY	1	GTTCAGCTTTTGTGTCAAAGTTGG	25	
ph	1	GTTCAGCTTTTGTGTCAAAGTTGG	25	

RESULT 16
US-09-498-074-16
; Sequence 16, Application US/09498074
; Patent No. 6534264
; GENERAL INFORMATION:
; APPLICANT: Hatley, James L.
; APPLICANT: Brasch, Michael A.

1. The first step is to identify the problem or question that needs to be answered. This involves understanding the context and the specific requirements of the task.

CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/09/233,492
APPLICATION NUMBER: US/09/233,492
FILING DATE: 20-JAN-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/563,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
US-09-233-492-16

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Query Match          93.6%; Score 23.4; DB 3; Length 25;
Best Local Similarity 96.0%; Pred. NO. 0.34;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  GTTCAGCTTTTTTGTACAAAGTTGG 25
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RESULT 14
US-09-296-280-16
; Sequence 16, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850007
; CURRENT APPLICATION NUMBER: US/09/296.280
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-296-280-16

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Query Match	93.6%	Score 23.4;	DB 3;	Length 25;
Best Local Similarity	96.0%	Pred. No. 0.34;		

1

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; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-498-074-16

Query Match 93.6%; Score 23.4; DB 4; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.34;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 17
PCT-US96-10082A-11
; Sequence 11, Application PC/TUS9610082A
; GENERAL INFORMATION:
; APPLICANT: Life Technologies, Inc.
; APPLICANT: 8717 Grovemont Circle
; APPLICANT: Gaithersburg, MD 20884-9980
; APPLICANT: United States of America
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10082A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10082A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; PCT-US96-10082A-16

Query Match 93.6%; Score 23.4; DB 5; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.34;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 18
PCT-US96-10082A-16
; Sequence 16, Application PC/TUS9610082A
; GENERAL INFORMATION:
; APPLICANT: Life Technologies, Inc.
; APPLICANT: 8717 Grovemont Circle
; APPLICANT: Gaithersburg, MD 20884-9980
; APPLICANT: United States of America
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10082A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; PCT-US96-10082A-16

Query Match 93.6%; Score 23.4; DB 5; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.34;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10082A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; PCT-US96-10082A-11

Query Match 93.6%; Score 23.4; DB 5; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.34;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 18
PCT-US96-10082A-16
; Sequence 16, Application PC/TUS9610082A
; GENERAL INFORMATION:
; APPLICANT: Life Technologies, Inc.
; APPLICANT: 8717 Grovemont Circle
; APPLICANT: Gaithersburg, MD 20884-9980
; APPLICANT: United States of America
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10082A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; PCT-US96-10082A-16

Query Match 93.6%; Score 23.4; DB 5; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.34;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25

```

```
Db 1 GTTCAGCTTTCTGTACAAAGTTG 25
|||||
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
TITLE OF INVENTION: Recombinational Cloning Using Engineered
RECOMBINATION SITES
NUMBER OF SEQUENCES: 35
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,476
FILING DATE: herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
US-09-005-476-9
Query Match 89.6%; Score 22.4; DB 3; Length 25;
Best Local Similarity 95.8%; Pred. No. 0.88;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAAGTTG 24
|||||
Db 1 GTTCAGCTTTCTGTACAAAGTTG 24
|||||

RESULT 21
US-09-233-492-9
; Sequence 9, Application US/09233492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; RECOMBINATION SITES
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,492
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 05/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; US-09-233-493-9
Query Match 89.6%; Score 22.4; DB 3; Length 25;
Best Local Similarity 95.8%; Pred. No. 0.88;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAAGTTG 24
|||||
Db 1 GTTCAGCTTTCTGTACAAAGTTG 24
|||||

RESULT 20
US-09-005-476-9
; Sequence 9, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; RECOMBINATION SITES
; NUMBER OF SEQUENCES: 35
```

```
;
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-233-492-9
;
; Query Match 89.6%; Score 22.4; DB 3; Length 25;
; Best Local Similarity 95.8%; Pred. No. 0.88;
; Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; Qy 1 GTTCAGCTTTTGTACAAAGTTG 24
; |||||
; Db 1 GTTCAGCTTTTGTACAAAGTTG 24
;
; RESULT 22
; US-09-296-280-9
; Sequence 9, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.285007
; CURRENT APPLICATION NUMBER: US/09/296.280
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177.387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065.930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; US-09-296-280-9
;
; Query Match 89.6%; Score 22.4; DB 3; Length 25;
; Best Local Similarity 95.8%; Pred. No. 0.88;
; Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; Qy 1 GTTCAGCTTTTGTACAAAGTTG 24
; |||||
; Db 1 GTTCAGCTTTTGTACAAAGTTG 24
;
; RESULT 23
; US-09-498-074-9
; Sequence 9, Application US/09498074
; Patent No. 6534264
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
```

```
;
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-498-074-9
;
; Query Match 89.6%; Score 22.4; DB 4; Length 25;
; Best Local Similarity 95.8%; Pred. No. 0.88;
; Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; Qy 1 GTTCAGCTTTTGTACAAAGTTG 24
; |||||
; Db 1 GTTCAGCTTTTGTACAAAGTTG 24
;
; RESULT 24
; PCT-US96-10082A-9
; Sequence 9, Application PC/TUS9610082A
; GENERAL INFORMATION:
; APPLICANT: Life Technologies, Inc.
; APPLICANT: 8717 Grovemont Circle
; APPLICANT: Gaithersburg, MD 20884-9980
; APPLICANT: United States of America
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10082A
; FILING DATE: 07-JUN-1996
```

```

; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
PCT-US96-10082A-9

Query Match      89.6%; Score 22.4; DB 5; Length 25;
Best Local Similarity 95.8%; Pred. No. 0.88;
Matches 23; Conservative 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTG 24
Db 1 GTTCAGCTTTTGTACAAAGTTG 24

RESULT 25
US-09-296-280-42
; Sequence 42, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850007
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-296-280-42

Query Match      88.0%; Score 22; DB 3; Length 25;
Best Local Similarity 79.2%; Pred. No. 1.3;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTG 24
Db 1 GTTCAGCTTTTGTACAAAGTTG 24

RESULT 26
US-08-021-667A-18
; Sequence 18, Application US/08021667A
; Patent No. 5434049
; GENERAL INFORMATION:
; APPLICANT: Okano, Kazunori
; APPLICANT: Kambara, Hideki
; TITLE OF INVENTION: POLYNUCLEOTIDE CAPTURING TIP AND
; TITLE OF INVENTION: POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION
; TITLE OF INVENTION: METHOD USING SAME
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Antonelli, Terry, Stout & Kraus

```

```

; STREET: Suite 600, 1919 Pennsylvania Ave., NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/021,667A
; FILING DATE: 19930224
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Terry, David T.
; REGISTRATION NUMBER: 20,178
; REFERENCE/DOCKET NUMBER: 520.31930X00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-828-0300
; TELEFAX: 202-828-0380
; TELEX: 440280/248545
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 201 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
US-08-021-667A-18

Query Match      87.2%; Score 21.8; DB 1; Length 201;
Best Local Similarity 92.0%; Pred. No. 1.7;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTG 25
Db 40 GTTCAGCTTTTGTACAAAGTTG 64

RESULT 27
US-08-410-544-18
; Sequence 18, Application US/08410544
; Patent No. 5607646
; GENERAL INFORMATION:
; APPLICANT: Okano, Kazunori
; APPLICANT: Kambara, Hideki
; TITLE OF INVENTION: POLYNUCLEOTIDE CAPTURING TIP AND
; TITLE OF INVENTION: POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION
; TITLE OF INVENTION: METHOD USING SAME
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Antonelli, Terry, Stout & Kraus
; STREET: Suite 600, 1919 Pennsylvania Ave., NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/410,544
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/021,667
; FILING DATE: 24-FEB-1993
; ATTORNEY/AGENT INFORMATION:

```

```
; NAME: Terry, David T.
; REGISTRATION NUMBER: 20,178
; REFERENCE/DOCKET NUMBER: 520.31930X00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-828-0300
; TELEFAX: 202-828-0380
; TELEX: 248545
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 201 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
US-08-410-544-18

Query Match      87.2%; Score 21.8; DB 1; Length 201;
Best Local Similarity 92.0%; Pred. No. 1.7;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
   |||||
Db 40 GTTCAGCTTTTATATACTAGTTGG 64

RESULT 28
US-08-728-785A-18
; Sequence 18, Application US/08728785A
; Patent No. 5817506
; GENERAL INFORMATION:
; APPLICANT: Okano, Kazunori
; APPLICANT: Kambara, Hideki
; TITLE OF INVENTION: POLYNUCLEOTIDE CAPTURING TIP AND
; TITLE OF INVENTION: POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION
; TITLE OF INVENTION: METHOD USING SAME
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Antoneilli, Terry, Stout & Kraus
; STREET: Suite 1800, 1300 No. 581/506th Seventeenth St.
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22209
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/728,785A
; FILING DATE: 10-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/410,544
; FILING DATE: 21-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/021,667
; FILING DATE: 24-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Terry, David T.
; REGISTRATION NUMBER: 20,178
; REFERENCE/DOCKET NUMBER: 520.31930X00
; TELEPHONE: 703-312-6600
; TELEFAX: 703-312-6666
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 201 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; NAME: Terry, David T.
; REGISTRATION NUMBER: 20,178
; REFERENCE/DOCKET NUMBER: 520.31930X00
; TELEPHONE: 703-312-6600
; TELEFAX: 703-312-6666
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 201 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
US-08-728-785A-18

Query Match      87.2%; Score 21.8; DB 1; Length 201;
Best Local Similarity 92.0%; Pred. No. 1.7;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
   |||||
Db 40 GTTCAGCTTTTATATACTAGTTGG 64

RESULT 29
US-08-556-978B-78/c
; Sequence 78, Application US/08556978B
; Patent No. 6268169
; GENERAL INFORMATION:
; APPLICANT: FARNESSTOCK, STEPHEN F.
; TITLE OF INVENTION: NOVEL RECOMBINANTLY PRODUCED
; TITLE OF INVENTION: SPIDER SILK ANALOGS
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINTON
; STATE: DELAWARE
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT WINDOWS 95
; SOFTWARE: MICROSOFT WORD FOR WINDOWS 95
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/556,978B
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,600
; FILING DATE: JUNE 15, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: FLOYD, LINDA AXAMETHY
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: CR-9389-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-892-8112
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4909 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
US-08-556-978B-78

Query Match      87.2%; Score 21.8; DB 3; Length 4909;
Best Local Similarity 92.0%; Pred. No. 2;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
   |||||
Db 2378 GTTCAGCTTTTATATACTAGTTGG 2354

RESULT 30
US-07-590-988A-1
; Sequence 1, Application US/07590988A
; Patent No. 5227288
; GENERAL INFORMATION:
; APPLICANT: Blattner, Frederick R.
```



```

/ CLASSIFICATION:
/ PRIOR APPLICATION DATA: 09/005,476
/ APPLICATION NUMBER: 09/005,476
/ FILING DATE: 12-JAN-1998
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA: 08/663,002
/ APPLICATION NUMBER: 08/663,002
/ FILING DATE: 07-JUN-1996
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA: 08/486,139
/ APPLICATION NUMBER: 08/486,139
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION:
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-371-2600
/ TELEFAX: 202-371-2540
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 25 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: both
/ TOPOLOGY: both
/ MOLECULE TYPE: CDNA
/ US-09-233-493-10
/
/ Query Match 83.2%; Score 20.8; DB 3; Length 25;
/ Best Local Similarity 91.7%; Pred. No. 4;
/ Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
/
QY 1 GTTCAGCTTTTGTGTACAAAGTTG 24
/ |||||
Db 1 GTTCAGCTTTTGTGTACAAAGTTG 24
/ |||||
/
RESULT 32
US-09-005-476-10
/ Sequence 10, Application US/09005476
/ Patent No. 6171861
/ GENERAL INFORMATION:
/ APPLICANT: Hartley, James L.
/ APPLICANT: Brasch, Michael A.
/ TITLE OF INVENTION: Recombinational Cloning Using Engineered
/ TITLE OF INVENTION: Recombination Sites
/ NUMBER OF SEQUENCES: 35
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: STERNE, KESSLER, GOLDBSTEIN & FOX, P.L.L.C.
/ STREET: 1100 New York Ave., N. W. Suite 600
/ CITY: Washington
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20005-3934
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/005,476
/ FILING DATE: herewith
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/663,002
/ FILING DATE: 07-JUN-1996
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-371-2600
/ TELEFAX: 202-371-2540
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 25 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: both
/ TOPOLOGY: both
/ MOLECULE TYPE: CDNA

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US-09-005-476-10

Query Match 83.2%; Score 20.8; DB 3; Length 25;
Best Local Similarity 91.7%; Pred. No. 4;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTCTGTACAAAGTTG 24
Db 1 GTTCAGCTTTCTGTACAAACTTG 24

RESULT 33
US-09-233-492-10
; Sequence 10, Application US/09233492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,492
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-233-492-10

Query Match 83.2%; Score 20.8; DB 3; Length 25;
Best Local Similarity 91.7%; Pred. No. 4;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTCTGTACAAAGTTG 24
Db 1 GTTCAGCTTTCTGTACAAACTTG 24

RESULT 34
US-09-296-280-10
; Sequence 10, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.

; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCES: 0942.2850007
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-296-280-10

Query Match 83.2%; Score 20.8; DB 3; Length 25;
Best Local Similarity 91.7%; Pred. No. 4;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTCTGTACAAAGTTG 24
Db 1 GTTCAGCTTTCTGTACAAACTTG 24

RESULT 35
US-09-296-280-11
; Sequence 11, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCES: 0942.2850007
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-296-280-11

Query Match 83.2%; Score 20.8; DB 3; Length 25;
Best Local Similarity 91.7%; Pred. No. 4;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTCTGTACAAAGTTG 24
Db 1 GTTCAGCTTTCTGTACAAACTTG 24

RESULT 36
US-09-498-074-10
; Sequence 10, Application US/09498074
; Patent No. 6534264

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; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Bransch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2540
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-498-074-10

Query Match 83.2%; Score 20.8; DB 4; Length 25;
Best Local Similarity 91.7%; Pred. No. 4;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTG 24
Db 1 GTTCAGCTTTTGTACAAAGTTG 24

RESULT 37
PCT-US96-10082A-10
; Sequence 10, Application PC/TUS9610082A
; GENERAL INFORMATION:
; APPLICANT: Life Technologies, Inc.
; APPLICANT: 8717 Grovemont Circle
; APPLICANT: Gaithersburg, MD 20884-9980
; APPLICANT: United States of America
; APPLICANT: Bransch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA

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; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10082A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; PCT-US96-10082A-10

Query Match 83.2%; Score 20.8; DB 5; Length 25;
Best Local Similarity 91.7%; Pred. No. 4;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTG 24
Db 1 GTTCAGCTTTTGTACAAAGTTG 24

RESULT 38
US-09-233-493-5
; Sequence 5, Application US/09233493
; Patent No. 6,143,557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Bransch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 5:

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Search completed: November 7, 2003, 00:22:53
Job time : 29 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 6, 2003, 22:12:53 ; Search time 28 Seconds

(without alignments)
394.092 Million cell updates/sec

Title: US-10-055-001A-11

Perfect score: 25

Sequence: 1 gttcagcttctgtacaaagtgg 25

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
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- 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	25	100.0	25	3	US-09-233-493-16
3	25	100.0	25	3	US-09-005-476-11
4	25	100.0	25	3	US-09-005-476-16
5	25	100.0	25	3	US-09-233-492-11
6	25	100.0	25	3	US-09-233-492-16
7	25	100.0	25	3	US-09-296-280-16
8	25	100.0	25	4	US-09-498-074-11
9	25	100.0	25	4	US-09-498-074-16
10	25	100.0	25	5	PCT-US96-10082A-11
11	25	100.0	25	5	PCT-US96-10082A-16
12	23.8	95.2	25	3	US-09-296-280-43
13	23.4	93.6	25	3	US-09-233-493-15
14	23.4	93.6	25	3	US-09-005-476-15
15	23.4	93.6	25	3	US-09-233-492-15
16	23.4	93.6	25	3	US-09-296-280-15
17	23.4	93.6	25	4	US-09-498-074-15
18	23.4	93.6	25	5	PCT-US96-10082A-15
19	22.4	89.6	25	3	US-09-233-493-10
20	22.4	89.6	25	3	US-09-005-476-10
21	22.4	89.6	25	3	US-09-233-492-10
22	22.4	89.6	25	3	US-09-296-280-10
23	22.4	89.6	25	3	US-09-236-280-11
24	22.4	89.6	25	4	US-09-498-074-10
25	22.4	89.6	25	5	PCT-US96-10082A-10
26	22	88.0	25	3	US-09-233-493-14
27	22	88.0	25	3	US-09-005-476-14

28	22	88.0	25	3	US-09-233-492-14	Sequence 14, Appl
29	22	88.0	25	3	US-09-296-280-14	Sequence 14, Appl
30	22	88.0	25	3	US-09-296-280-42	Sequence 42, Appl
31	22	88.0	25	4	US-09-498-074-14	Sequence 14, Appl
32	22	88.0	25	5	PCT-US96-10082A-14	Sequence 14, Appl
33	20.8	83.2	25	3	US-09-233-493-9	Sequence 9, Appl
34	20.8	83.2	25	3	US-09-005-476-9	Sequence 9, Appl
35	20.8	83.2	25	3	US-09-233-492-9	Sequence 9, Appl
36	20.8	83.2	25	3	US-09-296-280-9	Sequence 9, Appl
37	20.8	83.2	25	4	US-09-498-074-9	Sequence 9, Appl
38	20.8	83.2	25	5	PCT-US96-10082A-9	Sequence 9, Appl
39	20.4	81.6	25	3	US-09-233-493-5	Sequence 5, Appl
40	20.4	81.6	25	3	US-09-233-493-13	Sequence 13, Appl
41	20.4	81.6	25	3	US-09-005-476-5	Sequence 5, Appl
42	20.4	81.6	25	3	US-09-005-476-13	Sequence 13, Appl
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44	20.4	81.6	25	3	US-09-233-492-13	Sequence 13, Appl
45	20.4	81.6	25	3	US-09-296-280-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1

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US-09-233-493-11
; Sequence 11, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-233-493-11

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us-10-055-001a-11.rni

Fri Nov 7 08:08:38 2003

; FILING DATE: 07-JUN-1996
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-371-2600
 ; TELEFAX: 202-371-2540
 ; INFORMATION FOR SEQ ID NO: 16:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 25 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: both
 ; MOLECULE TYPE: cdna
 ; US-09-005-476-16

Query Match 100.0%; Score 25; DB 3; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.015;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTTGTACAAAGTTGG 25
 Db 1 GTTCAGCTTCTTGTACAAAGTTGG 25

RESULT 5
 US-09-233-492-11
 ; Sequence 11, Application US/09233492
 ; Patent No. 6270969
 ; GENERAL INFORMATION:
 ; APPLICANT: Hartley, James L.
 ; APPLICANT: Brasch, Michael A.
 ; TITLE OF INVENTION: Recombinational Cloning Using Engineered
 ; TITLE OF INVENTION: Recombination Sites
 ; NUMBER OF SEQUENCES: 35
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
 ; STREET: 1100 New York Ave., N. W. Suite 600
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005-3934
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/233,492
 ; FILING DATE: 20-JAN-1999
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/663,002
 ; FILING DATE: 07-JUN-1996
 ; CLASSIFICATION:
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-371-2600
 ; TELEFAX: 202-371-2540
 ; INFORMATION FOR SEQ ID NO: 11:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 25 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: both
 ; MOLECULE TYPE: cdna
 ; US-09-233-492-11

Query Match 100.0%; Score 25; DB 3; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.015;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTTGTACAAAGTTGG 25

Db 1 GTTCAGCTTCTTGTACAAAGTTGG 25

RESULT 6
 US-09-233-492-16
 ; Sequence 16, Application US/09233492
 ; Patent No. 6270969
 ; GENERAL INFORMATION:
 ; APPLICANT: Hartley, James L.
 ; APPLICANT: Brasch, Michael A.
 ; TITLE OF INVENTION: Recombinational Cloning Using Engineered
 ; TITLE OF INVENTION: Recombination Sites
 ; NUMBER OF SEQUENCES: 35
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
 ; STREET: 1100 New York Ave., N. W. Suite 600
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005-3934
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/233,492
 ; FILING DATE: 20-JAN-1999
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/663,002
 ; FILING DATE: 07-JUN-1996
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/486,139
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION:
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-371-2600
 ; TELEFAX: 202-371-2540
 ; INFORMATION FOR SEQ ID NO: 16:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 25 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: both
 ; MOLECULE TYPE: cdna
 ; US-09-233-492-16

Query Match 100.0%; Score 25; DB 3; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.015;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTTGTACAAAGTTGG 25
 Db 1 GTTCAGCTTCTTGTACAAAGTTGG 25

RESULT 7
 US-09-296-280-16
 ; Sequence 16, Application US/09296280
 ; Patent No. 6277608
 ; GENERAL INFORMATION:
 ; APPLICANT: Hartley, James L.
 ; APPLICANT: Brasch, Michael A.
 ; APPLICANT: Temple, Gary F.
 ; APPLICANT: Fox, Donna K.
 ; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
 ; TITLE OF INVENTION: Recombination Sites
 ; FILE REFERENCE: 0942.2850007
 ; CURRENT APPLICATION NUMBER: US/09/296,280
 ; CURRENT FILING DATE: 1999-04-22

EARLIER APPLICATION NUMBER: US 09/177,387
EARLIER FILING DATE: 1998-10-23
EARLIER APPLICATION NUMBER: US 60/065,930
EARLIER FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 16
LENGTH: 25
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: recombination
OTHER INFORMATION: products
US-09-296-280-16

Query Match 100.0%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.015; 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGTCACAAAGTTGG 25
|||||
Db 1 GTTCAGCTTTCTTGTCACAAAGTTGG 25

RESULT 8
US-09-498-074-11
Sequence 11, Application US/09498074
Patent No. 6534264
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,074
FILING DATE: (Herewith)
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION:
TELEPHONE: 202-371-2540
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
US-09-498-074-11

Query Match 100.0%; Score 25; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.015; 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTCTTGTCACAAAGTTGG 25
|||||
Db 1 GTTCAGCTTTCTTGTCACAAAGTTGG 25

RESULT 9
US-09-498-074-16
Sequence 16, Application US/09498074
Patent No. 6534264
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,074
FILING DATE: (Herewith)
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
US-09-498-074-16

Query Match 100.0%; Score 25; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.015; 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTCTTGTCACAAAGTTGG 25
|||||
Db 1 GTTCAGCTTTCTTGTCACAAAGTTGG 25

RESULT 10
PCT-US96-10082A-11
Sequence 11, Application PC/TUS9610082A
GENERAL INFORMATION:

APPLICANT: Life Technologies, Inc.
APPLICANT: 8717 Grovemont Circle
APPLICANT: Gaithersburg, MD 20884-9980
APPLICANT: United States of America
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10082A
FILING DATE: 07-JUN-1996
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
PCT-US96-10082A-11

Query Match 100.0%; Score 25; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTCACAAAGTTGG 25
|||||
DB 1 GTTCAGCTTCTTGTCACAAAGTTGG 25

RESULT 11
PCT-US96-10082A-16
Sequence 16, Application PC/TUS9610082A
GENERAL INFORMATION:
APPLICANT: Life Technologies, Inc.
APPLICANT: 8717 Grovemont Circle
APPLICANT: Gaithersburg, MD 20884-9980
APPLICANT: United States of America
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10082A
FILING DATE: 07-JUN-1996
CLASSIFICATION:

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
PCT-US96-10082A-16

Query Match 100.0%; Score 25; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTCACAAAGTTGG 25
|||||
DB 1 GTTCAGCTTCTTGTCACAAAGTTGG 25

RESULT 12
US-09-296-280-43
Sequence 43, Application US/09296280
Patent No. 6277608
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
APPLICANT: Temple, Gary F.
APPLICANT: Fox, Donna K.
TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
TITLE OF INVENTION: Recombination Sites
FILE REFERENCE: 0942.2850007
CURRENT APPLICATION NUMBER: US/09/296.280
CURRENT FILING DATE: 1999-04-22
EARLIER APPLICATION NUMBER: US 09/177,387
EARLIER FILING DATE: 1998-10-23
EARLIER APPLICATION NUMBER: US 60/065,930
EARLIER FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn ver. 2.0
SEQ ID NO 43
LENGTH: 25
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: recombination
OTHER INFORMATION: products
US-09-296-280-43

Query Match 95.2%; Score 23.8; DB 3; Length 25;
Best Local Similarity 88.0%; Pred. No. 0.051;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTCACAAAGTTGG 25
|||||
DB 1 GTTCAGCTTCTTGTCACAAAGTTGG 25

RESULT 13
US-09-233-493-15
Sequence 15, Application US/09233493
Patent No. 6143557
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington

```

FILING DATE: 07-JUN-1996
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdNA
US-09-005-476-15

Query Match 93.6%; Score 23.4; DB 3; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.077; 1; Indels 0;
Matches 24; Conservative 0; Mismatches 1; Indels 0;

1 GTTCAGCTTTCTTTGTACAAAGTTGG 25
1 GTTCAGCTTTTTTGTACAAAGTTGG 25

DB

RESULT 15
US-09-233-492-15
Sequence 15, Application US/09233492
Patent No. 6270969
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESSES:
ADDRESS: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,492
FILING DATE: 20-JAN-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdNA
US-09-233-492-15

Query Match 93.6%; Score 23.4; DB 3; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.077; 1; Indels
Matches 24; Conservative 0; Mismatches 1; Indels

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QY
1 GTTCAGCTTTCTTGTACAAAGTTGG 25

Db 1 GTTCAGCTTTTGTACAAAGTTG 25

RESULT 19
US-09-233-493-10
; Sequence 10, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-233-493-10

Query Match 89.6%; Score 22.4; DB 3; Length 25;
Best Local Similarity 95.8%; Pred. No. 0.22;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTG 24
Db 1 GTTCAGCTTTTGTACAAAGTTG 24

RESULT 20
US-09-005-476-10
; Sequence 10, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-005-476-10

Query Match 89.6%; Score 22.4; DB 3; Length 25;
Best Local Similarity 95.8%; Pred. No. 0.22;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTG 24
Db 1 GTTCAGCTTTTGTACAAAGTTG 24

RESULT 21
US-09-233-492-10
; Sequence 10, Application US/09233492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,492
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995

us-10-055-001a-11.rni

Fri Nov 7 08:08:38 2003

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;
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; US-09-233-492-10
;
; Query Match      89.6%; Score 22.4; DB 3; Length 25;
; Best Local Similarity 95.8%; Pred. No. 0.22;
; Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 1 GTTCAGCTTCTTGACAAAGTTG 24
;    |||||||||||||||||||||
; Db 1 GTTCAGCTTCTTGACAAACTTG 24
;
; RESULT 22
; US-09-296-280-10
; Sequence 10, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.285007
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; NUMBER OF SEQ ID NOS: 60
; SEQUENCE: PatentIn Ver. 2.0
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
; US-09-296-280-10
;
; Query Match      89.6%; Score 22.4; DB 3; Length 25;
; Best Local Similarity 95.8%; Pred. No. 0.22;
; Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 1 GTTCAGCTTCTTGACAAAGTTG 24
;    |||||||||||||||||||||
; Db 1 GTTCAGCTTCTTGACAAACTTG 24
;
; RESULT 24
; US-09-498-074-10
; Sequence 10, Application US/09498074
; Patent No. 6534264
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/498,074
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
;
; US-10-055-001a-11.rni
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US-09-498-074-10
Query Match      89.6%; Score 22.4; DB 4; Length 25;
Best Local Similarity 95.8%; Pred. No. 0.22;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTTACAAAGTTG 24
    |||||
Db 1 GTTCAGCTTCTTGTTACAAAGTTG 24

RESULT 25
PCT-US96-10082A-10
; Sequence 10, Application PC/TUS9610082A
; GENERAL INFORMATION:
; APPLICANT: Life Technologies, Inc.
; APPLICANT: 8717 Grovemont Circle
; APPLICANT: Gaithersburg, MD 20884-9980
; APPLICANT: United States of America
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10082A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; PCT-US96-10082A-10

Query Match      89.6%; Score 22.4; DB 5; Length 25;
Best Local Similarity 95.8%; Pred. No. 0.22;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTTACAAAGTTG 24
    |||||
Db 1 GTTCAGCTTCTTGTTACAAAGTTG 24

RESULT 26
US-09-233-493-14
; Sequence 14, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
```

```
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA: 09/005,476
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-233-493-14

Query Match      88.0%; Score 22; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTTCTTGTTACAAAGTTG 25
    |||||
Db 4 CAGCTTTCTTGTTACAAAGTTG 25

RESULT 27
US-09-005-476-14
; Sequence 14, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
```

APPLICATION NUMBER: 08/663,002
 FILING DATE: 07-JUN-1996
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2600
 TELEFAX: 202-371-2540
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 25 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: both
 MOLECULE TYPE: cDNA
 US-09-005-476-14

Query Match 88.0%; Score 22; DB 3; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.33;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTCTTGTACAAAGTTGG 25
 |||||
 Db 4 CAGCTTCTTGTACAAAGTTGG 25

RESULT 28

US-09-233-492-14
 ; Sequence 14, Application US/09233492
 ; Patent No. 6270969
 ; GENERAL INFORMATION:
 ; APPLICANT: Hartley, James L.
 ; APPLICANT: Brasch, Michael A.
 ; TITLE OF INVENTION: Recombinational Cloning Using Engineered
 ; TITLE OF INVENTION: Recombination Sites
 ; NUMBER OF SEQUENCES: 35
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C
 ; STREET: 1100 New York Ave., N. W. Suite 600
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005-3934
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/233,492
 ; FILING DATE: 20-JAN-1999
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/663,002
 ; FILING DATE: 07-JUN-1996
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/486,139
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION:
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-371-2600
 ; TELEFAX: 202-371-2540
 ; INFORMATION FOR SEQ ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 25 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: both
 ; MOLECULE TYPE: cDNA
 ; US-09-233-492-14

Query Match 88.0%; Score 22; DB 3; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.33;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTCTTGTACAAAGTTGG 25
 |||||
 Db 4 CAGCTTCTTGTACAAAGTTGG 25

RESULT 29

US-09-296-280-14
 ; Sequence 14, Application US/09296280
 ; Patent No. 6277608
 ; GENERAL INFORMATION:
 ; APPLICANT: Hartley, James L.
 ; APPLICANT: Brasch, Michael A.
 ; APPLICANT: Temple, Gary F.
 ; APPLICANT: Fox, Donna K.
 ; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
 ; TITLE OF INVENTION: Recombination Sites
 ; FILE REFERENCE: 0942.2850007
 ; CURRENT APPLICATION NUMBER: US/09/296,280
 ; CURRENT FILING DATE: 1999-04-22
 ; EARLIER APPLICATION NUMBER: US 09/177,387
 ; EARLIER FILING DATE: 1998-10-23
 ; EARLIER APPLICATION NUMBER: US 60/065,930
 ; EARLIER FILING DATE: 1997-10-24
 ; NUMBER OF SEQ ID NOS: 60
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 14
 ; TYPE: DNA
 ; LENGTH: 25
 ; ORGANISM: Unknown
 ; FEATURE:
 ; OTHER INFORMATION: Description of Unknown Organism: recombination
 ; OTHER INFORMATION: products
 ; OTHER INFORMATION: products
 ; US-09-296-280-14

Query Match 88.0%; Score 22; DB 3; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.33;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTCTTGTACAAAGTTGG 25
 |||||
 Db 4 CAGCTTCTTGTACAAAGTTGG 25

RESULT 30

US-09-296-280-42
 ; Sequence 42, Application US/09296280
 ; Patent No. 6277608
 ; GENERAL INFORMATION:
 ; APPLICANT: Hartley, James L.
 ; APPLICANT: Brasch, Michael A.
 ; APPLICANT: Temple, Gary F.
 ; APPLICANT: Fox, Donna K.
 ; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
 ; TITLE OF INVENTION: Recombination Sites
 ; FILE REFERENCE: 0942.2850007
 ; CURRENT APPLICATION NUMBER: US/09/296,280
 ; CURRENT FILING DATE: 1999-04-22
 ; EARLIER APPLICATION NUMBER: US 09/177,387
 ; EARLIER FILING DATE: 1998-10-23
 ; EARLIER APPLICATION NUMBER: US 60/065,930
 ; EARLIER FILING DATE: 1997-10-24
 ; NUMBER OF SEQ ID NOS: 60
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 42
 ; TYPE: DNA
 ; LENGTH: 25
 ; ORGANISM: Unknown
 ; FEATURE:
 ; OTHER INFORMATION: Description of Unknown Organism: recombination
 ; OTHER INFORMATION: products
 ; OTHER INFORMATION: products
 ; US-09-296-280-42

Query Match 88.0%; Score 22; DB 3; Length 25;

Best Local Similarity 79.2%; Pred. No. 0.33; Indels 0; Gaps 0;
Matches 19; Conservative 5; Mismatches 0;

Qy 1 GTTCAGCTTCTGTACAAAGTTG 24
Db 1 GTTCAGCTTCTGTACAAAGTTG 24

RESULT 31
US-09-498-074-14
; Sequence 14, Application US/09498074
; Patent No. 6534264
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-498-074-14

Query Match 88.0%; Score 22; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CAGCTTCTGTACAAAGTTG 25
Db 4 CAGCTTCTGTACAAAGTTG 25

RESULT 32
PCT-US96-10082A-14
; Sequence 14, Application PC/TUS9610082A
; GENERAL INFORMATION:
; APPLICANT: Life Technologies, Inc.
; APPLICANT: 8717 Grovemont Circle

; APPLICANT: Gaithersburg, MD 20884-9980
; APPLICANT: United States Of America
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10082A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; PCT-US96-10082A-14

Query Match 88.0%; Score 22; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CAGCTTCTGTACAAAGTTG 25
Db 4 CAGCTTCTGTACAAAGTTG 25

RESULT 33
US-09-233-493-9
; Sequence 9, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:

;; PRIOR APPLICATION DATA: 83.2%; Score 20.8; DB 3; Length 25;
;; APPLICATION NUMBER: 08/663,002
;; FILING DATE: 07-JUN-1996
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA: 08/486,139
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION:
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-2600
;; TELEFAX: 202-371-2540
;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 25 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: both
;; TOPOLOGY: both
;; MOLECULE TYPE: cdna
US-09-233-493-9

Query Match 83.2%; Score 20.8; DB 3; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.1;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAAGTTG 24
Db 1 GTTCAGCTTTTGTACAAACTTG 24

RESULT 34
US-09-005-476-9
; Sequence 9, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-005-476-9

QY 1 GTTCAGCTTTCTGTACAAAGTTG 24
Db 1 GTTCAGCTTTTGTACAAACTTG 24

RESULT 35
US-09-233-492-9
; Sequence 9, Application US/09233492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,492
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-233-492-9

Query Match 83.2%; Score 20.8; DB 3; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.1;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAAGTTG 24
Db 1 GTTCAGCTTTTGTACAAACTTG 24

RESULT 36
US-09-296-280-9
; Sequence 9, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850007

;; CURRENT APPLICATION NUMBER: US/09/296,280
;; CURRENT FILING DATE: 1998-04-22
;; EARLIER APPLICATION NUMBER: US 09/177,387
;; EARLIER FILING DATE: 1998-10-23
;; EARLIER APPLICATION NUMBER: US 60/065,930
;; EARLIER FILING DATE: 1997-10-24
;; NUMBER OF SEQ ID NOS: 60
;; SOFTWARE: Patent In Ver. 2.0
;; SEQ ID NO 9
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Unknown
;; FEATURE:
;; OTHER INFORMATION: Description of Unknown Organism: recombination
;; OTHER INFORMATION: products
US-09-296-280-9

Query Match 83.2%; Score 20.8; DB 3; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.1;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAAGTTG 24
|||
DB 1 GTTCAGCTTTCTGTACAAACTTG 24

RESULT 37
US-09-498-074-9
; Sequence 9, Application US/09498074
; Patent No. 6534264
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both

;; MOLECULE TYPE: CDNA
US-09-498-074-9
Query Match 83.2%; Score 20.8; DB 4; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.1;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAAGTTG 24
|||
DB 1 GTTCAGCTTTCTGTACAAACTTG 24

RESULT 38
PCT-US96-10082A-9
; Sequence 9, Application PC/TUS9610082A
; GENERAL INFORMATION:
; APPLICANT: Life Technologies, Inc.
; APPLICANT: 8717 Grovemont Circle
; APPLICANT: Gaithersburg, MD 20884-9980
; APPLICANT: United States of America
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10082A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
PCT-US96-10082A-9

Query Match 83.2%; Score 20.8; DB 5; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.1;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAAGTTG 24
|||
DB 1 GTTCAGCTTTCTGTACAAACTTG 24

RESULT 39
US-09-233-493-5
; Sequence 5, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C

```

; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; US-09-233-493-5

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Query Match      81.6%; Score 20.4; DB 3; Length 25;
Best Local Similarity 76.0%; Pred. No. 1.7;
Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

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Qy 1 GTTCAGCTTTCTTGTCACAAAGTTGG 25
Db 1 GTTCAGCTTTCTTGTCACAAAGTTGG 25

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RESULT 40
US-09-233-493-13
; Sequence 13, Application US/09233493
; Patent No. 6,435,57
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; US-09-233-493-13

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```

Query Match      81.6%; Score 20.4; DB 3; Length 25;
Best Local Similarity 95.5%; Pred. No. 1.7;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 4 CAGCTTTCTTGTCACAAAGTTGG 25
Db 4 CTGCTTTCTTGTCACAAAGTTGG 25

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Search completed: November 7, 2003, 00:22:53
Job time : 28 secs

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OM nucleic - nucleic search, using sw model

Run on: November 6, 2003, 22:12:53 ; Search time 28 Seconds
(without alignments)
394.092 Million cell updates/sec

Title: US-10-055-001A-5

Perfect score: 25

Sequence: 1 gttcagctttctgtacaaactgt 25

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: /cgn2_6/ptodata/1/ina/5A.COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTCUS.COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	25	3	US-09-233-493-10
2	25	100.0	25	3	US-09-005-476-10
3	25	100.0	25	3	US-09-233-492-10
4	25	100.0	25	3	US-09-296-280-10
5	25	100.0	25	4	US-09-498-074-10
6	25	100.0	25	5	PCT-US96-10082A-10
7	23.4	93.6	25	3	US-09-233-493-9
8	23.4	93.6	25	3	US-09-005-476-9
9	23.4	93.6	25	3	US-09-233-492-9
10	23.4	93.6	25	3	US-09-296-280-9
11	23.4	93.6	25	4	US-09-498-074-9
12	23.4	93.6	25	5	PCT-US96-10082A-9
13	22.6	90.4	25	3	US-09-296-280-42
14	22.4	89.6	25	3	US-09-233-493-11
15	22.4	89.6	25	3	US-09-233-493-16
16	22.4	89.6	25	3	US-09-005-476-11
17	22.4	89.6	25	3	US-09-005-476-16
18	22.4	89.6	25	3	US-09-233-492-11
19	22.4	89.6	25	3	US-09-233-492-16
20	22.4	89.6	25	3	US-09-296-280-16
21	22.4	89.6	25	4	US-09-498-074-11
22	22.4	89.6	25	4	US-09-498-074-16
23	22.4	89.6	25	5	PCT-US96-10082A-11
24	22.4	89.6	25	5	PCT-US96-10082A-16
25	22	88.0	25	3	US-09-233-493-8
26	22	88.0	25	3	US-09-005-476-8
27	22	88.0	25	3	US-09-233-492-8

28	22	88.0	25	4	US-09-498-074-8	Sequence 8, Appli
29	22	88.0	25	5	PCT-US96-10082A-8	Sequence 8, Appli
30	21.8	87.2	25	3	US-09-296-280-11	Sequence 11, Appl
31	21.2	84.8	25	3	US-09-296-280-43	Sequence 43, Appl
32	20.8	83.2	25	3	US-09-233-493-3	Sequence 3, Appli
33	20.8	83.2	25	3	US-09-233-493-15	Sequence 15, Appl
34	20.8	83.2	25	3	US-09-005-476-3	Sequence 3, Appli
35	20.8	83.2	25	3	US-09-005-476-15	Sequence 15, Appl
36	20.8	83.2	25	3	US-09-233-492-3	Sequence 3, Appli
37	20.8	83.2	25	3	US-09-233-492-15	Sequence 15, Appl
38	20.8	83.2	25	3	US-09-296-280-3	Sequence 3, Appli
39	20.8	83.2	25	3	US-09-296-280-15	Sequence 15, Appl
40	20.8	83.2	25	4	US-09-498-074-3	Sequence 3, Appli
41	20.8	83.2	25	4	US-09-498-074-15	Sequence 15, Appl
42	20.8	83.2	25	5	PCT-US96-10082A-3	Sequence 3, Appli
43	20.8	83.2	25	5	PCT-US96-10082A-15	Sequence 15, Appl
44	20.4	81.6	25	3	US-09-233-493-7	Sequence 7, Appli
45	20.4	81.6	25	3	US-09-233-493-34	Sequence 34, Appli

ALIGNMENTS

RESULT 1
US-09-233-493-10
; Sequence 10, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; US-09-233-493-10

Query Match 100.0%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTTACAAACTTGT 25
DB 1 GTTCAGCTTCTTGTTACAAACTTGT 25

RESULT 2

US-09-005-476-10
; Sequence 10, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2540
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-005-476-10

Query Match 100.0%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTTACAAACTTGT 25
DB 1 GTTCAGCTTCTTGTTACAAACTTGT 25

RESULT 3

US-09-233-492-10
; Sequence 10, Application US/09233492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington

STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,492
FILING DATE: 20-JAN-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
US-09-233-492-10

Query Match 100.0%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTTACAAACTTGT 25
DB 1 GTTCAGCTTCTTGTTACAAACTTGT 25

RESULT 4

US-09-296-280-10
; Sequence 10, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942 2850007
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-296-280-10

Query Match 100.0%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGACAACTTGT 25
Db 1 GTTCAGCTTCTTGACAACTTGT 25

RESULT 5

US-09-498-074-10
; Sequence 10, Application US/09498074
; Patent No. 6534264
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-498-074-10
Query Match 100.0%; Score 25; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGACAACTTGT 25
Db 1 GTTCAGCTTCTTGACAACTTGT 25

RESULT 6

PCT-US96-10082A-10
; Sequence 10, Application PC/TUS9610082A
; GENERAL INFORMATION:
; APPLICANT: Life Technologies, Inc.
; APPLICANT: 8717 Grovemont Circle
; APPLICANT: Gaithersburg, MD 20884-9980
; APPLICANT: United States of America

; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10082A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
PCT-US96-10082A-10

Query Match 100.0%; Score 25; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGACAACTTGT 25
Db 1 GTTCAGCTTCTTGACAACTTGT 25

RESULT 7

US-09-233-493-9
; Sequence 9, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002

1 GTTCAGCTTCTTGTA^ACAACTGT 25

;; EARLIER APPLICATION NUMBER: US 09/177,387
;; EARLIER FILING DATE: 1998-10-23
;; EARLIER APPLICATION NUMBER: US 60/065,930
;; EARLIER FILING DATE: 1997-10-24
;; NUMBER OF SEQ ID NOS: 60
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 9
;; TYPE: DNA
;; LENGTH: 25
;; ORGANISM: Unknown
;; FEATURE:
;; OTHER INFORMATION: Description of Unknown Organism: recombination
;; OTHER INFORMATION: products
US-09-296-280-9

Query Match 93.6%; Score 23.4; DB 3; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.065;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTTGTACAAACTTGT 25
|||||
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 11
US-09-498-074-9
; Sequence 9, Application US/09498074
; Patent No. 6534264
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/563,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-498-074-9

Query Match 93.6%; Score 23.4; DB 4; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.065;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTCTTTGTACAAACTTGT 25
|||||
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 12
PCT-US96-10082A-9
; Sequence 9, Application PC/TUS9610082A
; GENERAL INFORMATION:
; APPLICANT: Life Technologies, Inc.
; APPLICANT: 8717 Grovemont Circle
; APPLICANT: Gaithersburg, MD 20884-9980
; APPLICANT: United States of America
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10082A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
PCT-US96-10082A-9

Query Match 93.6%; Score 23.4; DB 5; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.065;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTCTTTGTACAAACTTGT 25
|||||
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 13
US-09-296-280-42
; Sequence 42, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850007
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22

; EARLIER APPLICATION NUMBER: US 09/177,387
 ; EARLIER FILING DATE: 1998-10-23
 ; EARLIER APPLICATION NUMBER: US 60/065,930
 ; EARLIER FILING DATE: 1997-10-24
 ; NUMBER OF SEQ ID NOS: 60
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 42
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Unknown
 ; FEATURE:
 ; OTHER INFORMATION: Description of Unknown Organism: recombination
 ; OTHER INFORMATION: products
 US-09-296-280-42

Query Match 90.4%; Score 22.6; DB 3; Length 25;
 Best Local Similarity 76.0%; Pred. No. 0.15;
 Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTACAACTTGT 25
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 Db 1 GTTCAGCTTCTTGTACAACTTGT 25

RESULT 14
 US-09-233-493-11
 ; Sequence 11, Application US/092333493
 ; Patent No. 6143557
 ; GENERAL INFORMATION:
 ; APPLICANT: Hartley, James L.
 ; APPLICANT: Brasch, Michael A.
 ; TITLE OF INVENTION: Recombinational Cloning Using Engineered
 ; TITLE OF INVENTION: Recombination Sites
 ; NUMBER OF SEQUENCES: 35
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
 ; STREET: 1100 New York Ave., N. W. Suite 600
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005-3934
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/233,493
 ; FILING DATE: 20-JAN-1999
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/005,476
 ; FILING DATE: 12-JAN-1998
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/663,002
 ; FILING DATE: 07-JUN-1996
 ; CLASSIFICATION:
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-371-2600
 ; TELEFAX: 202-371-2540
 ; INFORMATION FOR SEQ ID NO: 11:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 25 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: both
 ; MOLECULE TYPE: cdna
 US-09-233-493-11

Query Match 89.6%; Score 22.4; DB 3; Length 25;
 Best Local Similarity 95.8%; Pred. No. 0.18;
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTACAACTTGT 24
 |||||
 Db 1 GTTCAGCTTCTTGTACAACTTGT 24

Query Match 89.6%; Score 22.4; DB 3; Length 25;
 Best Local Similarity 95.8%; Pred. No. 0.18;
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTACAACTTGT 24
 |||||
 Db 1 GTTCAGCTTCTTGTACAACTTGT 24

RESULT 15
 US-09-233-493-16
 ; Sequence 16, Application US/092333493
 ; Patent No. 6143557
 ; GENERAL INFORMATION:
 ; APPLICANT: Hartley, James L.
 ; APPLICANT: Brasch, Michael A.
 ; TITLE OF INVENTION: Recombinational Cloning Using Engineered
 ; TITLE OF INVENTION: Recombination Sites
 ; NUMBER OF SEQUENCES: 35
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
 ; STREET: 1100 New York Ave., N. W. Suite 600
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005-3934
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/233,493
 ; FILING DATE: 20-JAN-1999
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/005,476
 ; FILING DATE: 12-JAN-1998
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/663,002
 ; FILING DATE: 07-JUN-1996
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/486,139
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION:
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-371-2600
 ; TELEFAX: 202-371-2540
 ; INFORMATION FOR SEQ ID NO: 16:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 25 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: both
 ; MOLECULE TYPE: cdna
 US-09-233-493-16

Query Match 89.6%; Score 22.4; DB 3; Length 25;
 Best Local Similarity 95.8%; Pred. No. 0.18;
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTACAACTTGT 24
 |||||
 Db 1 GTTCAGCTTCTTGTACAACTTGT 24

RESULT 16
 US-09-005-476-11
 ; Sequence 11, Application US/09005476
 ; Patent No. 6171861

GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Bransch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,476
FILING DATE: herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
US-09-005-476-11

Query Match 89.6%; Score 22.4; DB 3; Length 25;
Best Local Similarity 95.8%; Pred. No. 0.18;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGTAACAATTG 24
|||||
DB 1 GTTCAGCTTTCTTGTAACAATTG 24

RESULT 17
US-09-005-476-16
Sequence 16, Application US/09005476
Patent No. 6171961
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Bransch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,476
FILING DATE: herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
US-09-005-476-16

Query Match 89.6%; Score 22.4; DB 3; Length 25;
Best Local Similarity 95.8%; Pred. No. 0.18;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGTAACAATTG 24
|||||
DB 1 GTTCAGCTTTCTTGTAACAATTG 24

RESULT 18
US-09-233-492-11
Sequence 11, Application US/09233492
Patent No. 6270969
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Bransch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,492
FILING DATE: 20-JAN-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
US-09-233-492-11

Query Match 89.6%; Score 22.4; DB 3; Length 25;
Best Local Similarity 95.8%; Pred. No. 0.18;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 GTTCAGCTTTCTGTACAAACTTG 24
| | | | | | | | | | | | | | | | | |
Db 1 GTTCAGCTTTCTGTACAAACTTG 24

RESULT 19
US-09-233-492-16
; Sequence 16, Application US/09233492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,492
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-233-492-16

Query Match 89.6%; Score 22.4; DB 3; Length 25;
Best Local Similarity 95.8%; Pred. No. 0.18;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAACTTG 24
| | | | | | | | | | | | | | | | | |
Db 1 GTTCAGCTTTCTGTACAAACTTG 24

RESULT 20
US-09-296-280-16
; Sequence 16, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850007
; CURRENT APPLICATION NUMBER: US/09/296,280
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; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 16
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-296-280-16

Query Match 89.6%; Score 22.4; DB 3; Length 25;
Best Local Similarity 95.8%; Pred. No. 0.18;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAACTTG 24
| | | | | | | | | | | | | | | | | |
Db 1 GTTCAGCTTTCTGTACAAACTTG 24

RESULT 21
US-09-498-074-11
; Sequence 11, Application US/09498074
; Patent No. 6534264
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
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US-09-498-074-11
Query Match      89.6%; Score 22.4; DB 4; Length 25;
Best Local Similarity 95.8%; Pred. No. 0.18;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTGTGACAACTTG 24
   |||||
Db 1 GTTCAGCTTCTGTGACAAAGTTG 24

RESULT 22
US-09-498-074-16
; Sequence 16, Application US/09498074
; Patent No. 6534264
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Bransch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09498,074
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/563,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-498-074-16
Query Match      89.6%; Score 22.4; DB 4; Length 25;
Best Local Similarity 95.8%; Pred. No. 0.18;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTGTGACAACTTG 24
   |||||
Db 1 GTTCAGCTTCTGTGACAAAGTTG 24

RESULT 23
PCT-US96-10082A-11
; Sequence 11, Application PC/TUS9610082A
; GENERAL INFORMATION:
; APPLICANT: Life Technologies, Inc.
; APPLICANT: 8717 Grovemont Circle
; APPLICANT: Gaithersburg, MD 20884-9980
; APPLICANT: United States of America
; APPLICANT: Bransch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10082A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
PCT-US96-10082A-11
Query Match      89.6%; Score 22.4; DB 5; Length 25;
Best Local Similarity 95.8%; Pred. No. 0.18;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTGTGACAACTTG 24
   |||||
Db 1 GTTCAGCTTCTGTGACAAAGTTG 24

RESULT 24
PCT-US96-10082A-16
; Sequence 16, Application PC/TUS9610082A
; GENERAL INFORMATION:
; APPLICANT: Life Technologies, Inc.
; APPLICANT: 8717 Grovemont Circle
; APPLICANT: Gaithersburg, MD 20884-9980
; APPLICANT: United States of America
; APPLICANT: Bransch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10082A
; FILING DATE: 07-JUN-1996
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CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
PCT-US96-10082A-16

Query Match 89.6%; Score 22.4; DB 5; Length 25;
Best Local Similarity 95.8%; Pred. No. 0.18;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTCAGCTTCTGTACAACTTG 24
DB 1 GTTCAGCTTCTGTACAAAGTIG 24

RESULT 25
US-09-233-493-8
; Sequence 8, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESS: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
US-09-233-493-8

Query Match 88.0%; Score 22; DB 3; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 CAGCTTCTGTACAACTTGT 25
DB 4 CAGCTTCTGTACAACTTGT 25

RESULT 26
US-09-005-476-8
; Sequence 8, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESS: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
US-09-005-476-8

Query Match 88.0%; Score 22; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 CAGCTTCTGTACAACTTGT 25
DB 4 CAGCTTCTGTACAACTTGT 25

RESULT 27
US-09-233-492-8
; Sequence 8, Application US/09233492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESS: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC

```

; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,492
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2540
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-233-492-8
;
; Query Match 88.0%; Score 22; DB 3; Length 25;
; Best Local Similarity 100.0%; Pred. No. 0.28;
; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
Qy 4 CAGCTTCTCTGTACAACTTGT 25
Db 4 CAGCTTCTCTGTACAACTTGT 25

;
; RESULT 28
; PCT-US96-10082A-8
; Sequence 8, Application US/09498074
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
;
;
; Query Match 88.0%; Score 22; DB 3; Length 25;
; Best Local Similarity 100.0%; Pred. No. 0.28;
; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
Qy 4 CAGCTTCTCTGTACAACTTGT 25
Db 4 CAGCTTCTCTGTACAACTTGT 25

;
; RESULT 29
; PCT-US96-10082A-8
; Sequence 8, Application PC/TUS9610082A
; GENERAL INFORMATION:
; APPLICANT: Life Technologies, Inc.
; APPLICANT: 8717 Grovemont Circle
; APPLICANT: Gaithersburg, MD 20894-9980
; APPLICANT: United States of America
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10082A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2540
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; PCT-US96-10082A-8
;
; Query Match 88.0%; Score 22; DB 5; Length 25;
; Best Local Similarity 100.0%; Pred. No. 0.28;
; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
Qy 4 CAGCTTCTCTGTACAACTTGT 25
Db 4 CAGCTTCTCTGTACAACTTGT 25

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US-09-296-280-11
; Sequence 11, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850007
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-296-280-11

Query Match      87.2%; Score 21.8; DB 3; Length 25;
Best Local Similarity 92.0%; Pred. No. 0.34;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGTCACAAACTGT 25
Db 1 GTTCAGCTTTCTTGTCACAAAGTGT 25

US-09-296-280-43
; Sequence 43, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850007
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-296-280-43

Query Match      84.8%; Score 21.2; DB 3; Length 25;
Best Local Similarity 83.3%; Pred. No. 0.63;
Matches 20; Conservative 3; Mismatches 3; Indels 1; Gaps 0;

QY 1 GTTCAGCTTTCTTGTCACAAACTGT 25
Db 1 GTTCAGCTTTCTTGTCACAAAGTGT 25

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QY 1 GTTCAGCTTTCTTGTCACAAACTGT 24
Db 1 GTTCAGCTTTCTTGTCACAAAGTGT 24

RESULT 32
US-09-233-493-3
; Sequence 3, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-233-493-3

Query Match      83.2%; Score 20.8; DB 3; Length 25;
Best Local Similarity 80.0%; Pred. No. 0.96;
Matches 20; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGTCACAAACTGT 25
Db 1 GTTCAGCTTTCTTGTCACAAAGTGT 25

RESULT 33
US-09-233-493-15
; Sequence 15, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites

```

NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESS: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,493
FILING DATE: 20-JAN-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
US-09-233-493-15

Query Match 83.2%; Score 20.8; DB 3; Length 25;
Best Local Similarity 91.7%; Pred. No. 0.96;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAACTTG 24
Db 1 GTTCAGCTTTCTGTACAACTTG 24

RESULT 34
US-09-005-476-3
Sequence 3, Application US/09005476
Patent No. 6171861
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/005,476
FILING DATE: herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
US-09-005-476-3

Query Match 83.2%; Score 20.8; DB 3; Length 25;
Best Local Similarity 80.0%; Pred. No. 0.96;
Matches 20; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAACTTG 25
Db 1 GTTCAGCTTTCTGTACAACTSG 25

RESULT 35
US-09-005-476-15
Sequence 15, Application US/09005476
Patent No. 6171861
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,476
FILING DATE: herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
US-09-005-476-15

Query Match 83.2%; Score 20.8; DB 3; Length 25;
Best Local Similarity 91.7%; Pred. No. 0.96;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAACTTG 24

Db 1 GTTCAGCTTTTGTACAAAGTTG 24
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RESULT 36
US-09-233-492-3
; Sequence 3, Application US/09233492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,492
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2540
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-233-492-3

Query Match 83.2%; Score 20.8; DB 3; Length 25;
Best Local Similarity 80.0%; Pred. No. 0.96;
Matches 20; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAACTTGT 25
|||||

Db 1 GTTCAGCTTTCTGTACAACTSGB 25
|||||

RESULT 37
US-09-233-492-15
; Sequence 15, Application US/09233492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington

STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,492
FILING DATE: 20-JAN-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
US-09-233-492-15

Query Match 83.2%; Score 20.8; DB 3; Length 25;
Best Local Similarity 91.7%; Pred. No. 0.96;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAACTTG 24
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Db 1 GTTCAGCTTTTGTACAAAGTTG 24
|||||

RESULT 38
US-09-296-280-3
; Sequence 3, Application US/09296280
; Patent No. 627608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850007
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 3
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 18
; OTHER INFORMATION: "n" may be any nucleotide
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: Products
US-09-296-280-3

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Query Match      83.2%; Score 20.8; DB 3; Length 25;
Best Local Similarity 80.0%; Pred. No. 0.96;
Matches 20; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTTGTACAAACTGTG 25
Db 1 GTTCAGCTTCTTGTACAAACTGSG 25

RESULT 39
US-09-296-280-15
; Sequence 15, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850007
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-296-280-15
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Query Match      83.2%; Score 20.8; DB 3; Length 25;
Best Local Similarity 91.7%; Pred. No. 0.96;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTTGTACAAACTTG 24
Db 1 GTTCAGCTTCTTGTACAAAGTTG 24

RESULT 40
US-09-498-074-3
; Sequence 3, Application US/09498074
; Patent No. 6534264
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: (Herewith)
; CLASSIFICATION:
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-498-074-3

Query Match      83.2%; Score 20.8; DB 4; Length 25;
Best Local Similarity 80.0%; Pred. No. 0.96;
Matches 20; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTTGTACAAACTGTG 25
Db 1 GTTCAGCTTCTTGTACAAACTGSG 25

Search completed: November 7, 2003, 00:22:52
Job time : 28 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 6, 2003, 22:12:53 : Search time 28 Seconds
(without alignments)
394.092 Million cell updates/sec

Title: US-10-055-001A-4

Perfect score: 25

Sequence: 1 gttcagctttttgtacaaacttgt 25

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PTUS COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	25	100.0	25	US-09-233-493-9	Sequence 9, Appli
2	25	100.0	25	US-09-005-476-9	Sequence 9, Appli
3	25	100.0	25	US-09-233-492-9	Sequence 9, Appli
4	25	100.0	25	US-09-296-280-9	Sequence 9, Appli
5	25	100.0	25	US-09-498-074-9	Sequence 9, Appli
6	25	100.0	25	PCT-US96-10082A-9	Sequence 9, Appli
7	23.4	93.6	25	US-09-233-493-10	Sequence 10, Appl
8	23.4	93.6	25	US-09-005-476-10	Sequence 10, Appl
9	23.4	93.6	25	US-09-233-492-10	Sequence 10, Appl
10	23.4	93.6	25	US-09-296-280-10	Sequence 10, Appl
11	23.4	93.6	25	US-09-498-074-10	Sequence 10, Appl
12	23.4	93.6	25	PCT-US96-10082A-10	Sequence 10, Appl
13	22.6	90.4	25	US-09-296-280-42	Sequence 42, Appl
14	22.4	89.6	25	US-09-233-493-15	Sequence 15, Appl
15	22.4	89.6	25	US-09-005-476-15	Sequence 15, Appl
16	22.4	89.6	25	US-09-233-492-15	Sequence 15, Appl
17	22.4	89.6	25	US-09-296-280-15	Sequence 15, Appl
18	22.4	89.6	25	US-09-498-074-15	Sequence 15, Appl
19	22.4	89.6	25	PCT-US96-10082A-15	Sequence 15, Appl
20	21.2	84.8	25	US-09-296-280-43	Sequence 43, Appl
21	20.8	83.2	25	US-09-233-493-11	Sequence 11, Appl
22	20.8	83.2	25	US-09-233-493-16	Sequence 16, Appl
23	20.8	83.2	25	US-09-005-476-11	Sequence 11, Appl
24	20.8	83.2	25	US-09-005-476-16	Sequence 16, Appl
25	20.8	83.2	25	US-09-233-492-11	Sequence 11, Appl
26	20.8	83.2	25	US-09-233-492-16	Sequence 16, Appl
27	20.8	83.2	25	US-09-296-280-16	Sequence 16, Appl

28 20.8 83.2 25 4 US-09-498-074-11 Sequence 11, Appli
29 20.8 83.2 25 4 US-09-498-074-16 Sequence 16, Appli
30 20.8 83.2 25 5 PCT-US96-10082A-11 Sequence 11, Appli
31 20.8 83.2 25 5 PCT-US96-10082A-16 Sequence 16, Appli
32 20.4 81.6 25 3 US-09-233-493-6 Sequence 6, Appli
33 20.4 81.6 25 3 US-09-233-493-8 Sequence 8, Appli
34 20.4 81.6 25 3 US-09-233-493-33 Sequence 33, Appli
35 20.4 81.6 25 3 US-09-005-476-6 Sequence 6, Appli
36 20.4 81.6 25 3 US-09-005-476-8 Sequence 8, Appli
37 20.4 81.6 25 3 US-09-005-476-33 Sequence 33, Appli
38 20.4 81.6 25 3 US-09-233-492-6 Sequence 6, Appli
39 20.4 81.6 25 3 US-09-233-492-8 Sequence 8, Appli
40 20.4 81.6 25 3 US-09-233-492-33 Sequence 33, Appli
41 20.4 81.6 25 3 US-09-296-280-6 Sequence 6, Appli
42 20.4 81.6 25 4 US-09-498-074-6 Sequence 6, Appli
43 20.4 81.6 25 4 US-09-498-074-8 Sequence 8, Appli
44 20.4 81.6 25 4 US-09-498-074-33 Sequence 33, Appli
45 20.4 81.6 25 5 PCT-US96-10082A-6 Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-09-233-493-9
: Sequence 9, Application US/09233493
: Patent No. 6143557
: GENERAL INFORMATION:
: APPLICANT: Hartley, James L.
: APPLICANT: Brasch, Michael A.
: TITLE OF INVENTION: Recombinational Cloning Using Engineered
: TITLE OF INVENTION: Recombination Sites
: NUMBER OF SEQUENCES: 35
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
: STREET: 1100 New York Ave., N. W. Suite 600
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20005-3934
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/233,493
: FILING DATE: 20-JAN-1999
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/005,476
: FILING DATE: 12-JAN-1998
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/663,002
: FILING DATE: 07-JUN-1996
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/486,139
: FILING DATE: 07-JUN-1995
: CLASSIFICATION:
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-371-2600
: TELEFAX: 202-371-2540
: INFORMATION FOR SEQ ID NO: 9:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 25 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: both
: TOPOLOGY: both
: MOLECULE TYPE: cdna
US-09-233-493-9

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Query Match      100.0%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 2
US-09-005-476-9
; Sequence 9, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2540
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-005-476-9

Query Match      100.0%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 3
US-09-233-492-9
; Sequence 9, Application US/09233492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
```

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STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,492
FILING DATE: 20-JAN-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
US-09-233-492-9

Query Match      100.0%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 4
US-09-296-280-9
; Sequence 9, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850007
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-296-280-9

Query Match      100.0%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GTTCAGCTTTTGTACAACTTGT 25
Db 1 GTTCAGCTTTTGTACAACTTGT 25

RESULT 5
US-09-498-074-9
Query Match 100.0%; Score 25; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 9, Application US/09498074
Patent No. 6534264
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10082A
FILING DATE: 07-JUN-1996
CLASSIFICATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
PCT-US96-10082A-9

QY 1 GTTCAGCTTTTGTACAACTTGT 25
Db 1 GTTCAGCTTTTGTACAACTTGT 25

RESULT 6
PCT-US96-10082A-9
Query Match 100.0%; Score 25; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 9, Application PC/TUS9610082A
Patent No. 6143557
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,493
FILING DATE: 20-JAN-1999
CLASSIFICATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
PCT-US96-10082A-9

QY 1 GTTCAGCTTTTGTACAACTTGT 25
Db 1 GTTCAGCTTTTGTACAACTTGT 25

RESULT 7
US-09-233-493-10
Query Match 100.0%; Score 25; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 10, Application US/09233493
Patent No. 6143557
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,493
FILING DATE: 20-JAN-1999
CLASSIFICATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
PCT-US96-10082A-9

QY 1 GTTCAGCTTTTGTACAACTTGT 25
Db 1 GTTCAGCTTTTGTACAACTTGT 25

RESULT 8
PCT-US96-10082A-9
Query Match 100.0%; Score 25; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 10, Application US/09233493
Patent No. 6143557
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,493
FILING DATE: 20-JAN-1999
CLASSIFICATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
PCT-US96-10082A-9

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; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2500
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-233-493-10

Query Match          93.6%; Score 23.4; DB 3; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.33;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAACTTGT 25
    |||||
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 8
US-09-005-476-10
; Sequence 10, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: herewith
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2500
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-005-476-10

Query Match          93.6%; Score 23.4; DB 3; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.33;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAACTTGT 25
    |||||
Db 1 GTTCAGCTTTTGTACAAACTTGT 25
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; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2500
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-233-492-10

Query Match          93.6%; Score 23.4; DB 3; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.33;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAACTTGT 25
    |||||
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 9
US-09-233-492-10
; Sequence 10, Application US/09233492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,492
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-233-492-10

Query Match          93.6%; Score 23.4; DB 3; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.33;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAACTTGT 25
    |||||
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 10
US-09-296-280-10
; Sequence 10, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850007
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22
```

;
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-296-280-10

Query Match 93.6%; Score 23.4; DB 3; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.33;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
|||||
Db 1 GTTCAGCTTCTGTACAAACTTGT 25

RESULT 11
US-09-498-074-10
; Sequence 10, Application US/09498074
; Patent No. 6534264
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-498-074-10

Query Match 93.6%; Score 23.4; DB 4; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.33;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
|||||
Db 1 GTTCAGCTTCTGTACAAACTTGT 25

RESULT 12
PCT-US96-10082A-10
; Sequence 10, Application PC/TUS9610082A
; GENERAL INFORMATION:
; APPLICANT: Life Technologies, Inc.
; APPLICANT: 8717 Grovemont Circle
; APPLICANT: Gaithersburg, MD 20884-9980
; APPLICANT: United States of America
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10082A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
PCT-US96-10082A-10

Query Match 93.6%; Score 23.4; DB 5; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.33;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
|||||
Db 1 GTTCAGCTTCTGTACAAACTTGT 25

RESULT 13
US-09-296-280-42
; Sequence 42, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.285007
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22

; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 42
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-296-280-42

Query Match 90.4%; Score 22.6; DB 3; Length 25;
Best Local Similarity 76.0%; Pred. No. 0.71;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTGT 25
Db 1 GTTCAGCTTTTGTACAACTTGT 25

RESULT 14
US-09-233-493-15
; Sequence 15, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-233-493-15

Query Match 89.6%; Score 22.4; DB 3; Length 25;
Best Local Similarity 95.8%; Pred. No. 0.86;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTTGTACAACTTG 24
Db 1 GTTCAGCTTTTGTACAACTTG 24

RESULT 15
US-09-005-476-15
; Sequence 15, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-005-476-15

Query Match 89.6%; Score 22.4; DB 3; Length 25;
Best Local Similarity 95.8%; Pred. No. 0.86;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTG 24
Db 1 GTTCAGCTTTTGTACAACTTG 24

RESULT 16
US-09-233-492-15
; Sequence 15, Application US/09233492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600

CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,492
FILING DATE: 20-JAN-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
US-09-233-492-15

Query Match 89.6%; Score 22.4; DB 3; Length 25;
Best Local Similarity 95.8%; Pred. No. 0.86;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAACTTG 24
Db 1 GTTCAGCTTTTGTACAAACTTG 24

RESULT 17
US-09-296-280-15
Sequence 15, Application US/09296280
Patent No. 6277608
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
APPLICANT: Temple, Gary F.
APPLICANT: Fox, Donna K.
TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
FILE REFERENCE: 0942.2850007
CURRENT APPLICATION NUMBER: US/09/296,280
CURRENT FILING DATE: 1999-04-22
EARLIER APPLICATION NUMBER: US 09/177,387
EARLIER FILING DATE: 1998-10-23
EARLIER APPLICATION NUMBER: US 60/065,930
EARLIER FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 15
LENGTH: 25
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: recombination
OTHER INFORMATION: products
US-09-296-280-15

Query Match 89.6%; Score 22.4; DB 3; Length 25;
Best Local Similarity 95.8%; Pred. No. 0.86;

Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GTTCAGCTTTTGTACAAACTTG 24
Db 1 GTTCAGCTTTTGTACAAACTTG 24

RESULT 18
US-09-498-074-15
Sequence 15, Application US/09498074
Patent No. 6534264
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,074
FILING DATE: (Herewith)
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
US-09-498-074-15

Query Match 89.6%; Score 22.4; DB 4; Length 25;
Best Local Similarity 95.8%; Pred. No. 0.86;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAACTTG 24
Db 1 GTTCAGCTTTTGTACAAACTTG 24

RESULT 19
PCT-US96-10082A-15
Sequence 15, Application PC/TUS9610082A
GENERAL INFORMATION:
APPLICANT: Life Technologies, Inc.
APPLICANT: 8717 Grovemont Circle
APPLICANT: Gaithersburg, MD 20884-9980

; APPLICANT: United States of America
 ; APPLICANT: Brasch, Michael A.
 ; TITLE OF INVENTION: Recombinational Cloning Using Engineered
 ; TITLE OF INVENTION: Recombination Sites
 ; NUMBER OF SEQUENCES: 31
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
 ; STREET: 1100 New York Ave., N. W. Suite 600
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005-3934
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US96/10082A
 ; FILING DATE: 07-JUN-1996
 ; CLASSIFICATION:
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-371-2600
 ; TELEFAX: 202-371-2540
 ; INFORMATION FOR SEQ ID NO: 15:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 25 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: both
 ; MOLECULE TYPE: cDNA
 ; PCT-US96-10082A-15

Query Match 89.6%; Score 22.4; DB 5; Length 25;
 Best Local Similarity 95.8%; Pred. No. 0.86;
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTG 24
 |||||
 DB 1 GTTCAGCTTTTGTACAAAGTTG 24

RESULT 20
 US-09-296-280-43
 ; Sequence 43, Application US/09296280
 ; Patent No. 6277608
 ; GENERAL INFORMATION:
 ; APPLICANT: Hartley, James L.
 ; APPLICANT: Brasch, Michael A.
 ; APPLICANT: Temple, Gary F.
 ; APPLICANT: Fox, Donna K.
 ; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
 ; TITLE OF INVENTION: Recombination Sites
 ; FILE REFERENCE: 0942.2850007
 ; CURRENT APPLICATION NUMBER: US/09/296,280
 ; CURRENT FILING DATE: 1999-04-22
 ; EARLIER APPLICATION NUMBER: US 09/177,387
 ; EARLIER FILING DATE: 1998-10-23
 ; EARLIER APPLICATION NUMBER: US 60/065,930
 ; EARLIER FILING DATE: 1997-10-24
 ; NUMBER OF SEQ ID NOS: 60
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 43
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Unknown
 ; FEATURE:
 ; OTHER INFORMATION: Description of Unknown Organism: recombination
 ; OTHER INFORMATION: products
 ; US-09-296-280-43

Query Match 84.8%; Score 21.2; DB 3; Length 25;
 Best Local Similarity 83.3%; Pred. No. 2.6;

Matches 20; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GTTCAGCTTTTGTACAAACTTG 24
 |||||
 DB 1 GTTCAGCTTTTGTACAAAGTTG 24

RESULT 21
 US-09-233-493-11
 ; Sequence 11, Application US/09233493
 ; Patent No. 6143557
 ; GENERAL INFORMATION:
 ; APPLICANT: Hartley, James L.
 ; APPLICANT: Brasch, Michael A.
 ; TITLE OF INVENTION: Recombinational Cloning Using Engineered
 ; TITLE OF INVENTION: Recombination Sites
 ; NUMBER OF SEQUENCES: 35
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
 ; STREET: 1100 New York Ave., N. W. Suite 600
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005-3934
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/233,493
 ; FILING DATE: 20-JAN-1999
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/005,476
 ; FILING DATE: 12-JAN-1998
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/663,002
 ; FILING DATE: 07-JUN-1996
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/486,139
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION:
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-371-2600
 ; TELEFAX: 202-371-2540
 ; INFORMATION FOR SEQ ID NO: 11:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 25 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: both
 ; MOLECULE TYPE: cDNA
 ; US-09-233-493-11

Query Match 83.2%; Score 20.8; DB 3; Length 25;
 Best Local Similarity 91.7%; Pred. No. 3.8;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTG 24
 |||||
 DB 1 GTTCAGCTTTTGTACAAAGTTG 24

RESULT 22
 US-09-233-493-16
 ; Sequence 16, Application US/09233493
 ; Patent No. 6143557
 ; GENERAL INFORMATION:
 ; APPLICANT: Hartley, James L.
 ; APPLICANT: Brasch, Michael A.

;; TITLE OF INVENTION: Recombinational Cloning Using Engineered
;; TITLE OF INVENTION: Recombination Sites
;; NUMBER OF SEQUENCES: 35
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
;; STREET: 1100 New York Ave., N. W. Suite 600
;; CITY: Washington
;; STATE: DC
;; COUNTRY: USA
;; ZIP: 20005-3934
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/233,493
;; FILING DATE: 20-JAN-1999
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 09/005,476
;; FILING DATE: 12-JAN-1998
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/663,002
;; FILING DATE: 07-JUN-1996
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/486,139
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION:
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-2600
;; TELEFAX: 202-371-2540
;; INFORMATION FOR SEQ ID NO: 16:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 25 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: both
;; TOPOLOGY: both
;; MOLECULE TYPE: cdna
US-09-233-493-16

Query Match 83.2%; Score 20.8; DB 3; Length 25;
Best Local Similarity 91.7%; Pred. No. 3.8;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAACTTG 24
|||||
Db 1 GTTCAGCTTTTGTACAAACTTG 24

RESULT 23
US-09-005-476-11
;; Sequence 11, Application US/09005476
;; Patent No. 6171861
;; GENERAL INFORMATION:
;; APPLICANT: Hartley, James L.
;; APPLICANT: Brasch, Michael A.
;; TITLE OF INVENTION: Recombinational Cloning Using Engineered
;; TITLE OF INVENTION: Recombination Sites
;; NUMBER OF SEQUENCES: 35
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
;; STREET: 1100 New York Ave., N. W. Suite 600
;; CITY: Washington
;; STATE: DC
;; COUNTRY: USA
;; ZIP: 20005-3934
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA: US/09/005,476
;; FILING DATE: herewith
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/663,002
;; FILING DATE: 07-JUN-1996
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-2600
;; TELEFAX: 202-371-2540
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 25 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: both
;; TOPOLOGY: both
;; MOLECULE TYPE: cdna
US-09-005-476-11

Query Match 83.2%; Score 20.8; DB 3; Length 25;
Best Local Similarity 91.7%; Pred. No. 3.8;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAACTTG 24
|||||
Db 1 GTTCAGCTTTTGTACAAACTTG 24

RESULT 24
US-09-005-476-16
;; Sequence 16, Application US/09005476
;; Patent No. 6171861
;; GENERAL INFORMATION:
;; APPLICANT: Hartley, James L.
;; APPLICANT: Brasch, Michael A.
;; TITLE OF INVENTION: Recombinational Cloning Using Engineered
;; TITLE OF INVENTION: Recombination Sites
;; NUMBER OF SEQUENCES: 35
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
;; STREET: 1100 New York Ave., N. W. Suite 600
;; CITY: Washington
;; STATE: DC
;; COUNTRY: USA
;; ZIP: 20005-3934
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA: US/09/005,476
;; FILING DATE: herewith
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/663,002
;; FILING DATE: 07-JUN-1996
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-2600
;; TELEFAX: 202-371-2540
;; INFORMATION FOR SEQ ID NO: 16:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 25 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: both
;; TOPOLOGY: both
;; MOLECULE TYPE: cdna
US-09-005-476-16

Query Match 83.2%; Score 20.8; DB 3; Length 25;
Best Local Similarity 91.7%; Pred. No. 3.8;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTG 24
|||||
DB 1 GTTCAGCTTTTGTACAAAGTTG 24

RESULT 25

US-09-233-492-11
; Sequence 11, Application US/09233492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,492
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-233-492-11

Query Match 83.2%; Score 20.8; DB 3; Length 25;
Best Local Similarity 91.7%; Pred. No. 3.8;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTG 24
|||||
DB 1 GTTCAGCTTTTGTACAAAGTTG 24

RESULT 26

US-09-233-492-16
; Sequence 16, Application US/09233492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C

STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,492
FILING DATE: 20-JAN-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
US-09-233-492-16

Query Match 83.2%; Score 20.8; DB 3; Length 25;
Best Local Similarity 91.7%; Pred. No. 3.8;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTG 24
|||||
DB 1 GTTCAGCTTTTGTACAAAGTTG 24

RESULT 27

US-09-296-280-16
; Sequence 16, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.285007
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: Products
US-09-296-280-16

Query Match 83.2%; Score 20.8; DB 3; Length 25;

Best Local Similarity 91.7%; Pred. No. 3.8; Indels 2; Gaps 0;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTG 24
|||||
Db 1 GTTCAGCTTTTGTACAAAGTTG 24

RESULT 28

US-09-498-074-11
; Sequence 11, Application US/09498074
; Patent No. 6534264
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,074
FILING DATE: (Herewith)

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
US-09-498-074-11

Query Match 83.2%; Score 20.8; DB 4; Length 25;
Best Local Similarity 91.7%; Pred. No. 3.8;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTG 24
|||||
Db 1 GTTCAGCTTTTGTACAAAGTTG 24

RESULT 29

US-09-498-074-16
; Sequence 16, Application US/09498074
; Patent No. 6534264
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.

APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,074
FILING DATE: (Herewith)

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995

CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
US-09-498-074-16

Query Match 83.2%; Score 20.8; DB 4; Length 25;
Best Local Similarity 91.7%; Pred. No. 3.8;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTG 24
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Db 1 GTTCAGCTTTTGTACAAAGTTG 24

RESULT 30

PCT-US96-10082A-11
; Sequence 11, Application PC/TUS9610082A
; GENERAL INFORMATION:
; APPLICANT: Life Technologies, Inc.
; APPLICANT: 8717 Grovemont Circle
; APPLICANT: Gaithersburg, MD 20884-9980
; APPLICANT: United States of America
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US96/10082A
;; FILING DATE: 07-JUN-1996
;; CLASSIFICATION:
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-2540
;; TELEFAX: 202-371-2540
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 25 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: both
;; TOPOLOGY: both
;; MOLECULE TYPE: cdna
PCT-US96-10082A-11

Query Match 83.2%; Score 20.8; DB 5; Length 25;
Best Local Similarity 91.7%; Pred. No. 3.8;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTG 24
Db 1 GTTCAGCTTTTGTACAACTTG 24

RESULT 31
PCT-US96-10082A-16
;; Sequence 16, Application PC/TUS9610082A
;; GENERAL INFORMATION:
;; APPLICANT: Life Technologies, Inc.
;; APPLICANT: 8717 Grovemont Circle
;; APPLICANT: Gaithersburg, MD 20884-9980
;; APPLICANT: United States of America
;; APPLICANT: Brasch, Michael A.
;; TITLE OF INVENTION: Recombinational Cloning Using Engineered
;; TITLE OF INVENTION: Recombination Sites
;; NUMBER OF SEQUENCES: 31
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
;; STREET: 1100 New York Ave., N. W. Suite 600
;; CITY: Washington
;; STATE: DC
;; COUNTRY: USA
;; ZIP: 20005-3934
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US96/10082A
;; FILING DATE: 07-JUN-1996
;; CLASSIFICATION:
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-2600
;; TELEFAX: 202-371-2540
;; INFORMATION FOR SEQ ID NO: 16:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 25 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: both
;; TOPOLOGY: both
;; MOLECULE TYPE: cdna
PCT-US96-10082A-16

Query Match 83.2%; Score 20.8; DB 5; Length 25;
Best Local Similarity 91.7%; Pred. No. 3.8;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTG 24
Db 1 GTTCAGCTTTTGTACAACTTG 24

RESULT 32
US-09-233-493-6
;; Sequence 6, Application US/09233493
;; Patent No. 6143557
;; GENERAL INFORMATION:
;; APPLICANT: Hartley, James L.
;; APPLICANT: Brasch, Michael A.
;; TITLE OF INVENTION: Recombinational Cloning Using Engineered
;; TITLE OF INVENTION: Recombination Sites
;; NUMBER OF SEQUENCES: 35
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
;; STREET: 1100 New York Ave., N. W. Suite 600
;; CITY: Washington
;; STATE: DC
;; COUNTRY: USA
;; ZIP: 20005-3934
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/233,493
;; FILING DATE: 20-JAN-1999
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 09/005,476
;; FILING DATE: 12-JAN-1998
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/663,002
;; FILING DATE: 07-JUN-1996
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/486,139
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION:
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-2540
;; TELEFAX: 202-371-2540
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 25 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: both
;; TOPOLOGY: both
;; MOLECULE TYPE: cdna
US-09-233-493-6

Query Match 81.6%; Score 20.4; DB 3; Length 25;
Best Local Similarity 95.5%; Pred. No. 5.6;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCTTTTGTACAACTTGT 25
Db 4 CTGCTTTTGTACAACTTGT 25

RESULT 33
US-09-233-493-8
;; Sequence 8, Application US/09233493
;; Patent No. 6143557
;; GENERAL INFORMATION:
;; APPLICANT: Hartley, James L.
;; APPLICANT: Brasch, Michael A.
;; TITLE OF INVENTION: Recombinational Cloning Using Engineered
;; TITLE OF INVENTION: Recombination Sites

NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,493
FILING DATE: 20-JAN-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 20-JAN-1999
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
US-09-233-493-8

Query Match 81.6%; Score 20.4; DB 3; Length 25;
Best Local Similarity 95.5%; Pred. No. 5.6;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CAGCTTTTGTACAAACTTGT 25
|||||
Db 4 CAGCTTTTGTACAAACTTGT 25

RESULT 34
US-09-233-493-33/c
Sequence 33, Application US/09233493
Patent No. 6143557
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/233,493
FILING DATE: 20-JAN-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
US-09-233-493-33

Query Match 81.6%; Score 20.4; DB 3; Length 25;
Best Local Similarity 95.5%; Pred. No. 5.6;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CAGCTTTTGTACAAACTTGT 25
|||||
Db 22 CTGCTTTTGTACAAACTTGT 1

RESULT 35
US-09-005-476-6
Sequence 6, Application US/09005476
Patent No. 6171861
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,476
FILING DATE: herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both

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; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-005-476-6

Query Match      81.6%; Score 20.4; DB 3; Length 25;
Best Local Similarity 95.5%; Pred. No. 5.6;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCTTTTGTACAAACTTGT 25
Db 4 CTGCTTTTGTACAAACTTGT 25

RESULT 36
US-09-005-476-8
; Sequence 8, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-005-476-33

Query Match      81.6%; Score 20.4; DB 3; Length 25;
Best Local Similarity 95.5%; Pred. No. 5.6;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCTTTTGTACAAACTTGT 25
Db 22 CTGCTTTTGTACAAACTTGT 1

RESULT 38
US-09-233-492-6
; Sequence 6, Application US/092333492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,492
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-005-476-8

Query Match      81.6%; Score 20.4; DB 3; Length 25;
Best Local Similarity 95.5%; Pred. No. 5.6;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCTTTTGTACAAACTTGT 25
Db 4 CAGCTTTTGTACAAACTTGT 25

RESULT 37
US-09-005-476-33/c
; Sequence 33, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
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CLASSIFICATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
US-09-233-492-6

Query Match 81.6%; Score 20.4; DB 3; Length 25;
Best Local Similarity 95.5%; Pred. No. 5.6;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CAGCTTTTGTACAACTTGT 25
Db 4 CTGCTTTTGTACAACTTGT 25

RESULT 39
US-09-233-492-8
; Sequence 8, Application US/092333492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,492
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
US-09-233-492-8

Query Match 81.6%; Score 20.4; DB 3; Length 25;
Best Local Similarity 95.5%; Pred. No. 5.6;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CAGCTTTTGTACAACTTGT 25

Db 4 CAGCTTTTGTACAACTTGT 25

RESULT 40
US-09-233-492-33/C
; Sequence 33, Application US/092333492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,492
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
US-09-233-492-33

Query Match 81.6%; Score 20.4; DB 3; Length 25;
Best Local Similarity 95.5%; Pred. No. 5.6;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CAGCTTTTGTACAACTTGT 25
Db 22 CTGCTTTTGTACAACTTGT 1

Search completed: November 7, 2003, 00:22:52
Job time : 28 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 6, 2003, 21:05:38 ; Search time 111.5 Seconds
(without alignments)
605.255 Million cell updates/sec

Title: US-10-055-001a-11

Perfect score: 25

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	25	100.0	25	22	Recombination site
4	25	100.0	25	22	Recombination site
5	25	100.0	25	22	Recombination site
6	25	100.0	25	22	Recombination site
7	25	100.0	25	22	Recombination site
8	25	100.0	25	22	Escherichia coli c

9	25	100.0	25	23	AAS14785
10	25	100.0	25	24	ABQ82123
11	25	100.0	25	24	ABQ82128
12	25	100.0	25	25	ACC44660
13	25	100.0	25	25	ACC44665
14	25	100.0	25	25	ABT16630
15	25	100.0	25	25	ABT16635
16	25	100.0	25	25	ABT16635
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25	25	100.0	27	22	ABT16635
26	25	100.0	27	22	ABT16635
27	25	100.0	27	22	ABT16635
28	25	100.0	27	22	ABT16635
29	25	100.0	27	22	ABT16635
30	25	100.0	27	22	ABT16635
31	25	100.0	27	22	ABT16635
32	25	100.0	27	22	ABT16635
33	25	100.0	27	22	ABT16635
34	25	100.0	27	22	ABT16635
35	25	100.0	27	22	ABT16635
36	25	100.0	27	22	ABT16635
37	25	100.0	27	22	ABT16635
38	25	100.0	27	22	ABT16635
39	25	100.0	27	22	ABT16635
40	25	100.0	27	22	ABT16635
41	25	100.0	27	22	ABT16635
42	25	100.0	27	22	ABT16635
43	25	100.0	27	22	ABT16635
44	25	100.0	27	22	ABT16635
45	25	100.0	27	22	ABT16635

ALIGNMENTS

RESULT 1
AAT48225
ID AAT48225 standard; DNA; 25 BP.
AC AAT48225;
DT 20-OCT-1997 (first entry)
XX attP2,P3 core region.
DE att recombination site; core region; mutation; enhance; recombination;
KW vector; subcloning; regulation; exchange; ss.
OS Synthetic.
PN WO9640724-A1.
XX 19-DEC-1996.
PD 07-JUN-1996; 96WO-US10082.
PF 07-JUN-1995; 95US-0486139.
PR (LIFE-) LIFE TECHNOLOGIES INC.
PA Brasch MA, Hartley JL;
PI WPI; 1997-065168/06.
DR Nucleic acids, vectors and methods to obtain chimeric nucleic acid -
XX using recombinant proteins and engineered recombination sites in
PT

PT vitro or in vivo
 XX
 PS Claim 14; Page 56; 106pp; English.
 XX

CC AAX48210-25 are att recombination site core region DNA sequences. The
 CC core region has at least one engineered mutation that enhances
 CC recombination in vitro in the formation of a Cointegrate or Product DNA.
 CC These core regions can be incorporated into novel vector donor DNA
 CC molecules. The nucleic acids, vectors and methods of the invention are
 CC used to obtain chimeric nucleic acid using recombination proteins and
 CC engineered recombination sites in vitro or in vivo. The improved
 CC specificity, speed and yields of the invention facilitates DNA or RNA
 CC subcloning, regulation or exchange useful for any related purpose, e.g.
 CC in vitro recombination of DNA segments, and in vitro or in vivo insertion
 CC or modification of transcribed, replicated, isolated or genomic DNA or
 CC RNA.
 XX

SQ Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;
 Query Match 100.0%; Score 25; DB 18; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTTGACAAAGTTGG 25
 |||||
 Db 1 GTTCAGCTTCTTGACAAAGTTGG 25

RESULT 2
 AAX78950
 ID AAX78950 standard; DNA; 25 BP.
 AC
 XX AAX78950;
 XX
 DT 17-AUG-1999 (first entry)
 XX
 DE Oligonucleotide #16 for recombination and cloning method.
 XX
 KW Cloning; donor; recombination site; vector; chimeric; ss.
 XX
 OS Synthetic.
 XX
 XX WO9921977-A1.
 XX
 PD 06-MAY-1999.
 XX
 XX 26-OCT-1998; 98WO-US22589.
 XX
 XX 23-OCT-1998; 98US-0177387.
 PR 24-OCT-1997; 97US-0065930.
 XX
 XX (LIFE-) LIFE TECHNOLOGIES INC.
 XX
 XX Brasch MA, Fox DK, Hartley JL, Temple GF;
 PI
 XX WPI; 1999-303011/25.
 DR
 XX New nucleic acid cloning methods
 PT
 XX Disclosure; Page 163; 185pp; English.
 PS
 XX

CC The invention relates to novel methods for cloning or subcloning one or
 CC more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or
 CC in vivo: (1) at least one insert donor molecules (IDMs) comprising one
 CC or more desired nucleic acid segments flanked by at least 2
 CC recombination sites which do not recombine with each other; (2) one or
 CC more vector donor molecules (VDMs) comprising at least 2 recombination
 CC sites which do not recombine with each other; and (3) one or more
 CC site-specific recombination proteins; (b) incubating the combination to
 CC transfer one or more of the desired segments into one or more of the
 CC VDMs, thereby producing one or more desired product molecules (PMs). The
 CC methods can be used for the efficient and specific recombination of NAM
 CC segments. They can be used to generate chimeric DNA or RNA molecules that

CC have the desired characteristics and/or nucleic acid segments. The
 CC methods can also be used for changing vectors. The oligonucleotides
 CC AAX78935-X78994 are used in the method of the invention.
 XX

SQ Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;
 Query Match 100.0%; Score 25; DB 20; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTTGACAAAGTTGG 25
 |||||
 Db 1 GTTCAGCTTCTTGACAAAGTTGG 25

RESULT 3
 AAD14439
 ID AAD14439 standard; DNA; 25 BP.
 AC
 XX AAD14439;
 XX
 DT 01-NOV-2001 (first entry)
 XX
 DE Recombination site attR3 DNA.
 XX
 KW Recombination site; copy number; replicon; recombinatorial cloning;
 KW attR3; ds.
 XX
 OS Unidentified.
 XX
 XX US6270969-B1.
 PN
 XX 07-AUG-2001.
 PD
 XX 20-JAN-1999; 99US-0233492.
 XX
 XX 07-JUN-1996; 96US-0663002.
 PR 07-JUN-1995; 95US-0486139.
 XX
 XX (INVI-) INVITROGEN CORP.
 FA
 XX Hartley JL, Brasch MA;
 PI
 XX WPI; 2001-488240/53.
 DR
 XX Methods for apposing nucleic acids comprising an expression signal and
 XX a gene/partial gene, using recombinatorial cloning by incubating the
 XX nucleic acids in the presence of a recombination protein under
 XX conditions for recombination -
 PS
 XX Claim 14; Column 18; 76pp; English.
 XX

CC The invention relates to a method for apposing an expression signal and
 CC a gene or partial gene, using recombinatorial cloning. The method
 CC incubates nucleic acids comprising the expression signal and the gene/
 CC partial gene in the presence of a recombination protein under conditions
 CC sufficient to cause recombination and therefore appose the expression
 CC signal and the gene or partial gene. The methods are useful for apposing
 CC an expression signal and a gene or partial gene using recombinatorial
 CC cloning. The methods are also useful for changing vectors, constructing
 CC genes for fusion proteins, changing copy number, changing replicons,
 CC cloning into phages, and cloning e.g., PCR products (with an attB site
 CC at one end and a loxP site at the other end), genomic DNAs, and cDNAs.
 CC The methods are highly specific, rapid, and less labour intensive than
 CC prior art methods. The present sequence is a recombination site
 CC useful for recombination cloning.
 XX

SQ Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;
 Query Match 100.0%; Score 25; DB 22; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Faraday Avenue Genoscope sequence ID : CS0DC002AC03QPI.

FEATURES

Location/Qualifiers

1..1190
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DC002YB05"
/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was normalized." 248 a 332 c 362 g 209 t 39 others

BASE COUNT
ORIGIN

Query Match 84.8%; Score 21.2; DB 13; Length 1190;
Best Local Similarity 90.9%; Pred. No. 5.5e+02;
Matches 20; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CAGCTTTTGTACAACTTGT 25
Db 38 CWGCTTTTGTACAACTTGT 17

RESULT 38
AL541966/c

LOCUS
DEFINITION AL541966 Homo sapiens PLACENTA Homo sapiens cDNA clone EST 12-MAY-2003
5-PRIME, mRNA sequence.
ACCESSION AL541966
VERSION AL541966.2 GI:30546649
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 15, 2001 this sequence version replaced gi:12873543.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 8896.f For more information about this cluster, see
http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DE007DA04QPI&cluster=8896.f. Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0DE007DA04QPI.

FEATURES

Location/Qualifiers

1..1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DE007YB08"
/tissue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized." 228 a 364 c 398 g 175 t 36 others

BASE COUNT
ORIGIN

Query Match 84.8%; Score 21.2; DB 9; Length 1201;
Best Local Similarity 90.9%; Pred. No. 5.5e+02;
Matches 20; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CAGCTTTTGTACAACTTGT 25
Db 31 CWGCTTTTGTACAACTTGW 10

RESULT 39
AL544813

LOCUS
DEFINITION AL544813 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CS0DI012YK20 3-PRIME, mRNA sequence.
ACCESSION AL544813
VERSION AL544813.2 GI:31266654
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 15, 2001 this sequence version replaced gi:12877293.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 79.r For more information about this cluster, see http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DI012BF10NP1&cluster=79.r. Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0DI012BF10NP1.

FEATURES

Location/Qualifiers

1..1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI012YK20"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was normalized." 324 a 240 c 255 g 315 t 67 others

BASE COUNT
ORIGIN

Query Match 84.8%; Score 21.2; DB 9; Length 1201;
Best Local Similarity 90.9%; Pred. No. 5.5e+02;
Matches 20; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CAGCTTTTGTACAACTTGT 25
Db 905 MWGCTTTTGTACAACTTGT 926

RESULT 40
BX355712/c

LOCUS
DEFINITION BX355712 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CS0DI002YL06 5-PRIME, mRNA sequence.
ACCESSION BX355712
VERSION BX355712.1 GI:30367959
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 612)
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization

```

BASE COUNT      188 a      264 c      221 g      188 t      134 others
ORIGIN

Query Match      84.8%; Score 21.2; DB 13; Length 995;
Best Local Similarity 90.9%; Pred. No. 5.4e+02;
Matches 20; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTTTGTGACAACTTGT 25
   |:::|||||
Db 37 CWGCTTTTGTGACAACTTGT 16

RESULT 35
BX375648/c
LOCUS      1067 bp      mRNA      linear      EST 08-MAY-2003
DEFINITION Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
CDNA clone CSODC015YH12 5-PRIME, mRNA sequence.
BX375648
ACCESSION  BX375648.1 GI:30434667
VERSION
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1067)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3245.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODG0015DD06QPI&cluster=3245.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODC015DD06QPI.

FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODG015YH12"
/tissue_type="B CELLS (RAMOS CELL LINE)"
/cell_line="RAMOS CELL LINE"
/clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE)"
/note="Vector: pCMVSPORT6; 1st strand cDNA was primed
with a NotI-oligo (dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
BASE COUNT      288 a      221 c      268 g      272 t      18 others
ORIGIN

Query Match      84.8%; Score 21.2; DB 13; Length 1067;
Best Local Similarity 95.5%; Pred. No. 5.4e+02;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTTTGTGACAACTTGT 25
   |:::|||||
Db 38 CDGCTTTTGTGACAACTTGT 17

RESULT 36
AL559630/c
LOCUS      1122 bp      mRNA      linear      EST 31-MAY-2003
DEFINITION Homo sapiens B CELLS (RAMOS CELL LINE) Homo sapiens CDNA
clone CSODG001YA01 5-PRIME, mRNA sequence.
AL559630
ACCESSION  AL559630.2 GI:31283761
VERSION
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1122)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9817.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODC002AC03QPI&cluster=9817.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

```

[illegible]

FEATURES	source
Location/Qualifiers	
1. .1201	
/organism="Homo sapiens"	
/mol_type="mRNA"	
/db_xref="taxon:9606"	
/clone="CS0DF006YI08"	
/tissue_type="PLACENTA"	
/clone_lib="Homo sapiens PLACENTA"	
/note="Vector: pCMVSPORT 6: 1st strand cDNA was primed with a NotI-oligo (dN) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."	

BASE COUNT	316 a	171 c	198 g	258 others
ORIGIN	Library was not normalized.			
Query Match	85.6%; Score 21.4; DB 13; Length 1201;			
Best Local Similarity	88.0%; Pred. No. 4.6e+02;			
Matches 22; Conservative	0; Mismatches 3; Indels 0; Gaps 0;			
Qy	1	GTCAGCTTTTTTGTACAAACTTGT	25	
Db	43	GNNCTGCTTTTTTGTACAAACTTGT	19	

RESULT	33
AL538458/c	
LOCUS	
DEFINITION	946 bp mRNA linear EST 31-MAY-2003 AL538458 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
ACCESSION	CSDDF027YP04 5-PRIME, mRNA sequence.
VERSION	AL538458
SOURCE	AL538458.2 GI:31263051
TITLE	Est.
ORGANISM	Homo sapiens (human)
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 946) Li,W.B., Gruber,C.; Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished JOURNAL COMMENT On Feb 13, 2001 this sequence version replaced gi:12801951.

Contact: Genoscope
Genoscope - Centre National de Sequençage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5628.f For

```

more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DF027DH02QP1&cluster=5628.f. Contact :
Peng Liang Email : filiang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DF027DH02QP1.
Location/Qualifiers
1. .946
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DF027YP04"
/tissue_type="FETAL BRAIN"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/notes="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
200 a 322 c 277 g 145 t 2 others
BASE COUNT
ORIGIN

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Query Match      84.8%  Score 21.2; DB 9; Length 946;
Best local Similarity 95.5%  Pred. No. 5.4e+02;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy  4  CAGCTTTTTTGTACAACTGT 25
      | | | | | | | | | |
Db 36 CDGCTTTTTTGTACAACTGT 15

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RESULT	34
LOCUS	BX445504/c
DEFINITION	995 bp mRNA linear EST 15-MAY-2003 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
ACCESSION	X8445504
VERSION	X8445504.1
KEYWORDS	EST.
SOURCE	GI:30774336 Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 995) Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished Contact: Genoscope
AUTHORS	
TITLE	
JOURNAL	
COMMENT	

Email: sef@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3874.r For
more information about this cluster, see
<http://www.genoscope.cns.fr/>
<http://bin/cluster.cgi?seq=CS1DA002ZA08QPI&cluster=3874.r>. Contact :
Peng Liang Email : liang@lifetech.com URL :
<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS1DA002ZA08QPI.

```

FEATURES
    source
        Location/Qualifiers
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                /clone_lib="Homo sapiens NEUROBLASTOMA"
                /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched, into
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

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[illegible]

/organism="Homo sapiens"			
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/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"			
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."			
BASE COUNT	327 a	257 c	281 g
ORIGIN			48 others
Query Match	85.6%	Score 21.4;	DB 13; Length 1201;
Best Local Similarity	95.7%;	Pred. No. 4.6e+02;	
Matches	22; Conservative	0; Mismatches	1; Indels 0; Gaps 0;
QY	3	TCAGCTTTTTTGTACAAACTTGT 25	
DB	39	TCGTGTTTTTGTACAAACTTGT 17	
RESULT 31			
EX399404/c			
LOCUS			
DEFINITION	EX399404 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI075YH01 5-PRIME, mRNA sequence.	1201 bp	mRNA linear EST 13-MAY-2000
ACCESSION	EX399404		
VERSION	EX399404.1	GI:30621878	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Li W.B., Gruber C., Jessee J. and Polayes D.		
TITLE	Full-length cDNA libraries and normalization		
JOURNAL	Unpublished		
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 622.f For more information about this cluster, see http://www.genoscope.cns.fr/ cgi-bin/cluster.cgi?seq=CS0DI075CD01Q1P1&cluster=622.f. Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Paradise Avenue Genoscope sequence ID : CS0DI075CD01Q1P1. Location/Qualifiers		
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source	1..1201		
	/organism="Homo sapiens"		
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	/clone="CS0DI075YH01"		
	/tissue_type="PLACENTA COT 25-NORMALIZED"		
	/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"		
	/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."		
BASE COUNT	254 a	316 c	356 g
ORIGIN			79 others
Query Match	85.6%	Score 21.4;	DB 13; Length 1201;
Best Local Similarity	95.7%;	Pred. No. 4.6e+02;	
Matches	22; Conservative	0; Mismatches	1; Indels 0; Gaps 0;

Qy 3 TCAGCTTTTGTACAACTTGT 25
|||
Db 38 TCTGCTTTTGTACAACTTGT 16

FEATURES
source

Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10184.r For
more information about this cluster, see

<http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0BAK013CF02NM1&cluster=10184.r>. Contact :
Feng Liang Email : fliang@lifetech.com URL :
<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0BAK013CF02NM1.

FEATURES

Location/Qualifiers
1. .1035
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DC005YB15"
/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 173 a 260 c 217 g 382 t 3 others
ORIGIN
Query Match 85.6%; Score 21.4; DB 13; Length 1035;
Best Local Similarity 95.7%; Pred.No. 4.5e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 TCAGCTTTTGTACAAACTTGT 25
Db 389 TCTGCTTTTGTACAAACTTGT 411

RESULT 27
BX329663
LOCUS 1071 bp mRNA linear EST 02-MAY-2003
DEFINITION BX329663 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
cDNA clone CS0DC023YN14 3-PRIME, mRNA sequence.
ACCESSION BX329663
VERSION BX329663.1 GI:30340861

KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1071)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9540.f For
more information about this cluster, see

<http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0BAK018DE01NM1&cluster=9540.f>. Contact :
Feng Liang Email : fliang@lifetech.com URL :
<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0BAK018DE01NM1.
Location/Qualifiers
1. .1071
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DC023YN14"
/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES

Location/Qualifiers
1. .1071
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DC023YN14"
/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 181 a 318 c 250 g 314 t 8 others
ORIGIN

Query Match 85.6%; Score 21.4; DB 13; Length 1071;
Best Local Similarity 95.7%; Pred.No. 4.5e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCAGCTTTTGTACAAACTTGT 25

Db 467 TCTGCTTTTGTACAAACTTGT 489

FEATURES

Location/Qualifiers
1. .1119
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0CAP004YN12"
/tissue_type="THYMUS"
/clone_lib="Homo sapiens THYMUS"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
BASE COUNT 253 a 338 c 256 g 206 t 66 others
ORIGIN
Query Match 85.6%; Score 21.4; DB 13; Length 1119;
Best Local Similarity 88.0%; Pred.No. 4.5e+02;
Matches 22; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 42 GCKTGTCTTTTGTACAAACTTGT 18

FEATURES

Location/Qualifiers
1. .1119
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0CAP004YN12"
/tissue_type="THYMUS"
/clone_lib="Homo sapiens THYMUS"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
BASE COUNT 253 a 338 c 256 g 206 t 66 others
ORIGIN
Query Match 85.6%; Score 21.4; DB 13; Length 1119;
Best Local Similarity 88.0%; Pred.No. 4.5e+02;
Matches 22; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 42 GCKTGTCTTTTGTACAAACTTGT 18

FEATURES

Location/Qualifiers
1. .1119
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0CAP004YN12"
/tissue_type="THYMUS"
/clone_lib="Homo sapiens THYMUS"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
BASE COUNT 253 a 338 c 256 g 206 t 66 others
ORIGIN
Query Match 85.6%; Score 21.4; DB 13; Length 1119;
Best Local Similarity 88.0%; Pred.No. 4.5e+02;
Matches 22; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 42 GCKTGTCTTTTGTACAAACTTGT 18

FEATURES

Location/Qualifiers
1. .1119
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0CAP004YN12"
/tissue_type="THYMUS"
/clone_lib="Homo sapiens THYMUS"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
BASE COUNT 253 a 338 c 256 g 206 t 66 others
ORIGIN
Query Match 85.6%; Score 21.4; DB 13; Length 1119;
Best Local Similarity 88.0%; Pred.No. 4.5e+02;
Matches 22; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 42 GCKTGTCTTTTGTACAAACTTGT 18

FEATURES

Location/Qualifiers
1. .1119
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0CAP004YN12"
/tissue_type="THYMUS"
/clone_lib="Homo sapiens THYMUS"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
BASE COUNT 253 a 338 c 256 g 206 t 66 others
ORIGIN
Query Match 85.6%; Score 21.4; DB 13; Length 1119;
Best Local Similarity 88.0%; Pred.No. 4.5e+02;
Matches 22; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 42 GCKTGTCTTTTGTACAAACTTGT 18

FEATURES

Location/Qualifiers
1. .1119
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0CAP004YN12"
/tissue_type="THYMUS"
/clone_lib="Homo sapiens THYMUS"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
BASE COUNT 253 a 338 c 256 g 206 t 66 others
ORIGIN
Query Match 85.6%; Score 21.4; DB 13; Length 1119;
Best Local Similarity 88.0%; Pred.No. 4.5e+02;
Matches 22; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 42 GCKTGTCTTTTGTACAAACTTGT 18

Oy

Query Match 86.4%; Score 21.6; DB 13; Length 1201;
 Best Local Similarity 95.5%; Pred. No. 3.8e+02;
 Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CAGCTTTTGTACAAACTTGT 25
 Db 39 CWGCTTTTGTACAAACTTGT 18

RESULT 21
 BX463202/c
 LOCUS BX463202 1201 bp mRNA linear EST 22-MAY-2003
 DEFINITION CSODM008YI09 5-PRIME, mRNA sequence.

ACCESSION BX463202
 VERSION BX463202.1 GI:31025494

KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1201)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 9373.r For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CSODM008AE05QP1&cluster=9373.r. Contact :

Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

Faraday Avenue Genoscope sequence ID : CSODM008AE05QP1.

FEATURES

source

1. .1201
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CSODM008YI09"
 /tissue_type="FETAL LIVER"
 /dev_stage="fetal"
 /clone_lib="Homo sapiens FETAL LIVER"
 /note="Organ: Liver; Vector: pCMVSPORT 6; 1st strand cDNA
 was primed with a NotI-oligo (dT) primer. Five prime end
 enriched, double-strand cDNA was digested with Not I and
 cloned into the Not I and EcoRV sites of the pCMVSPORT 6
 vector. Library was not normalized."
 BASE COUNT 253 a 318 c 262 g 291 t
 ORIGIN

Query Match 86.4%; Score 21.6; DB 13; Length 1201;
 Best Local Similarity 95.5%; Pred. No. 3.8e+02;
 Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CAGCTTTTGTACAAACTTGT 25

Db 23 CWGCTTTTGTACAAACTTGT 2

RESULT 22
 BX373155
 LOCUS BX373155 891 bp mRNA linear EST 08-MAY-2003
 DEFINITION BX373155 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 clone CS0DI015YF12 3-PRIME, mRNA sequence.

ACCESSION BX373155

VERSION BX373155.1 GI:30458167

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 891)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 1550.r For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0BAK052DH04NM1&cluster=1550.r. Contact :

Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0BAK052DH04NM1.

FEATURES

source

1. .891
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DI015YF12"
 /tissue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo (dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was normalized."
 BASE COUNT 292 a 181 c 161 g 257 t
 ORIGIN

Query Match 85.6%; Score 21.4; DB 13; Length 891;
 Best Local Similarity 95.7%; Pred. No. 4.5e+02;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TCAGCTTTTGTACAAACTTGT 25

Db 691 TCTGCTTTTGTACAAACTTGT 713

RESULT 23

BX448442/c

LOCUS BX448442 898 bp mRNA linear EST 22-MAY-2003

DEFINITION BX448442 Homo sapiens FETAL LIVER Homo sapiens cDNA clone

CSODM009YF22 5-PRIME, mRNA sequence.

ACCESSION BX448442

VERSION BX448442.1 GI:31019933

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 898)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 7793.f For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0AM009DC11QP1&cluster=7793.f. Contact :

Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0AM009DC11QP1.

FEATURES

source

1. .898
 Location/Qualifiers
 /organism="Homo sapiens"

DEFINITION BX363509 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
Homo sapiens cDNA clone CS0DL001YD08 5-PRIME, mRNA sequence.
ACCESSION BX363509
VERSION BX363509.1 GI:30376731
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Web : www.genoscope.cns.fr
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2356.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DL001YD04QP1&cluster=2356.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DL001YD04QP1.
Location/Qualifiers
1. .1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DL001YD08"
/cell_type="B CELLS (RAMOS CELL LINE)"
/clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT
25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 335 a 140 c 217 g 340 t 169 others
ORIGIN
1. .1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DL001YD08"
/cell_type="B CELLS (RAMOS CELL LINE)"
/clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT
25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES
source

Query Match 86.4%; Score 21.6; DB 13; Length 1201;
Best Local Similarity 95.5%; Pred. No. 3.8e+02;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 4 CAGCTTTTGTGACAACTTGT 25
|:|||||||||||||||||
Db 35 CMGCTTTTGTGACAACTTGT 14
|:|||||||||||||||||

RESULT 19
BX386369/c
LOCUS BX386369 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0DI071YA13 5-PRIME, mRNA sequence.
ACCESSION BX386369
VERSION BX386369.1 GI:30436794
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Web : www.genoscope.cns.fr
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 95.r For more

information about this cluster, see http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS1AI018ZE07QP1&cluster=95.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS1AI018ZE07QP1.
Location/Qualifiers
1. .1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI071YA13"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES
source

BASE COUNT 232 a 290 c 326 g 241 t 112 others
ORIGIN
1. .1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI071YA13"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
Query Match 86.4%; Score 21.6; DB 13; Length 1201;
Best Local Similarity 95.5%; Pred. No. 3.8e+02;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 4 CAGCTTTTGTGACAACTTGT 25
|:|||||||||||||||||
Db 30 CMGCTTTTGTGACAACTTGT 9
|:|||||||||||||||||

RESULT 20
BX400983/c

LOCUS BX400983 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
DEFINITION cDNA clone CS0DK005YD11 5-PRIME, mRNA sequence.
ACCESSION BX400983
VERSION BX400983.1 GI:30626325
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Web : www.genoscope.cns.fr
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1038.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DK005YD11&cluster=1038.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DK005YD11.
Location/Qualifiers
1. .1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DK005YD11"
/cell_type="HELA"
/clone_lib="HELA"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES
source

BASE COUNT 283 a 315 c 336 g 239 t 28 others
ORIGIN
1. .1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DK005YD11"
/cell_type="HELA"
/clone_lib="HELA"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT

Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3257.f,
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS1AF001ZF02QF1.
Location/Qualifiers

FEATURES

source

1. .1198
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DF003YB02"
/tissue_type="FETAL BRAIN"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo (dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
BASE COUNT 256 a 295 c 337 g 237 t 73 others
ORIGIN

Query Match 86.4%; Score 21.6; DB 13; Length 1198;
Best Local Similarity 95.5%; Pred. No. 3.8e+02;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CAGCTTTTGTACAAACTTGT 25
|:|||||
Db 39 CWGCTTTTGTACAAACTTGT 18

RESULT 16
AL544923/c
LOCUS
DEFINITION AL544923 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSODI012YM11 5-PRIME, mRNA sequence.
ACCESSION AL544923
VERSION AL544923.2 GI:31266764
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 15, 2001 this sequence version replaced gi:12877404.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1077.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODI012AG06QF1&cluster=1077.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODI012AG06QF1.
Location/Qualifiers

FEATURES

source

1. .1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI012YM11"
/tissue_type="PLACENTA COT 25-NORMALIZED"

BASE COUNT 223 a 339 c 352 g 250 t 37 others
ORIGIN
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoRV
sites of the pCMVSPORT 6 vector. Library was normalized."

Query Match 86.4%; Score 21.6; DB 9; Length 1201;
Best Local Similarity 95.5%; Pred. No. 3.8e+02;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CAGCTTTTGTACAAACTTGT 25
|:|||||
Db 33 CAGCTTTTGTACAAACTTGT 12

RESULT 17
AL554071/c
LOCUS
DEFINITION AL554071 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSODI081YF11 5-PRIME, mRNA sequence.
ACCESSION AL554071
VERSION AL554071.2 GI:31275884
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 15, 2001 this sequence version replaced gi:12894503.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5023.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODI081CC06QPI&cluster=5023.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODI081CC06QPI.
Location/Qualifiers

FEATURES

source

1. .1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI081YF11"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoRV
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 279 a 244 c 318 g 244 t 116 others
ORIGIN

Query Match 86.4%; Score 21.6; DB 9; Length 1201;
Best Local Similarity 95.5%; Pred. No. 3.8e+02;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CAGCTTTTGTACAAACTTGT 25
|:|||||
Db 33 CAGCTTTTGTACAAACTTGT 12

RESULT 18
BX363509/c
LOCUS
DEFINITION BX363509 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSODI081CC06QPI 5-PRIME, mRNA sequence.
ACCESSION BX363509
VERSION BX363509.1 GI:12894503
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 15, 2001 this sequence version replaced gi:12894503.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5023.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODI081CC06QPI&cluster=5023.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODI081CC06QPI.
Location/Qualifiers

Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0DI005B03QP1.

FEATURES

source

Location/Qualifiers
 1. .933
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DI005YI06"
 /tissue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo (dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 254 a 212 c 238 g 227 t
 ORIGIN

Query Match 86.4%; Score 21.6; DB 13; Length 933;
 Best Local Similarity 95.5%; Pred. No. 3.7e+02;
 Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTTTGTACAAACTTGT 25

Db 38 CAGCTTTTGTACAAACTTGT 17

RESULT 13

AL550767/c

LOCUS AL550767 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 clone CS0DI056YC22 5-PRIME, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Full-length cDNA libraries and normalization
 On Feb 15, 2001 this sequence version replaced gi:12888058.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 629.f For
 more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0DI056BB11QP1&cluster=629.f. Contact :

Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0DI056BB11QP1.

FEATURES

source

Location/Qualifiers
 1. .1060
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DI056YC22"
 /tissue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo (dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 243 a 276 c 226 g 257 t 58 others
 ORIGIN

Query Match 86.4%; Score 21.6; DB 9; Length 1060;
 Best Local Similarity 95.5%; Pred. No. 3.8e+02;

Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTTTGTACAAACTTGT 25

Db 40 CWGCTTTTGTACAAACTTGT 19

RESULT 14

BX338865/c

LOCUS BX338865 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 clone CS0DI064YH04 5-PRIME, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 5957.f For
 more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0DI064DD02QP1&cluster=5957.f. Contact :

Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0DI064DD02QP1.

FEATURES

source

Location/Qualifiers
 1. .1084
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DI064YH04"
 /tissue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo (dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 207 a 276 c 314 g 250 t 37 others

ORIGIN

Query Match 86.4%; Score 21.6; DB 13; Length 1084;
 Best Local Similarity 95.5%; Pred. No. 3.8e+02;

Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTTTGTACAAACTTGT 25

Db 33 CAGCTTTTGTACAAACTTGT 12

RESULT 15

BX463747/c

LOCUS BX463747 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
 CS0DF003YB02 5-PRIME, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 1198)
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

the Not I and EcoRV sites of the pCMVSPORT 6 vector.

Library was not normalized." 231 c 306 g 190 t 11 others

BASE COUNT
ORIGIN

Query Match 87.2%; Score 21.8; DB 13; Length 1006;
Best Local Similarity 92.0%; Pred. No. 3.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
|||
DB 42 GTCCTGCTTTTGTACAAACTTGT 18
|||

RESULT 10
BX333971/c
LOCUS
DEFINITION
BX333971 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens
CDNA clone CS0DD004YN23 5-PRIME, mRNA sequence.

ACCESSION
BX333971

VERSION
BX333971.1 GI:30337270

KEYWORDS
EST.

SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens

REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

TITLE
1 (bases 1 to 894)

JOURNAL
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

COMMENT
Full-length cDNA libraries and normalization

Unpublished

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 9435.f For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0DD004CG12QPI&cluster=9435.f. Contact :

Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0DD004CG12QPI.

Location/Qualifiers

1. .894

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DD004YN23"

/tissue_type="NEUROBLASTOMA COT 50-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo (GT)

/primer. Five prime end enriched, double-strand cDNA was

digested with Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

148 a 332 c 233 g 173 t 8 others

BASE COUNT

ORIGIN

Query Match 86.4%; Score 21.6; DB 13; Length 894;

Best Local Similarity 95.5%; Pred. No. 3.7e+02;

Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTTTGTACAAACTTGT 25

|||||

DB 37 CWGCTTTTGTACAAACTTGT 16

|||||

RESULT 11

AL538354/c

LOCUS

DEFINITION

AL538354 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone

CS0DF027YH18 5-PRIME, mRNA sequence.

ACCESSION

AL538354

VERSION

AL538354.2 GI:31262948

KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

EST.
Homo sapiens (human)
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 897)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished

On Feb 13, 2001 this sequence version replaced gi:12801847.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 1734.r For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0DF027DD09QPI&cluster=1734.r. Contact :

Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0DF027DD09QPI.

Location/Qualifiers

1. .897

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DF027YH18"

/tissue_type="FETAL BRAIN"

/dev_stage="fetal"

/clone_lib="Homo sapiens FETAL BRAIN"

/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA

was primed with a NotI-oligo (GT) primer. Five prime end

enriched, double-strand cDNA was digested with Not I and

cloned into the Not I and EcoRV sites of the pCMVSPORT 6

vector. Library was not normalized."

193 a 211 c 216 g 276 t 1 others

BASE COUNT

ORIGIN

Query Match 86.4%; Score 21.6; DB 9; Length 897;

Best Local Similarity 95.5%; Pred. No. 3.7e+02;

Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTTTGTACAAACTTGT 25

|||||

DB 30 CWGCTTTTGTACAAACTTGT 9

|||||

RESULT 12

BX334648/c

LOCUS

DEFINITION

BX334648 Homo sapiens sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA

clone CS0DI005YI06 5-PRIME, mRNA sequence.

ACCESSION

BX334648

VERSION

BX334648.1 GI:30341342

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 933)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 334.r For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0DI005BE03QPI&cluster=334.r. Contact :

```

BX457051/c
LOCUS      BX457051      956 bp      mRNA      linear      EST 22-MAY-2003
DEFINITION BX457051 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP005YP02
ACCESSION  BX457051
VERSION    BX457051.1 GI:31034832
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 956)
AUTHORS   Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE     Full-length cDNA libraries and normalization
JOURNAL   Unpublished
COMMENT   Contact: Genoscope
          Genoscope - Centre National de Sequencage
          BP 191 91006 EVRY cedex - France
          Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
          Library was constructed by Life Technologies, a division of
          Invitrogen. This sequence belongs to sequence cluster 6437.r For
          more information about this cluster, see
          http://www.genoscope.cns.fr/
          cgi-bin/cluster.cgi?seq=CS0CAP005DH01QPI&cluster=6437.r. Contact :
          Feng Liang Email : fliang@lifetech.com URL :
          http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
          Faraday Avenue Genoscope sequence ID : CS0CAP005DH01QPI.

FEATURES             Location/Qualifiers
     source            1..956
     organism="Homo sapiens"
     mol_type="mRNA"
     db_xref="taxon:9606"
     clone="CS0CAP005YP02"
     tissue_type="THYMUS"
     clone_lib="Homo sapiens THYMUS"
     note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
           with a NotI-oligo(dT) primer. Five prime end enriched,
           double-strand cDNA was digested with Not I and cloned into
           the Not I and EcoRV sites of the pCMVSPORT 6 vector.
           Library was not normalized."
BASE COUNT      209 a 286 c 234 g 220 t 7 others
ORIGIN
Query Match      87.2%; Score 21.8; DB 13; Length 956;
Best Local Similarity 92.0%; Pred. No. 3.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GTTCAGCTTTTGTACAACTTGT 25
        |||
DB      40 GCTCTGCTTTTGTACAACTTGT 16
        |||

RESULT 8
BX422399/c
LOCUS      BX422399      973 bp      mRNA      linear      EST 13-MAY-2003
DEFINITION BX422399 Homo sapiens FETAL LIVER Homo sapiens cDNA clone
          CS0DM004YD15 5-PRIME, mRNA sequence.
ACCESSION  BX422399
VERSION    BX422399.1 GI:30655319
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 973)
AUTHORS   Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE     Full-length cDNA libraries and normalization
JOURNAL   Unpublished
COMMENT   Contact: Genoscope
          Genoscope - Centre National de Sequencage
          BP 191 91006 EVRY cedex - France
          Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
          Library was constructed by Life Technologies, a division of
          Invitrogen. This sequence belongs to sequence cluster 7333.f For
          more information about this cluster, see
          http://www.genoscope.cns.fr/
          cgi-bin/cluster.cgi?seq=CS0AS009ZC07QPI&cluster=7333.f. Contact :
          Feng Liang Email : fliang@lifetech.com URL :
          http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
          Faraday Avenue Genoscope sequence ID : CS0AS009ZC07QPI.

FEATURES             Location/Qualifiers
     source            1..1006
     organism="Homo sapiens"
     mol_type="mRNA"
     db_xref="taxon:9606"
     clone="CS0DG005YP18"
     tissue_type="B CELLS (RAMOS CELL LINE)"
     cell_line="RAMOS CELL LINE"
     clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE)"
     note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
           with a NotI-oligo(dT) primer. Five prime end enriched,
           double-strand cDNA was digested with Not I and cloned into

```

Invitrogen. This sequence belongs to sequence cluster 7228.f For more information about this cluster, see <http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DM004CB08QPI&cluster=7228.f>. Contact : Feng Liang Email : fliang@lifetech.com URL : <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0DM004CB08QPI.

```

FEATURES             Location/Qualifiers
     source            1..973
     organism="Homo sapiens"
     mol_type="mRNA"
     db_xref="taxon:9606"
     clone="CS0DM004YD15"
     tissue_type="FETAL LIVER"
     dev_stage="fetal"
     clone_lib="Homo sapiens FETAL LIVER"
     note="Organ: liver; Vector: pCMVSPORT 6; 1st strand cDNA
           was primed with a NotI-oligo(dT) primer. Five prime end
           enriched, double-strand cDNA was digested with Not I and
           cloned into the Not I and EcoRV sites of the pCMVSPORT 6
           vector. Library was not normalized."
BASE COUNT      287 a 205 c 218 g 260 t 3 others
ORIGIN
Query Match      87.2%; Score 21.8; DB 13; Length 973;
Best Local Similarity 92.0%; Pred. No. 3.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GTTCAGCTTTTGTACAACTTGT 25
        |||
DB      29 GCTCTGCTTTTGTACAACTTGT 5
        |||

RESULT 9
BX428996/c
LOCUS      BX428996      1006 bp      mRNA      linear      EST 15-MAY-2003
DEFINITION BX428996 Homo sapiens B CELLS (RAMOS CELL LINE) Homo sapiens cDNA
          clone CS0DG005YF18 5-PRIME, mRNA sequence.
ACCESSION  BX428996
VERSION    BX428996.1 GI:30780782
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 1006)
AUTHORS   Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE     Full-length cDNA libraries and normalization
JOURNAL   Unpublished
COMMENT   Contact: Genoscope
          Genoscope - Centre National de Sequencage
          BP 191 91006 EVRY cedex - France
          Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
          Library was constructed by Life Technologies, a division of
          Invitrogen. This sequence belongs to sequence cluster 7333.f For
          more information about this cluster, see
          http://www.genoscope.cns.fr/
          cgi-bin/cluster.cgi?seq=CS0AS009ZC07QPI&cluster=7333.f. Contact :
          Feng Liang Email : fliang@lifetech.com URL :
          http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
          Faraday Avenue Genoscope sequence ID : CS0AS009ZC07QPI.

FEATURES             Location/Qualifiers
     source            1..1006
     organism="Homo sapiens"
     mol_type="mRNA"
     db_xref="taxon:9606"
     clone="CS0DG005YF18"
     tissue_type="B CELLS (RAMOS CELL LINE)"
     cell_line="RAMOS CELL LINE"
     clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE)"
     note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
           with a NotI-oligo(dT) primer. Five prime end enriched,
           double-strand cDNA was digested with Not I and cloned into

```

```

JOURNAL
COMMENT
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6911.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DC019BC08QP1&cluster=6911.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue Genoscope sequence ID : CS0DC019BC08QP1.
Location/Qualifiers
1. .1145
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DC019YE16"
/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoRV sites of the Not I and EcoRV
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 298 a 226 c 244 g 308 t 69 others
ORIGIN

Query Match 88.0%; Score 22; DB 13; Length 1145;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTTTGTACAACTTGT 25
|||||
Db 39 CAGCTTTTGTACAACTTGT 18

RESULT 5
BX361644/c 1201 bp mRNA linear EST 05-MAY-2003
LOCUS
DEFINITION
BX361644 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
Homo sapiens cDNA clone CS0D0001YF12 5-PRIME, mRNA sequence.
ACCESSION
BX361644
VERSION
BX361644.1 GI:30366552
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7763.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0D001DC06QP1&cluster=7763.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue Genoscope sequence ID : CS0D001DC06QP1.
Location/Qualifiers
1. .1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D001YF12"
/cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
/cell_line="JURKAT"

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/clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT
10-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoRV sites of the Not I and EcoRV
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 278 a 308 c 341 g 205 t 69 others
ORIGIN

Query Match 88.0%; Score 22; DB 13; Length 1201;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTTTGTACAACTTGT 25
|||||
Db 35 CAGCTTTTGTACAACTTGT 14

RESULT 6
AL519260/c 914 bp mRNA linear EST 12-MAY-2003
LOCUS
DEFINITION
AL519260 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
CS0DA012YH14 5-PRIME, mRNA sequence.
ACCESSION
AL519260
VERSION
AL519260.2 GI:30538367
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3874.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DA012DD07QP1&cluster=3874.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue Genoscope sequence ID : CS0DA012DD07QP1.
Location/Qualifiers
1. .914
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DA012YH14"
/tissue_type="NEUROBLASTOMA"
/clone_lib="Homo sapiens NEUROBLASTOMA"
/note="Vector: pCMVSPORT.6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and EcoRV sites of
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
BASE COUNT 186 a 310 c 254 g 158 t 6 others
ORIGIN

Query Match 87.2%; Score 21.8; DB 9; Length 914;
Best Local Similarity 92.0%; Pred. No. 3.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTGT 25
|||||
Db 39 GCTCTGCTTTTGTACAACTTGT 15

RESULT 7

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Faraday Avenue Genoscope sequence ID : CS0BAK021BF12NM1.

FEATURES

source

Location/Qualifiers

1..996

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DD005YC15"

/tissue_type="NEUROBLASTOMA COT 50-NORMALIZED"

/clone_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo (dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. library was normalized."

BASE COUNT 212 a 291 c 107 g 373 t 13 others

ORIGIN

Query Match 89.6%; Score 22.4; DB 13; Length 996;

Best Local Similarity 95.8%; Pred. No. 1.8e+02;

Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTTCAGCTTTTGTACAAACTTGT 25

Db 425 TTTCAGCTTTTGTACAAACTTGT 448

RESULT 2

EX441089/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 2850.r For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0DF014BA04QP1&cluster=2850.r. Contact :

Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0DF014BA04QP1.

Location/Qualifiers

1..934

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DF014YA08"

/tissue_type="FETAL BRAIN"

/dev_stage="fetal"

/clone_lib="Homo sapiens FETAL BRAIN"

/notes="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA

was primed with a NotI-oligo(dT) primer. Five prime end

enriched, double-strand cDNA was digested with Not I and

cloned into the Not I and EcoRV sites of the pCMVSPORT 6

vector. Library was not normalized."

BASE COUNT 233 a 233 c 278 g 189 t 1 others

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CAGCTTTTGTACAAACTTGT 25

Db 35 CAGCTTTTGTACAAACTTGT 14

RESULT 3

EX359829/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 6269.r For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0DI062AD12QP1&cluster=6269.r. Contact :

Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0DI062AD12QP1.

Location/Qualifiers

1..1092

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DI062YG23"

/tissue_type="PLACENTA COT 25-NORMALIZED"

/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo (dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. library was normalized."

BASE COUNT 237 a 268 c 322 g 207 t 58 others

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CAGCTTTTGTACAAACTTGT 25

Db 36 CAGCTTTTGTACAAACTTGT 15

RESULT 4

EX394655/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 2850.r For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0DF014BA04QP1&cluster=2850.r. Contact :

Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0DF014BA04QP1.

Location/Qualifiers

1..934

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DF014YA08"

/tissue_type="FETAL BRAIN"

/dev_stage="fetal"

/clone_lib="Homo sapiens FETAL BRAIN"

/notes="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA

was primed with a NotI-oligo(dT) primer. Five prime end

enriched, double-strand cDNA was digested with Not I and

cloned into the Not I and EcoRV sites of the pCMVSPORT 6

vector. Library was not normalized."

BASE COUNT 233 a 233 c 278 g 189 t 1 others

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CAGCTTTTGTACAAACTTGT 25

Db 35 CAGCTTTTGTACAAACTTGT 14

EX359829

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 6269.r For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0DI062AD12QP1&cluster=6269.r. Contact :

Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0DI062AD12QP1.

Location/Qualifiers

1..1092

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DI062YG23"

/tissue_type="PLACENTA COT 25-NORMALIZED"

/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo (dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. library was normalized."

BASE COUNT 237 a 268 c 322 g 207 t 58 others

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CAGCTTTTGTACAAACTTGT 25

Db 36 CAGCTTTTGTACAAACTTGT 15

RESULT 4

EX394655

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 2850.r For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0DF014BA04QP1&cluster=2850.r. Contact :

Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0DF014BA04QP1.

Location/Qualifiers

1..934

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DF014YA08"

/tissue_type="FETAL BRAIN"

/dev_stage="fetal"

/clone_lib="Homo sapiens FETAL BRAIN"

/notes="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA

was primed with a NotI-oligo(dT) primer. Five prime end

enriched, double-strand cDNA was digested with Not I and

cloned into the Not I and EcoRV sites of the pCMVSPORT 6

vector. Library was not normalized."

BASE COUNT 233 a 233 c 278 g 189 t 1 others

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 6, 2003, 22:08:13 ; Search time 1093.75 Seconds

(without alignments)
555.531 Million cell updates/sec

Title: US-10-055-001A-4

Perfect score: 25

Sequence: 1 gttcagctttttgtacaaacttgt 25

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.*

1: em_estba.*

2: em_esthm.*

3: em_estin.*

4: em_estmu.*

5: em_estov.*

6: em_estopl.*

7: em_estro.*

8: em_htc.*

9: gb_est1.*

10: gb_est2.*

11: gb_htc.*

12: gb_est3.*

13: gb_est4.*

14: gb_est5.*

15: em_estfun.*

16: em_eston.*

17: em_gss_hum.*

18: em_gss_inv.*

19: em_gss_pln.*

20: em_gss_vrt.*

21: em_gss_fun.*

22: em_gss_mam.*

23: em_gss_mus.*

24: em_gss_pro.*

25: em_gss_rod.*

26: em_gss_phg.*

27: em_gss_vrl.*

28: gb_gsl.*

29: gb_gsl2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22.4	89.6	996	13	BX329816
C 2	22	88.0	934	13	BX441089
C 3	22	88.0	1092	13	BX359829
C 4	22	88.0	1145	13	BX394655

C 5	22	88.0	1201	13	BX361644
C 6	21.8	87.2	914	9	AL519260
C 7	21.8	87.2	956	13	BX457051
C 8	21.8	87.2	973	13	BX422399
C 9	21.8	87.2	1006	13	BX428996
C 10	21.6	86.4	894	13	BX333971
C 11	21.6	86.4	897	9	AL538354
C 12	21.6	86.4	933	13	BX334648
C 13	21.6	86.4	1060	9	AL550767
C 14	21.6	86.4	1084	13	BX338865
C 15	21.6	86.4	1198	13	BX463747
C 16	21.6	86.4	1201	9	AL544923
C 17	21.6	86.4	1201	9	AL554071
C 18	21.6	86.4	1201	13	BX363509
C 19	21.6	86.4	1201	13	BX386369
C 20	21.6	86.4	1201	13	BX400983
C 21	21.6	86.4	1201	13	BX463202
C 22	21.4	85.6	891	13	BX373155
C 23	21.4	85.6	898	13	BX448442
C 24	21.4	85.6	953	13	BX373524
C 25	21.4	85.6	965	13	BX372532
C 26	21.4	85.6	1035	13	BX372606
C 27	21.4	85.6	1071	13	BX329663
C 28	21.4	85.6	1119	13	BX437057
C 29	21.4	85.6	1132	13	BX456900
C 30	21.4	85.6	1201	13	BX332991
C 31	21.4	85.6	1201	13	BX399404
C 32	21.4	85.6	1201	13	BX417226
C 33	21.2	84.8	946	9	AL538458
C 34	21.2	84.8	995	13	BX445504
C 35	21.2	84.8	1067	13	BX375648
C 36	21.2	84.8	1122	9	AL559630
C 37	21.2	84.8	1190	13	BX374761
C 38	21.2	84.8	1201	9	AL541966
C 39	21.2	84.8	1201	9	AL544813
C 40	21	84.0	612	13	BX355712
C 41	21	84.0	834	13	BX358772
C 42	21	84.0	906	13	BX418181
C 43	21	84.0	911	9	AL520832
C 44	21	84.0	935	13	BX367104
C 45	21	84.0	953	13	BX403441

ALIGNMENTS

RESULT 1
BX329816
LOCUS
DEFINITION BX329816 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens
CDNA clone CS0DD005YC15 3-PRIME, mRNA sequence.
ACCESSION BX329816
VERSION BX329816.1 GI:30342879
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 996)
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 4354.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0BAK021BF12NM1&cluster=4354.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

CC recombination site; and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (I), (II), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (I), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.

XX
SQ Sequence 204 BP; 80 A; 35 C; 31 G; 58 T; 0 other;

Query Match 93.6%; Score 23.4; DB 21; Length 204;
Best Local Similarity 96.0%; Pred. No. 0.73;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAACTTGT 25
|||||
Db 184 GTTCAGCTTTCTGTACAACTTGT 160

RESULT 40
AAC55476/c
ID AAC55476 standard; DNA; 204 BP.
XX
AC AAC55476;
XX
DT 11-JAN-2001 (first entry)
XX
DE Destination vector pDEST11 fragment nucleotide sequence.
XX
KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
KW mutant; recombinational cloning; entry vector; destination vector;
KW gene product targeting; fusion tag cleavage; ds.
XX
OS Bacteriophage lambda.
OS Synthetic.
XX
PN WO200052027-A1.
XX
PD 08-SEP-2000.
XX
PF 02-MAR-2000; 2000WO-US05432.
XX
PR 02-MAR-1999; 99US-0122389.
PR 23-MAR-1999; 99US-0126049.
PR 28-MAY-1999; 99US-0136744.
XX
PA (LIFE-) LIFE TECHNOLOGIES INC.
XX
PI Hartley JL, Brasch MA, Temple GF, Cheo D;
XX WPI; 2000-543948/49.
XX
DR
XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides -
XX
XX Example 13; Fig 31; 459pp; English.

XX The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence. Also described are: (1) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att

CC recombination site; and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (I), (II), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (I), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.

XX
SQ Sequence 204 BP; 60 A; 53 C; 50 G; 41 T; 0 other;

Query Match 93.6%; Score 23.4; DB 21; Length 204;
Best Local Similarity 96.0%; Pred. No. 0.73;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAACTTGT 25
|||||
Db 181 GTTCAGCTTTCTGTACAACTTGT 157

Search completed: November 6, 2003, 22:26:29
Job time : 112.5 secs

CC recombination site; and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (I), (II), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing fusion tags, targeting gene products to intracellular locations, cleaving fusion tags, from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (I), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.

XX
SQ Sequence 153 BP; 50 A; 28 C; 40 G; 35 T; 0 other;

Query Match 93.6%; Score 23.4; DB 21; Length 153;
Best Local Similarity 96.0%; Pred. No. 0.71;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAACTTGT 25
||||| ||||| ||||| ||||| |||||
Db 127 GTTCAGCTTTTGTACAAACTTGT 103

RESULT 38
AAC55465/c
ID AAC55465 standard; DNA; 204 BP.
XX
AC AAC55465;
XX
DT 11-JAN-2001 (first entry)
XX
DE Destination vector pDEST6 fragment nucleotide sequence #1.
XX
KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
KW mutant; recombinational cloning; entry vector; destination vector;
KW gene product targeting; fusion tag cleavage; ds.
XX
OS Bacteriophage lambda.
OS Synthetic.
XX
FN WO200052027-A1.
XX
PD 08-SEP-2000.
XX
PF 02-MAR-2000; 2000WO-US05432.
XX
PR 02-MAR-1999; 99US-0122389.
PR 23-MAR-1999; 99US-0126049.
PR 28-MAY-1999; 99US-0136744.
XX
PA (LIFE-) LIFE TECHNOLOGIES INC.
XX
PI Hartley JL, Brasch MA, Temple GF, Cheo D;
XX
XX WPI; 2000-543948/49.
DR
XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides -
XX
XX Example 15; Fig 26; 459pp; English.

XX The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence. Also described are: (1) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att

CC recombination site; and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (I), (II), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing fusion tags, targeting gene products to intracellular locations, cleaving fusion tags, from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (I), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.

XX
SQ Sequence 204 BP; 70 A; 40 C; 46 G; 48 T; 0 other;

Query Match 93.6%; Score 23.4; DB 21; Length 204;
Best Local Similarity 96.0%; Pred. No. 0.73;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAACTTGT 25
||||| ||||| ||||| ||||| |||||
Db 166 GTTCAGCTTTTGTACAAACTTGT 142

RESULT 39
AAC55470/c
ID AAC55470 standard; DNA; 204 BP.
XX
AC AAC55470;
XX
DT 11-JAN-2001 (first entry)
XX
DE Destination vector pDEST8 fragment nucleotide sequence.
XX
KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
KW mutant; recombinational cloning; entry vector; destination vector;
KW gene product targeting; fusion tag cleavage; ds.
XX
OS Bacteriophage lambda.
OS Synthetic.
XX
FN WO200052027-A1.
XX
PD 08-SEP-2000.
XX
PF 02-MAR-2000; 2000WO-US05432.
XX
PR 02-MAR-1999; 99US-0122389.
PR 23-MAR-1999; 99US-0126049.
PR 28-MAY-1999; 99US-0136744.
XX
PA (LIFE-) LIFE TECHNOLOGIES INC.
XX
PI Hartley JL, Brasch MA, Temple GF, Cheo D;
XX
XX WPI; 2000-543948/49.
DR
XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides -
XX
XX Example 15; Fig 28; 459pp; English.

XX The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence. Also described are: (1) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att

CC recombination site; and (2) an isolated nucleic acid molecule (III)
 CC comprising one or more mutated att recombination sites comprising at
 CC least one mutation in its core region that enhances the efficiency of
 CC recombination between a first nucleic acid molecule comprising the
 CC mutated att recombination site and a second nucleic acid molecule
 CC comprising a second recombination site that interacts with the mutated
 CC att recombination site. (I), (II), (III), primers, vectors and methods
 CC from the present invention are used for the recombinational cloning of
 CC nucleic acid molecules. They can be used for changing vectors, targeting
 CC gene products to intracellular locations, cleaving fusion tags from
 CC desired proteins, operably linking nucleic acid molecules of interest to
 CC regulatory genetic sequences, constructing genes for fusion proteins,
 CC changing copy number, changing replicons, cloning into phages and
 CC cloning. (I), (II), (III), host cells and vectors can be used in the
 CC production of polypeptides and antibodies. The present sequence is
 CC used in the exemplification of the present invention.
 XX
 SQ Sequence 125 BP; 61 A; 18 C; 14 G; 32 T; 0 other;

Query Match 93.6%; Score 23.4; DB 21; Length 125;
 Best Local Similarity 96.0%; Pred. No. 0.69;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAACTTGT 25
 |||||
 DB 25 GTTCAGCTTTTGTACAACTTGT 1

RESULT 36
 AAC55485/c
 ID AAC55485 standard; DNA; 153 BP.
 XX
 AC AAC55485;
 XX
 DT 11-JAN-2001 (first entry)
 XX
 DE Destination vector pBEST15 fragment nucleotide sequence #2.
 XX
 KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
 XX mutant; recombinational cloning; entry vector; destination vector;
 XX gene product targeting; fusion tag cleavage; ds.
 XX
 OS Bacteriophage lambda.
 OS Synthetic.
 XX
 PN WC200052027-A1.
 XX
 PD 08-SEP-2000.
 XX
 PF 02-MAR-2000; 2000WO-US05432.
 XX
 PR 02-MAR-1999; 99US-0122389.
 PR 23-MAR-1999; 99US-0126049.
 PR 28-MAY-1999; 99US-0136744.
 XX
 XX (LIFE-) LIFE TECHNOLOGIES INC.
 XX
 XX Hartley JL, Brasch MA, Temple GF, Cheo D;
 XX WPI; 2000-543948/49.
 XX
 XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 XX attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 XX recombinational cloning of polypeptides -
 XX
 XX Disclosure; Fig 35; 459pp; English.

XX The present invention describes isolated nucleic acid molecules (I)
 CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
 CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity
 CC of interaction between the recombination site and a second att

CC recombination site; and (2) an isolated nucleic acid molecule (III)
 CC comprising one or more mutated att recombination sites comprising at
 CC least one mutation in its core region that enhances the efficiency of
 CC recombination between a first nucleic acid molecule comprising the
 CC mutated att recombination site and a second nucleic acid molecule
 CC comprising a second recombination site that interacts with the mutated
 CC att recombination site. (I), (II), (III), primers, vectors and methods
 CC from the present invention are used for the recombinational cloning of
 CC nucleic acid molecules. They can be used for changing vectors, targeting
 CC gene products to intracellular locations, cleaving fusion tags from
 CC desired proteins, operably linking nucleic acid molecules of interest to
 CC regulatory genetic sequences, constructing genes for fusion proteins,
 CC changing copy number, changing replicons, cloning into phages and
 CC cloning. (I), (II), (III), host cells and vectors can be used in the
 CC production of polypeptides and antibodies. The present sequence is
 CC used in the exemplification of the present invention.
 XX

SQ Sequence 153 BP; 52 A; 29 C; 33 G; 39 T; 0 other;

Query Match 93.6%; Score 23.4; DB 21; Length 153;
 Best Local Similarity 96.0%; Pred. No. 0.71;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAACTTGT 25
 |||||
 DB 103 GTTCAGCTTTTGTACAACTTGT 79

RESULT 37
 AAC55488/c
 ID AAC55488 standard; DNA; 153 BP.
 XX
 AC AAC55488;
 XX
 DT 11-JAN-2001 (first entry)
 XX
 DE Destination vector pBEST16 fragment nucleotide sequence #2.
 XX
 KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
 XX mutant; recombinational cloning; entry vector; destination vector;
 XX gene product targeting; fusion tag cleavage; ds.
 XX
 OS Bacteriophage lambda.
 OS Synthetic.
 XX
 PN WC200052027-A1.
 XX
 PD 08-SEP-2000.
 XX
 PF 02-MAR-2000; 2000WO-US05432.
 XX
 PR 02-MAR-1999; 99US-0122389.
 PR 23-MAR-1999; 99US-0126049.
 PR 28-MAY-1999; 99US-0136744.
 XX
 XX (LIFE-) LIFE TECHNOLOGIES INC.
 XX
 XX Hartley JL, Brasch MA, Temple GF, Cheo D;
 XX WPI; 2000-543948/49.
 XX
 XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 XX attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 XX recombinational cloning of polypeptides -
 XX
 XX Disclosure; Fig 36; 459pp; English.

XX The present invention describes isolated nucleic acid molecules (I)
 CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
 CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity
 CC of interaction between the recombination site and a second att

of interaction between the recombination site and a second att recombination site; and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (I), (II), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (I), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.

XX SQ Sequence 102 BP; 37 A; 24 C; 19 G; 21 T; 1 other;

Query Match 93.6%; Score 23.4; DB 21; Length 102;
Best Local Similarity 96.0%; Pred. No. 0.68;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGACAACTTGT 25
|||||||
Db 92 GTTCAGCTTTTGTACAACTTGT 68

RESULT 34
AAC55453/c
ID AAC55453 standard; DNA; 120 BP.
XX
AC AAC55453;
XX
DT 11-JAN-2001 (first entry)
XX
DE Ttc expression cassette for destination vector pDBST1.
XX
KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
KW mutant; recombinational cloning; entry vector; destination vector;
KW gene product targeting; fusion tag cleavage; ds.
XX
OS Bacteriophage lambda.
OS Escherichia coli.
XX
FN WO200052027-A1.
XX
PD 08-SEP-2000.
XX
PF 02-MAR-2000; 2000WO-US05432.
XX
PR 02-MAR-1999; 99US-0122389.
PR 23-MAR-1999; 99US-0126049.
PR 28-MAY-1999; 99US-0136744.
XX
PA (LIFE-) LIFE TECHNOLOGIES INC.
XX
PI Hartley JL, Brasch MA, Temple GF, Cheo D;
XX
DR WPI; 2000-543948/49.
XX
PT Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
PT recombinational cloning of polypeptides -
XX
PS Disclosure; Fig 21; 459pp; English.
XX

The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence. Also described are: (1) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity

of interaction between the recombination site and a second att recombination site; and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (I), (II), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (I), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.

XX SQ Sequence 120 BP; 44 A; 19 C; 28 G; 29 T; 0 other;

Query Match 93.6%; Score 23.4; DB 21; Length 120;
Best Local Similarity 96.0%; Pred. No. 0.69;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGACAACTTGT 25
|||||||
Db 118 GTTCAGCTTTTGTACAACTTGT 94

RESULT 35
AAC55384/c
ID AAC55384 standard; DNA; 125 BP.
XX
AC AAC55384;
XX
DT 11-JAN-2001 (first entry)
XX
DE Recombination site nucleotide sequence attR1.
XX
KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
KW mutant; recombinational cloning; entry vector; destination vector;
KW gene product targeting; fusion tag cleavage; ds.
XX
OS Bacteriophage lambda.
XX
FN WO200052027-A1.
XX
PD 08-SEP-2000.
XX
PF 02-MAR-2000; 2000WO-US05432.
XX
PR 02-MAR-1999; 99US-0122389.
PR 23-MAR-1999; 99US-0126049.
PR 28-MAY-1999; 99US-0136744.
XX
PA (LIFE-) LIFE TECHNOLOGIES INC.
XX
PI Hartley JL, Brasch MA, Temple GF, Cheo D;
XX
DR WPI; 2000-543948/49.
XX
PT Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
PT recombinational cloning of polypeptides -
XX
PS Claim 1; Fig 9; 459pp; English.
XX

The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence. Also described are: (1) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att

of interaction between the recombination site and a second att recombination site; and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (I), (II), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing fusion tags, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (I), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.

XX SQ Sequence 102 BP; 40 A; 22 C; 18 G; 22 T; 0 other;

Query Match 93.6%; Score 23.4; DB 21; Length 102;
 Best Local Similarity 96.0%; Pred. No. 0.68;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTGTACAACTTGT 25
 |||||
 DB 83 GTTCAGCTTCTGTACAACTTGT 59

RESULT 32
 AAC55508/c
 ID AAC55508 standard; DNA; 102 BP.
 XX
 AC AAC55508;
 XX
 DT 11-JAN-2001 (first entry)
 XX
 DE Destination vector pDEST24 fragment nucleotide sequence #1.
 XX
 KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
 KW mutant; recombinational cloning; entry vector; destination vector;
 KW gene product targeting; fusion tag cleavage; ds.
 XX
 OS Bacteriophage lambda.
 OS Synthetic.
 XX
 PN WO200052027-A1.
 XX
 PD 08-SEP-2000.
 XX
 PF 02-MAR-2000; 2000WO-US05432.
 XX
 PR 02-MAR-1999; 99US-0122389.
 PR 23-MAR-1999; 99US-0126049.
 PR 28-MAY-1999; 99US-0136744.
 XX
 PA (LIFE-) LIFE TECHNOLOGIES INC.
 XX
 PI Hartley JL, Brasch MA, Temple GF, Cheo D;
 XX
 DR WPI; 2000-543948/49.
 XX
 XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 PT recombinational cloning of polypeptides -
 XX
 PS Example 5; Fig 44; 459pp; English.
 XX
 CC The present invention describes isolated nucleic acid molecules (I)
 CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
 CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity

of interaction between the recombination site and a second att recombination site; and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (I), (II), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing fusion tags, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (I), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.

XX SQ Sequence 102 BP; 37 A; 25 C; 19 G; 21 T; 0 other;

Query Match 93.6%; Score 23.4; DB 21; Length 102;
 Best Local Similarity 96.0%; Pred. No. 0.68;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTGTACAACTTGT 25
 |||||
 DB 95 GTTCAGCTTCTGTACAACTTGT 71

RESULT 33
 AAC55511/c
 ID AAC55511 standard; DNA; 102 BP.
 XX
 AC AAC55511;
 XX
 DT 11-JAN-2001 (first entry)
 XX
 DE Destination vector pDEST25 fragment nucleotide sequence #1.
 XX
 KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
 KW mutant; recombinational cloning; entry vector; destination vector;
 KW gene product targeting; fusion tag cleavage; ds.
 XX
 OS Bacteriophage lambda.
 OS Synthetic.
 XX
 PN WO200052027-A1.
 XX
 PD 08-SEP-2000.
 XX
 PF 02-MAR-2000; 2000WO-US05432.
 XX
 PR 02-MAR-1999; 99US-0122389.
 PR 23-MAR-1999; 99US-0126049.
 PR 28-MAY-1999; 99US-0136744.
 XX
 PA (LIFE-) LIFE TECHNOLOGIES INC.
 XX
 PI Hartley JL, Brasch MA, Temple GF, Cheo D;
 XX
 DR WPI; 2000-543948/49.
 XX
 XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 PT recombinational cloning of polypeptides -
 XX
 PS Example 5; Fig 45; 459pp; English.
 XX
 CC The present invention describes isolated nucleic acid molecules (I)
 CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
 CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity

CC of interaction between the recombination site and a second att
 CC recombination site; and (2) an isolated nucleic acid molecule (III)
 CC comprising one or more mutated att recombination sites comprising at
 CC least one mutation in its core region that enhances the efficiency of
 CC recombination between a first nucleic acid molecule comprising the
 CC mutated att recombination site and a second nucleic acid molecule
 CC comprising a second recombination site that interacts with the mutated
 CC att recombination site. (I), (II), (III), primers, vectors and methods
 CC from the present invention are used for the recombinational cloning of
 CC nucleic acid molecules. They can be used for changing vectors, targeting
 CC gene products to intracellular locations, cleaving fusion tags from
 CC desired proteins, operably linking nucleic acid molecules of interest to
 CC regulatory genetic sequences, constructing genes for fusion proteins,
 CC changing copy number, changing replicons, cloning into phages and
 CC cloning. (I), (II), (III), host cells and vectors can be used in the
 CC production of polypeptides and antibodies. The present sequence is
 CC used in the exemplification of the present invention.

XX
 SQ Sequence 102 BP; 35 A; 19 C; 20 G; 28 T; 0 other;

Query Match 93.6%; Score 23.4; DB 21; Length 102;
 Best Local Similarity 96.0%; Pred. No. 0.69;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAACTTGT 25
 |||||
 Db 70 GTTCAGCTTTCTGTACAAACTTGT 46

RESULT 30
 AAC55500/c
 ID AAC55500 standard; DNA; 102 BP.
 XX
 AC AAC55500;
 XX
 DT 11-JAN-2001 (first entry)
 XX
 DE Destination vector pDEST21 fragment nucleotide sequence #2.
 XX
 KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
 KW mutant; recombinational cloning; entry vector; destination vector;
 KW gene product targeting; fusion tag cleavage; ds.

OS Bacteriophage lambda.
 OS Synthetic.
 XX WO200052027-A1.
 XX
 PD 08-SEP-2000.
 XX
 XX 02-MAR-2000; 2000WO-US05432.
 XX
 PR 02-MAR-1999; 99US-0122389.
 PR 23-MAR-1999; 99US-0126049.
 PR 28-MAY-1999; 99US-0136744.
 XX
 XX (LIFE-) LIFE TECHNOLOGIES INC.
 XX
 XX Hartley JL, Brasch MA, Temple GF, Cheo D;
 XX
 DR WPI; 2000-543948/49.

Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 recombinational cloning of polypeptides -
 PS Disclosure; Fig 41; 459pp; English.

XX The present invention describes isolated nucleic acid molecules (I)
 CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
 CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity

CC of interaction between the recombination site and a second att
 CC recombination site; and (2) an isolated nucleic acid molecule (III)
 CC comprising one or more mutated att recombination sites comprising at
 CC least one mutation in its core region that enhances the efficiency of
 CC recombination between a first nucleic acid molecule comprising the
 CC mutated att recombination site and a second nucleic acid molecule
 CC comprising a second recombination site that interacts with the mutated
 CC att recombination site. (I), (II), (III), primers, vectors and methods
 CC from the present invention are used for the recombinational cloning of
 CC nucleic acid molecules. They can be used for changing vectors, targeting
 CC gene products to intracellular locations, cleaving fusion tags from
 CC desired proteins, operably linking nucleic acid molecules of interest to
 CC regulatory genetic sequences, constructing genes for fusion proteins,
 CC changing copy number, changing replicons, cloning into phages and
 CC cloning. (I), (II), (III), host cells and vectors can be used in the
 CC production of polypeptides and antibodies. The present sequence is
 CC used in the exemplification of the present invention.

XX
 SQ Sequence 102 BP; 45 A; 13 C; 24 G; 20 T; 0 other;

Query Match 93.6%; Score 23.4; DB 21; Length 102;
 Best Local Similarity 96.0%; Pred. No. 0.68;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAACTTGT 25
 |||||
 Db 82 GTTCAGCTTTCTGTACAAACTTGT 58

RESULT 31
 AAC55505/c
 ID AAC55505 standard; DNA; 102 BP.
 XX
 AC AAC55505;
 XX
 DT 11-JAN-2001 (first entry)
 XX
 DE Destination vector pDEST23 fragment nucleotide sequence #1.
 XX
 KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
 KW mutant; recombinational cloning; entry vector; destination vector;
 KW gene product targeting; fusion tag cleavage; ds.

OS Bacteriophage lambda.
 OS Synthetic.
 XX WO200052027-A1.
 XX
 PD 08-SEP-2000.
 XX
 XX 02-MAR-2000; 2000WO-US05432.
 XX
 PR 02-MAR-1999; 99US-0122389.
 PR 23-MAR-1999; 99US-0126049.
 PR 28-MAY-1999; 99US-0136744.
 XX
 XX (LIFE-) LIFE TECHNOLOGIES INC.
 XX
 XX Hartley JL, Brasch MA, Temple GF, Cheo D;
 XX
 DR WPI; 2000-543948/49.

Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 recombinational cloning of polypeptides -
 PS Example 5; Fig 43; 459pp; English.

XX The present invention describes isolated nucleic acid molecules (I)
 CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
 CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity

CC of interaction between the recombination site and a second att
CC recombination site; and (2) an isolated nucleic acid molecule (III)
CC comprising one or more mutated att recombination sites comprising at
CC least one mutation in its core region that enhances the efficiency of
CC recombination between a first nucleic acid molecule comprising the
CC mutated att recombination site and a second nucleic acid molecule
CC comprising a second recombination site that interacts with the mutated
CC att recombination site. (I), (II), (III), primers, vectors and methods
CC from the present invention are used for the recombinational cloning of
CC nucleic acid molecules. They can be used for changing vectors, targeting
CC gene products to intracellular locations, cleaving fusion tags from
CC desired proteins, operably linking nucleic acid molecules of interest to
CC regulatory genetic sequences, constructing genes for fusion proteins,
CC changing copy number, changing replicons, cloning into phages and
CC cloning. (I), (II), (III), host cells and vectors can be used in the
CC production of polypeptides and antibodies. The present sequence is
CC used in the exemplification of the present invention.

XX Sequence 87 BP; 26 A; 19 C; 21 G; 21 T; 0 other;
SQ

Query Match 93.6%; Score 23.4; DB 21; Length 87;
Best Local Similarity 96.0%; Pred. No. 0.67;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAACTTGT 25
|||||
DB 79 GTTCAGCTTTCTGTACAACTTGT 55
|||||

RESULT 28
AAC55497/c
ID AAC55497 standard; DNA; 95 BP.
XX
AC AAC55497;
XX
DT 11-JAN-2001 (first entry)
XX
DE Destination vector pDEST20 fragment nucleotide sequence #2.
XX
KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
KW mutant; recombinational cloning; entry vector; destination vector;
KW gene product targeting; fusion tag cleavage; ds.
XX
OS Bacteriophage lambda.
OS Synthetic.
XX
PN WO200052027-A1.
XX
PD 08-SEP-2000.
XX
PF 02-MAR-2000; 2000WO-US05432.
XX
PR 02-MAR-1999; 99US-0122389.
PR 23-MAR-1999; 99US-0126049.
PR 28-MAY-1999; 99US-0136744.
XX
PA (LIFE-) LIFE TECHNOLOGIES INC.
XX
PI Hartley JL, Brasch MA, Temple GF, Cheo D;
XX
XX WPI; 2000-543948/49.
XX
PT Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
PT recombinational cloning of polypeptides -
XX
PS Example 23; Fig 40; 459pp; English.
XX
XX The present invention describes isolated nucleic acid molecules (I)
CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
CC molecule (II) comprising one or more att recombination sites comprising
CC at least one mutation in its core region that increases the specificity

CC of interaction between the recombination site and a second att
CC recombination site; and (2) an isolated nucleic acid molecule (III)
CC comprising one or more mutated att recombination sites comprising at
CC least one mutation in its core region that enhances the efficiency of
CC recombination between a first nucleic acid molecule comprising the
CC mutated att recombination site and a second nucleic acid molecule
CC comprising a second recombination site that interacts with the mutated
CC att recombination site. (I), (II), (III), primers, vectors and methods
CC from the present invention are used for the recombinational cloning of
CC nucleic acid molecules. They can be used for changing vectors, targeting
CC gene products to intracellular locations, cleaving fusion tags from
CC desired proteins, operably linking nucleic acid molecules of interest to
CC regulatory genetic sequences, constructing genes for fusion proteins,
CC changing copy number, changing replicons, cloning into phages and
CC cloning. (I), (II), (III), host cells and vectors can be used in the
CC production of polypeptides and antibodies. The present sequence is
CC used in the exemplification of the present invention.

XX Sequence 95 BP; 41 A; 13 C; 15 G; 26 T; 0 other;
SQ

Query Match 93.6%; Score 23.4; DB 21; Length 95;
Best Local Similarity 96.0%; Pred. No. 0.68;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAACTTGT 25
|||||
DB 52 GTTCAGCTTTCTGTACAACTTGT 28
|||||

RESULT 29
AAC55458/c
ID AAC55458 standard; DNA; 102 BP.
XX
AC AAC55458;
XX
DT 11-JAN-2001 (first entry)
XX
DE GST expression cassette for destination vector pDEST3 #2.
XX
KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
KW mutant; recombinational cloning; entry vector; destination vector;
KW gene product targeting; fusion tag cleavage; ds.
XX
OS Bacteriophage lambda.
OS Escherichia coli.
XX
PN WO200052027-A1.
XX
PD 08-SEP-2000.
XX
PF 02-MAR-2000; 2000WO-US05432.
XX
PR 02-MAR-1999; 99US-0122389.
PR 23-MAR-1999; 99US-0126049.
PR 28-MAY-1999; 99US-0136744.
XX
PA (LIFE-) LIFE TECHNOLOGIES INC.
XX
PI Hartley JL, Brasch MA, Temple GF, Cheo D;
XX
XX WPI; 2000-543948/49.
XX
PT Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
PT recombinational cloning of polypeptides -
XX
PS Example 15; Fig 23; 459pp; English.
XX
XX The present invention describes isolated nucleic acid molecules (I)
CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
CC molecule (II) comprising one or more att recombination sites comprising
CC at least one mutation in its core region that increases the specificity

XX Example 7; Page 209; 357pp; English.
 XX AAS06174-AAS06322 represent Bacteriophage lambda att recombination
 CC site nucleic acid sequences, and PCR primers of the invention. The
 CC att sequences are recognised by the recombination protein lambda
 CC integrase (Int). The invention is a new method of producing a population
 CC of hybrid nucleic acids comprising mixing at least a first population of
 CC nucleic acids comprising one or more recombination sites with at least
 CC one target nucleic acid comprising one or more recombination sites and
 CC causing some or all of the nucleic acids to recombine with all or some of
 CC the target nucleic acids. The method is useful for producing a population
 CC of hybrid nucleic acids which may be the same or different. The nucleic
 CC acids may be used to express therapeutic proteins or peptides and they
 CC may also be used to create novel fusion proteins by expressing different
 CC sequences linked to each other. The method allows simultaneous cloning of
 CC two or more different nucleic acids.
 XX Sequence 43 BP; 20 A; 5 C; 11 G; 7 T; 0 other;
 SQ

Query Match 93.6%; Score 23.4; DB 22; Length 43;
 Best Local Similarity 96.0%; Pred. No. 0.62; Indels 0; Gaps 0;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAACTTGT 25
 Db 29 GTTCAGCTTTCTGTACAAACTTGT 5

RESULT 26
 AAC5503/c
 ID AAC5503 standard; DNA; 82 BP.
 XX
 AC AAC5503;
 XX
 DT 11-JAN-2001 (first entry)
 XX
 DE Destination vector pDEST22 fragment nucleotide sequence #2.
 XX Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
 KW mutant; recombinational cloning; entry vector; destination vector;
 KW gene product targeting; fusion tag cleavage; ds.
 XX Bacteriophage lambda.
 OS Synthetic.
 OS
 XX WO200052027-A1.
 XX
 XX 08-SEP-2000.
 XX
 XX 02-MAR-2000; 2000WO-US05432.
 XX
 XX 02-MAR-1999; 99US-0122389.
 XX 23-MAR-1999; 99US-0126049.
 XX 28-MAY-1999; 99US-0136744.
 XX
 XX (LIFE-) LIFE TECHNOLOGIES INC.
 XX
 XX Hartley JL, Brasch MA, Temple GF, Cheo D;
 XX WPI; 2000-543948/49.
 XX
 XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 PT recombinational cloning of polypeptides -
 XX
 XX Disclosure; Fig 42; 459pp; English.
 XX
 XX The present invention describes isolated nucleic acid molecules (I)
 CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
 CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity

CC of interaction between the recombination site and a second att
 CC recombination site; and (2) an isolated nucleic acid molecule (III)
 CC comprising one or more mutated att recombination sites comprising at
 CC least one mutation in its core region that enhances the efficiency of
 CC recombination between a first nucleic acid molecule comprising the
 CC mutated att recombination site and a second nucleic acid molecule
 CC comprising a second recombination site that interacts with the mutated
 CC att recombination site. (I), (II), (III), primers, vectors and methods
 CC from the present invention are used for the recombinational cloning of
 CC nucleic acid molecules. They can be used for changing vectors, targeting
 CC gene products to intracellular locations, cleaving fusion tags from
 CC desired proteins, operably linking nucleic acid molecules of interest to
 CC regulatory genetic sequences, constructing genes for fusion proteins,
 CC changing copy number, changing replicons, cloning into phages and
 CC cloning. (I), (II), (III), host cells and vectors can be used in the
 CC production of polypeptides and antibodies. The present sequence is
 CC used in the exemplification of the present invention.
 XX
 XX Sequence 82 BP; 39 A; 16 C; 17 G; 10 T; 0 other;
 SQ

Query Match 93.6%; Score 23.4; DB 21; Length 82;
 Best Local Similarity 96.0%; Pred. No. 0.67; Indels 0; Gaps 0;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAACTTGT 25
 Db 70 GTTCAGCTTTCTGTACAAACTTGT 46

RESULT 27
 AAC5517/c
 ID AAC5517 standard; DNA; 87 BP.
 XX
 AC AAC5517;
 XX
 DT 11-JAN-2001 (first entry)
 XX
 DE Destination vector pDEST27 fragment nucleotide sequence #2.
 XX Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
 KW mutant; recombinational cloning; entry vector; destination vector;
 KW gene product targeting; fusion tag cleavage; ds.
 XX Bacteriophage lambda.
 OS Synthetic.
 OS
 XX WO200052027-A1.
 XX
 XX 08-SEP-2000.
 XX
 XX 02-MAR-2000; 2000WO-US05432.
 XX
 XX 02-MAR-1999; 99US-0122389.
 XX 23-MAR-1999; 99US-0126049.
 XX 28-MAY-1999; 99US-0136744.
 XX
 XX (LIFE-) LIFE TECHNOLOGIES INC.
 XX
 XX Hartley JL, Brasch MA, Temple GF, Cheo D;
 XX WPI; 2000-543948/49.
 XX
 XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 PT recombinational cloning of polypeptides -
 XX
 XX Disclosure; Fig 47; 459pp; English.
 XX
 XX The present invention describes isolated nucleic acid molecules (I)
 CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
 CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity

XX The invention relates to improving the production of a secondary
CC metabolite by a fungus. This involves modulating the expression of at
CC least one ZBC (zinc binuclear cluster protein) gene in a manner to
CC improve the yield of the secondary metabolite. Methods of the invention
CC may be used for improving the production of the secondary metabolite e.g.
CC antibacterial (such as beta-lactam), an anti-hypercholesterolaemic (such
CC as lovastatin or mevastatin), an immunosuppressant (such as cyclosporin A),
CC an ergot alkaloid (such as ergotamine), an angiogenesis inhibitor (such
CC as ovalicin), a glucan synthase inhibitor, gliotoxin family of compounds,
CC a fungal toxin, a modulator of cell surface receptor signalling, a plant
CC growth regulator, a pigment, an insecticide, or an antineoplastic
CC compound. The method results in a decrease in fermentor run-time, a
CC decrease in the size of the fermentor required for the production of
CC equivalent amounts of the secondary metabolite, or a decrease in the
CC biomass required for the production, which translates into decreased
CC waste that must be handled in downstream processing. The sequences given
CC in records AB158587-AB158598 represent primers that are used in
CC construction of vectors containing the ZBC genes of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 35 BP; 14 A; 7 C; 7 G; 7 T; 0 other;

Query Match 93.6%; Score 23.4; DB 24; Length 35;
Best Local Similarity 96.0%; Pred. No. 0.61;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGACAACTTGT 25
DB 35 GTTCAGCTTTCTTGACAACTTGT 11

RESULT 24
AAC55545/c
ID AAC55545 standard; DNA; 43 BP.
XX
XX AAC55545;
DT 11-JAN-2001 (first entry)
XX
XX att site PCR primer attR1.
XX
XX Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
XX mutant; recombinational cloning; entry vector; destination vector;
XX gene product targeting; fusion tag cleavage; PCR primer; ss.
XX
XX Bacteriophage lambda.
XX Synthetic.
XX
XX WO200052027-A1.
XX
XX 08-SEP-2000.
XX
XX 02-MAR-2000; 2000WO-US05432.
XX
XX 02-MAR-1999; 99US-0122389.
XX
XX 23-MAR-1999; 99US-0126049.
XX
XX 28-MAY-1999; 99US-0136744.
XX
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX
XX Hartley JL, Brasch MA, Temple GF, Cheo D;
XX WPI; 2000-543948/49.
XX
XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
XX attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
XX recombinational cloning of polypeptides -
XX Example 19; Page 142; 459pp; English.
XX
XX

CC The present invention describes isolated nucleic acid molecules (I)
CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
CC molecule (II) comprising one or more att recombination sites comprising
CC at least one mutation in its core region that increases the specificity
CC of interaction between the recombination site and a second att
CC recombination site; and (2) an isolated nucleic acid molecule (III)
CC comprising one or more mutated att recombination sites comprising at
CC least one mutation in its core region that enhances the efficiency of
CC recombination between a first nucleic acid molecule comprising the
CC mutated att recombination site and a second nucleic acid molecule
CC comprising a second recombination site that interacts with the mutated
CC att recombination site. (I), (II), (III), primers, vectors and methods
CC from the present invention are used for the recombinational cloning of
CC nucleic acid molecules. They can be used for changing fusion tags, targeting
CC gene products to intracellular locations, cleaving fusion tags from
CC desired proteins, operably linking nucleic acid molecules of interest to
CC regulatory genetic sequences, constructing genes for fusion proteins,
CC changing copy number, changing replicons, cloning into phages and
CC cloning. (I), (II), (III), host cells and vectors can be used in the
CC production of polypeptides and antibodies. The present sequence is
CC used in the exemplification of the present invention.
XX
XX Sequence 43 BP; 20 A; 5 C; 11 G; 7 T; 0 other;

Query Match 93.6%; Score 23.4; DB 21; Length 43;
Best Local Similarity 96.0%; Pred. No. 0.62;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGACAACTTGT 25
DB 29 GTTCAGCTTTCTTGACAACTTGT 5

RESULT 25
AAS06217/c
ID AAS06217 standard; DNA; 43 BP.
XX
XX AAS06217;
DT 12-SEP-2001 (first entry)
XX
XX PCR primer attR1 used to produce a population of hybrid DNA molecules.
DE Bacteriophage lambda; recombination; att site; PCR primer; lambda Int;
XX lambda integrase; therapeutic; ss.
XX
XX Bacteriophage lambda.
XX Synthetic.
XX
XX WO200142509-A1.
XX
XX 14-JUN-2001.
XX
XX 11-DEC-2000; 2000WO-US33546.
XX
XX 10-DEC-1999; 99US-0169983.
XX
XX 09-MAR-2000; 2000US-0188020.
XX
XX (CHEO/) CHEO D.
XX (BRAS/) BRASCH M A.
XX (TEMP/) TEMPLE G F.
XX (HART/) HARTLEY J L.
XX (BYRD/) BYRD D R N.
XX
XX Cheo D, Brasch MA, Temple GF, Hartley JL, Byrd DRN;
XX WPI; 2001-356174/37.
XX
XX Producing hybrid nucleic acids, useful for expressing novel therapeutic
XX polypeptides, by mixing the same or different nucleic acids having one
XX or more recombination sites in the presence of recombination proteins,
XX e.g. Cre -
XX

PT nucleic acids -
XX
PS Disclosure; Page 262; 269pp; English.
XX
CC The invention relates to a novel method for producing plant artificial
chromosomes. The invention also relates to methods for targeting
insertion of heterologous DNA into plant artificial chromosomes, methods
for delivery of plant chromosomes to selected cells and tissues. The
CC isolated plant artificial chromosome (PAC) is useful for producing a
transgenic plant, which involves introducing the PAC into a plant cell.
CC The PAC comprises a heterologous nucleic acid encoding a gene product
such as enzymes, antisense RNA, tRNA, rDNA, structural proteins, marker
proteins, ligands, receptors, ribozymes, therapeutic proteins, and
CC biopharmaceutical proteins, vaccines, blood factors, antigens, hormones,
cytokines, growth factors, antibodies, or a product that provides for
resistance to diseases, insects, herbicides, or stress in a plant. The
CC heterologous nucleic acid optionally encodes a product that provides an
agronomically important trait in the plant, e.g. a product that alters
nutrient use and/or improves the nutrient quality of the plant. The
CC heterologous nucleic acid is contained within a bacterial artificial
chromosome (BAC) or a yeast artificial chromosome (YAC). This
CC polynucleotide sequence represents an oligo relating to the method for
producing plant artificial chromosomes of the invention.
XX
SQ Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 other;
Query Match 93.6%; Score 23.4; DB 25; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.59;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GTTCAGCTTCTTGTACAAACTTGT 25
Db 1 GTTCAGCTTCTTGTACAAACTTGT 25
RESULT 22
AAH19591/c
ID AAH19591 standard; DNA; 35 BP.
XX
AC AAH19591;
XX
DT 30-JUL-2001 (first entry)
XX
DE Plasmid pEZC7201 ccdB cassette PCR oligo M0511.
XX
KW Secondary metabolite production; gene expression modulation;
genetically modified fungus; antibacterial; antihypercholesterolaemic;
KW immunosuppressant; cell surface receptor signalling; pigment;
KW plant growth regulator; insecticide; anti-neoplastic; ccdB; death gene;
KW pEZC7201; PCR primer; ss.
XX
OS Unidentified.
XX
PN WO200129073-A1.
XX
PD 26-APR-2001.
XX
PF 18-OCT-2000; 2000WO-US28903.
XX
PR 20-OCT-1999; 99US-0160587.
PR 19-JAN-2000; 2000US-0487559.
XX
PA (MICR-) MICROBIA INC.
XX
PI Busby R, Doten R, Cali B, Hecht P, Holtzman D, Madden K, Maxon M;
PI Milne T, Norman T, Royer J, Salama S, Sherman A, Silva J;
PI Summers E, Zhang L, Mayorga M, Feibelman T;
XX
DR WPI; 2001-374304/39.
XX
PT Improving production of secondary metabolite by fungus, for producing
proteins of interest, involves modulating the expression of gene
involved in regulation of secondary metabolite production -

XX
PS Example 1; Page 67; 139pp; English.
XX
CC The present sequence is a primer which was used in an example
illustrating an invention relating to a method for improving production
of a secondary metabolite by a fungus. The method involves modulating
CC the expression of a gene involved in the regulation of secondary
metabolite production. The gene may be modulated in a manner that
increases the yield or productivity of metabolite, increases
CC efflux or excretion of the metabolite, decreases production of side
effects or competing metabolites, alters the characteristics of the
fungus in a manner that is beneficial to the production of the
metabolite, causes conditional lysis of the fungus, or increases the
resistance of the fungus to deleterious effects of exposure to the
secondary metabolite. The method is useful for producing
CC genetically modified fungi, which are useful for producing
secondary metabolites such as antibacterial compounds,
CC antihypercholesterolaemic compounds, immunosuppressants, modulators
of cell surface receptor signalling, plant growth regulators, pigments,
insecticides or anti-neoplastic compounds. The present sequence was
used in the preparation of clones to regulate secondary metabolite
production.
XX
SQ Sequence 35 BP; 14 A; 7 C; 7 G; 7 T; 0 other;
Query Match 93.6%; Score 23.4; DB 22; Length 35;
Best Local Similarity 96.0%; Pred. No. 0.61;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GTTCAGCTTCTTGTACAAACTTGT 25
Db 35 GTTCAGCTTCTTGTACAAACTTGT 11
RESULT 23
ABL58593/c
ID ABL58593 standard; DNA; 35 BP.
XX
AC ABL58593;
XX
DT 24-JUL-2002 (first entry)
XX
DE Oligonucleotide M0511.
XX
KW Secondary metabolite; fungus; ZBC gene; zinc binuclear cluster protein;
antibacterial; beta-lactam; anti-hypercholesterolaemic; lovastatin;
KW mevastatin; immunosuppressant; cyclosporin A; ergot alkaloid; ergotamine;
KW angiogenesis inhibitor; ovalicin; glucan synthase inhibitor; gliotoxin;
KW fungal toxin; cell surface receptor; plant growth regulator; pigment;
KW insecticide; antineoplastic; PCR; primer; ss.
XX
OS Unidentified.
XX
PN WO200224865-A2.
XX
PD 28-MAR-2002.
XX
PF 19-SEP-2001; 2001WO-US29288.
XX
PR 19-SEP-2000; 2000US-233564P.
XX
PA (MICR-) MICROBIA INC.
XX
PI Holtzman D, Madden K, Maxon M, Sherman A;
XX
DR WPI; 2002-352005/38.
XX
PT New method for improving the production of a secondary metabolite e.g.
antineoplastic agent, ergot alkaloid from a fungus involves modulation
of the expression of at least one zinc binuclear cluster protein gene
-
XX
PS Example 1; SEQ ID 7; 49pp + sequence listing; English.

30-MAY-2002; 2002WO-US17452.
30-MAY-2001; 2001US-294758P.
21-MAR-2002; 2002US-366891P.
(CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
Perkins E, Perez C, Lindenbaum M, Greene A, Leung J, Fleming E;
Stewart S, Shellard J;
WPI; 2003-140461/13.
Novel eukaryotic chromosome comprising one or many att sites which
permits site-directed integration in the presence of lambda-integrase,
useful for site-specific recombination-directed integration of DNA of
interest
Claim 43; Page 143; 272pp; English.
The present invention describes a eukaryotic chromosome (I) comprising
one or several att sites, where an att site is heterologous to the
chromosome, and permits site-directed integration in the presence of
lambda-integrase. Also described: (1) a platform artificial chromosome
expression system (ACes) (II) comprising several sites that participate
in recombining a heterologous nucleic acid into a platform artificial
chromosome. (I) can be used in gene therapy. (M1) is useful for
introducing a heterologous nucleic acid molecule into a platform
artificial chromosome, preferably an ACes. (II) is useful for producing a
transgenic animal (e.g. a fish, insect, reptile, amphibian, arachnid, or
mammal) by introducing (II) by cell fusion, lipid-mediated transfection,
by a carrier system, microinjection, microcell fusion, electroporation,
microprojectile bombardment or direct DNA transfer into an embryonic
cell, preferably a stem cell or an embryo. (II) comprises a heterologous
nucleic acid that encodes a therapeutic product which is useful for
making a library of ACes comprising random portions of a genome. ACC44612
to ACC44732 and ABP96650 to ABP96657 represent sequences used in the
exemplification of the present invention.
Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 other;
Query Match 93.6%; Score 23.4; DB 25; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.59;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTCTTGACAACTTGT 25
Db 1 GTTCAGCTTTTGTACAACTTGT 25
RESULT 20
ABZ58734
ID ABZ58734 standard; DNA; 25 BP.
AC ABZ58734;
XX
XX
XX 01-MAY-2003 (first entry)
XX
XX Att site nucleotide sequence attR1.
XX
XX Nucleic acid insertion; recombination; nucleic acid selection;
KW nucleic acid isolation; att; ds.
XX
XX Synthetic.
XX
XX WO200295055-A2.
XX
XX 28-NOV-2002.
XX
XX 21-MAY-2002; 2002WO-US15947.
XX
XX 21-MAY-2001; 2001US-291973P.
XX

(INVI-) INVITROGEN CORP.
Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN;
WPI; 2003-129436/12.
Inserting a population of nucleic acids into a second target molecule
for selecting and isolating nucleic acid molecules by mixing the second
population of nucleic acid with a second target nucleic acid
Disclosure; Fig 13A; 273pp; English.
The invention relates to inserting a population of nucleic acids into a
second target molecule. The method involves (a) mixing a first population
of nucleic acid comprising one or more recombination sites with a target
nucleic acid; (b) causing some or all of the nucleic acid molecules of
the first population to recombine with the first target nucleic acid
molecules to form a second population; (c) mixing the second population
of nucleic acid with a second target nucleic acid; and (d) causing some
or all of the nucleic acid molecules of the second population to
recombine with some or all of the second target nucleic acid molecules to
form a third population of nucleic acid. The method is useful for
selecting and isolating nucleic acid molecules. Sequences ABZ58727-762
represent att recombination site sequences used in the method of the
invention.
Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 other;
Query Match 93.6%; Score 23.4; DB 25; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.59;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTCTTGACAACTTGT 25
Db 1 GTTCAGCTTTTGTACAACTTGT 25
RESULT 21
ABT16628
ID ABT16628 standard; DNA; 25 BP.
AC ABT16628;
XX
XX 03-APR-2003 (first entry)
XX
XX Artificial plant chromosome related oligo SEQ ID No 40.
DE
XX Plant artificial chromosome; PAC; transgenic plant; vaccine;
KW blood factor; herbicide; stress; agronomical; nutrient quality;
KW bacterial artificial chromosome; BAC; yeast artificial chromosome; YAC;
KW ds.
XX
XX Unidentified.
XX
XX WO200296923-A1.
XX
XX 05-DEC-2002.
XX
XX 30-MAY-2002; 2002WO-US17451.
XX
XX 30-MAY-2001; 2001US-294687P.
PR 04-JUN-2001; 2001US-296329P.
XX
XX (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
PA (AGRI-) AGRISOMA INC.
XX
XX Perez C, Fabijanski SF, Perkins E;
XX
XX WPI; 2003-140436/13.
XX
XX Producing artificial chromosome by introducing a nucleic acid into
PT plant cell, selecting artificial chromosome that has one or more repeat
PT regions with equivalent amounts of euchromatic and heterochromatic

XX OS Bacteriophage lambda.
 XX PN WO200174861-A2.
 XX PD 11-OCT-2001.
 XX PF 30-MAR-2001; 2001WO-US10250.
 XX PR 31-MAR-2000; 2000US-193977P.
 XX PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
 XX PI Vile RG, Harrington K, Murphy S, Bateman A;
 XX DR WPI; 2001-656985/75.
 XX PT Recombinant nucleic acid vector for reducing tumour size, has expression cassette comprising a promoter linked to nucleic acid sequence encoding a syncytium-inducing polypeptide and flanked on either side by a recombinase -
 XX PS Disclosure; Page 42; 84pp; English.
 XX CC The invention relates to a recombinant nucleic acid vector comprising a first expression cassette, comprising a first promoter operably linked to a nucleic acid sequence encoding a syncytium-inducing polypeptide (such as a fusogenic membrane glycoprotein) and flanked on either side by a sequence recognised by a recombinase, and/or a second expression cassette comprising a tumour-specific promoter operably linked to a nucleic acid sequence encoding a recombinase. The nucleic acid of the first expression cassette may be linked to a hypoxic response element (HRE), the second expression cassette may contain a promoter linked to a nucleic acid encoding a cytokine, and a third cassette may contain a tumour specific promoter linked to the nucleic acid encoding the recombinase. The tumour specific promoter is, for example, a carcinoembryonic antigen (CEA) promoter or a tyrosinase promoter and the recombinase is, for example, Cre recombinase or FLP recombinase. The invention is useful for reducing tumour size by administering the compositions as retroviral vectors, or in a cell containing the vector, to an individual in need of treatment for a disease caused by malignant cells. This sequence represents an Int recombinase site core region attR2, required for excisive recombination.
 XX SQ Sequence 25 BP; 5 A; 5 C; 4 G; 10 T; 1 other;
 Query Match 93.6%; Score 23.4; DB 23; Length 25;
 Best Local Similarity 96.0%; Pred. No. 0.59;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 GTTCAGCTTCTTGACAACTTGT 25
 Db 1 GTTCAGCTTCTTGACAACTTGT 25
 RESULT 18
 ABQ82121
 ID ABQ82121 standard; DNA; 25 BP.
 AC ABQ82121;
 XX ABQ82121;
 XX 11-DEC-2002 (first entry)
 DE Core sequence of recombination site attR1 SEQ ID NO:4.
 XX Chimeric nucleic acid construct; recombinational cloning; silencing;
 KW recombination site; double stranded RNA; plant; ss.
 XX Synthetic.
 OS WO200259294-A1.
 XX PN 01-AUG-2002.
 XX PD

PF 24-JAN-2002; 2002WO-AU000073.
 XX 26-JAN-2001; 2001US-264067P.
 PR 29-NOV-2001; 2001US-333743P.
 XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
 PA Wesley S, Waterhouse P, Helliwell C;
 XX WPI; 2002-682669/73.
 XX New vectors comprising operably linked DNA fragments having an origin of replication, a selectable marker and a chimeric DNA construct, useful for silencing target nucleic acids and for producing large amounts of double-stranded RNA -
 XX PS Disclosure; Page 14; 104pp; English.
 XX CC The present invention describes a vector (I) comprising operably linked DNA fragments having: (a) origin of replication allowing replication in a recipient cell, preferably in bacteria such as *Escherichia coli*;
 CC (b) selectable marker region capable of being expressed in the recipient cell; and (c) a chimeric DNA construct comprising: (i) promoter or promoter region capable of being recognized by RNA polymerases of a eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second, third and fourth recombination sites; (iii) 3' transcription terminating and polyadenylation region functional in the eukaryotic cell. The first and fourth recombination sites, or the second and third recombination sites are capable of reacting with a same recombination site, and preferably are identical. The first and second recombination sites, or the third and fourth recombination sites, do not recombine with each other or with a same recombination site. The vector is useful for producing large amounts of double-stranded RNA which can be used for silencing target nucleic acid sequences. The vectors can also be used to convert a DNA fragment into an inverted repeat structure. Plants transformed with a vector from the present invention can be used in a conventional breeding scheme to produce more plants with the same characteristics or to introduce a chimeric gene for reduction of the phenotypic expression of nucleic acids. The present sequence represents the core sequence of recombination site attB1 which is given in the exemplification of the present invention.
 XX SQ Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 other;
 Query Match 93.6%; Score 23.4; DB 24; Length 25;
 Best Local Similarity 96.0%; Pred. No. 0.59;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 GTTCAGCTTCTTGACAACTTGT 25
 Db 1 GTTCAGCTTCTTGACAACTTGT 25
 RESULT 19
 ACC44658
 ID ACC44658 standard; DNA; 25 BP.
 XX ACC44658;
 XX 29-MAY-2003 (first entry)
 DE Recombination site related oligonucleotide SEQ ID NO:49.
 XX Chromosome-based platform; artificial chromosome; eukaryotic chromosome; att site; integrase; recombinase; A/Ces; gene therapy; transgenic animal; platform artificial chromosome expression system; PCR primer; ss.
 XX Synthetic.
 OS WO200297059-A2.
 XX PN 05-DEC-2002.
 XX PD

```
Db      1 GTTCAGCTTTTGTGACAACTTGT 25

RESULT 15
AAF55743
ID  AAF55743 standard; DNA; 25 BP.
XX
AC  AAF55743;
XX
DT  12-APR-2001 (first entry)
XX
DE  Recombination site attr1.
XX
KW  Recombination site; cloning; att; ss.
XX
OS  Unidentified.
XX
PN  US6171861-B1.
XX
PD  09-JAN-2001.
XX
PF  12-JAN-1998; 98US-0005476.
XX
PR  07-JUN-1996; 96US-0663002.
XX  07-JUN-1995; 95US-0486139.
XX
PA  (LIFE-) LIFE TECHNOLOGIES INC.
XX
PI  Hartley JL, Brasch MA;
XX  WPI; 2001-136877/14.
XX
PT  In vitro cloning of nucleic acid involves mixing vectors comprising
PT  recombination sites and/or nucleic acid, incubating mixture to produce
PT  chimeric molecule, contacting hosts with mixture and selecting host -
XX
PS  Claim 25; Column 46; 73pp; English.
XX
CC  The present invention relates to a method for in vitro cloning of a
CC  nucleic acid of interest. The method involves mixing in vitro two vectors
CC  each comprising at least one recombination site and the nucleic acid of
CC  interest; incubating the mixture in the presence of at least one
CC  recombination protein to result in recombination of the recombination
CC  sites, leading to production of a chimeric nucleic acid molecule
CC  comprising the nucleic acid of interest; contacting hosts with the
CC  mixture; and selecting for a host comprising the chimeric nucleic acid
CC  molecule, and selecting against a host comprising the vectors comprising
CC  the second vector, to clone the nucleic acid. The present sequence is a
CC  recombination site, which may be used in the method of the present
XX  invention.
XX
SQ  Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 other;

Query Match      93.6%; Score 23.4; DB 22; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.59;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GTTCAGCTTTTGTGACAACTTGT 25
Db      1 GTTCAGCTTTTGTGACAACTTGT 25

RESULT 16
AAC87874
ID  AAC87874 standard; DNA; 25 BP.
XX
AC  AAC87874;
XX
DT  02-MAR-2001 (first entry)
XX
DE  Escherichia coli core region recombinant site attr1 SEQ ID NO:9.
XX
KW  Escherichia coli core region recombinant site; cloning; chimeric DNA;
KW  characteristic; mutation; att site; lox site; ss.
XX
OS  Escherichia coli.
XX
PN  US6143557-A.
XX
PD  07-NOV-2000.
XX
PF  20-JAN-1999; 99US-0233493.
XX
PR  07-JUN-1996; 96US-0663002.
XX  12-JAN-1998; 98US-0005476.
XX  07-JUN-1995; 95US-0486139.
XX
PA  (LIFE-) LIFE TECHNOLOGIES INC.
XX
PI  Brasch MA, Hartley JL;
XX  WPI; 2001-049004/06.
XX
PT  Isolated nucleic acid molecules comprising a DNA segment having two
PT  engineered recombination sites, derived from att or lox, which flank a
PT  selectable marker and comprise a core region having an engineered
PT  mutation -
XX
PS  Claim 1; Column 18; 73pp; English.
XX
CC  The present invention describes an isolated nucleic acid molecule (I)
CC  comprising a first nucleic acid sequence having a defined sequence
CC  (AAC87866 to AAC87881), sequences complementary to AAC87866 to AAC87881,
CC  or an RNA sequence corresponding to AAC87866 to AAC87881. Also described
CC  are: (1) an isolated nucleic acid molecule (II) comprising a first
CC  mutated recombination site that removes one or more stop codons from the
CC  recombination site or avoids hairpin formation, the recombination site
CC  being an att or lox site; (2) an isolated nucleic acid molecule (III)
CC  comprising a first att recombination site comprising a mutation that
CC  enhances recombination specificity; (3) vectors (IV) comprising the
CC  above mentioned nucleic acids; and (4) cells comprising the above
CC  mentioned nucleic acids or (IV). The nucleic acids are used in
CC  engineering a core region of a given recombination site to provide
CC  mutative sites suitable for subcloning reactions. The use of nucleic
CC  acids for obtaining engineered recombination in vitro or in vivo makes
CC  the methods for DNA or RNA subcloning, highly specific, rapid, and
XX  less labour intensive.
XX
SQ  Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 other;

Query Match      93.6%; Score 23.4; DB 22; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.59;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GTTCAGCTTTTGTGACAACTTGT 25
Db      1 GTTCAGCTTTTGTGACAACTTGT 25

RESULT 17
AAS14785
ID  AAS14785 standard; DNA; 25 BP.
XX
AC  AAS14785;
XX
DT  27-FEB-2002 (first entry)
XX
DE  Lambda phage Int recombinase site core region DNA sequence attrN2.
XX
KW  Recombinant nucleic acid vector; carcinoembryonic antigen; CEA; cytokine;
KW  syncytium-inducing polypeptide; fusogenic membrane glycoprotein; tumour;
KW  recombinase; tumour-specific promoter; hypoxic response element; HRE; ss;
KW  tyrosinase promoter; Cre; FLP; retroviral vector; malignant cell; cancer;
KW  cytosstatic; gene therapy; Int recombinase site core region; attrN2;
XX  exclusive recombination.
```

CC site-specific recombination proteins; (b) incubating the combination to
CC transfer one or more of the desired segments into one or more of the
CC VDMs, thereby producing one or more desired product molecules (PMs). The
CC methods can be used for the efficient and specific recombination of NAM
CC segments. They can be used to generate chimeric DNA or RNA molecules that
CC have the desired characteristics and/or nucleic acid segments. The
CC methods can also be used for changing vectors. The oligonucleotides
CC AAX78935-X78994 are used in the method of the invention.

XX
SQ Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 other;

Query Match 93.6%; Score 23.4; DB 20; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.59;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGACAAACTTGT 25
Db 1 GTTCAGCTTTCTTGACAAACTTGT 25

RESULT 13

AAD14437
ID AAD14437 standard; DNA; 25 BP.

XX AAD14437;

XX 01-NOV-2001 (first entry)

XX Recombination site attB3 DNA.

XX Recombination site; copy number; replicon; recombinatorial cloning;
XX attB3; ds.

XX Unidentified.

XX US6270969-B1.

XX 07-AUG-2001.

XX 20-JAN-1999; 99US-0233492.

XX 07-JUN-1996; 96US-0663002.

XX 07-JUN-1995; 95US-0486139.

XX (INVI-) INVITROGEN CORP.

XX Hartley JL, Brasch MA;

XX WPI; 2001-488248/53.

XX Methods for apposing nucleic acids comprising an expression signal and
XX a gene/partial gene, using recombinatorial cloning by incubating the
XX nucleic acids in the presence of a recombination protein under
XX conditions for recombination -

PS Claim 14; Column 18; 76pp; English.

XX The invention relates to a method for apposing an expression signal and
XX a gene or partial gene, using recombinatorial cloning. The method
XX incubates nucleic acids comprising the expression signal and the gene/
XX partial gene in the presence of a recombination protein under conditions
XX sufficient to cause recombination and therefore appose the expression
XX signal and the gene or partial gene. The methods are useful for apposing
XX an expression signal and a gene or partial gene using recombinatorial
XX cloning. The methods are also useful for changing vectors, constructing
XX genes for fusion proteins, changing copy number, changing replicons,
XX cloning into phages, and cloning e.g., PCR products (with an attB site
XX at one end and a loxP site at the other end), genomic DNAs, and cDNAs.
XX The methods are highly specific, rapid, and less labour intensive than
XX prior art methods. The present sequence is a recombination site
XX useful for recombination cloning.

XX Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 other;

Query Match 93.6%; Score 23.4; DB 22; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.59;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGACAAACTTGT 25
Db 1 GTTCAGCTTTCTTGACAAACTTGT 25

RESULT 14

AAS06181
ID AAS06181 standard; DNA; 25 BP.

XX AAS06181;

XX 12-SEP-2001 (first entry)

XX Phage-lambda recombination site attR1.

XX Bacteriophage lambda; recombination; att site; PCR primer; lambda Int;
XX lambda integrase; therapeutic; ss.

XX Bacteriophage lambda.

XX WO200142509-A1.

XX 14-JUN-2001.

XX 11-DEC-2000; 2000WO-US33546.

XX 10-DEC-1999; 99US-0169983.

XX 09-MAR-2000; 2000US-0188020.

XX (CHEO/) CHEO D.

XX (BRAS/) BRASCH M A.

XX (TEMP/) TEMPLE G F.

XX (HART/) HARTLEY J L.

XX (BYRD/) BYRD D R N.

XX Cheo D, Brasch MA, Temple GF, Hartley JL, Byrd DRN;

XX WPI; 2001-356174/37.

XX Producing hybrid nucleic acids, useful for expressing novel therapeutic
XX polypeptides, by mixing the same or different nucleic acids having one
XX or more recombination sites in the presence of recombination proteins,
XX e.g. Cre -

PS Disclosure; Fig 24A; 357pp; English.

XX AAS06174-AAS06322 represent Bacteriophage lambda att recombination
XX site nucleic acid sequences, and PCR primers of the invention. The
XX att sequences are recognised by the recombination protein lambda
XX integrase (Int). The invention is a new method of producing a population
XX of hybrid nucleic acids comprising mixing at least a first population of
XX nucleic acids comprising one or more recombination sites with at least
XX one target nucleic acid comprising one or more recombination sites and
XX causing some or all of the nucleic acids to recombine with all or some of
XX the target nucleic acids. The method is useful for producing a population
XX of hybrid nucleic acids which may be the same or different. The nucleic
XX acids may be used to express therapeutic proteins or peptides and they
XX may also be used to create novel fusion proteins by expressing different
XX sequences linked to each other. The method allows simultaneous cloning of
XX two or more different nucleic acids.

XX Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 other;

Query Match 93.6%; Score 23.4; DB 22; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.59;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGACAAACTTGT 25


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XX 10-DEC-1999; 99US-0169983.
PR 09-MAR-2000; 2000US-0188020.
XX (CHEO/) CHEO D.
PA (BRAS/) BRASCH M A.
PA (TEMP/) TEMPLE G F.
PA (HART/) HARTLEY J L.
PA (BYRD/) BYRD D R N.
XX
XX Chco D, Brasch MA, Temple GF, Hartley JL, Byrd DRN;
FI WPI; 2001-356174/37.
XX
XX Producing hybrid nucleic acids, useful for expressing novel therapeutic
PT polypeptides, by mixing the same or different nucleic acids having one
PT or more recombination sites in the presence of recombination proteins,
PT e.g. Cre -
XX
XX Example 7; Page 209; 357pp; English.
XX
XX AAS06174-AAS06322 represent Bacteriophage lambda att recombination
CC site nucleic acid sequences, and PCR primers of the invention. The
CC att sequences are recognised by the recombination protein lambda
CC integrase (Int). The invention is a new method of producing a population
CC of hybrid nucleic acids comprising mixing at least a first population of
CC nucleic acids comprising one or more recombination sites with at least
CC one target nucleic acid comprising one or more recombination sites and
CC causing some or all of the nucleic acids to recombine with all or some of
CC the target nucleic acids. The method is useful for producing a population
CC of hybrid nucleic acids which may be the same or different. The nucleic
CC acids may be used to express therapeutic proteins or peptides and they
CC may also be used to create novel fusion proteins by expressing different
CC sequences linked to each other. The method allows simultaneous cloning of
CC two or more different nucleic acids.
XX
XX Sequence 43 BP; 19 A; 5 C; 12 G; 7 T; 0 other;
SQ
    Query Match      100.0%; Score 25; DB 22; Length 43;
    Best Local Similarity 100.0%; Pred. No. 0.12;
    Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 GTTCAGCTTTCTGTACAAACTTGT 25
Db 29 GTTCAGCTTTCTGTACAAACTTGT 5
XX
RESULT 11
AAT48218
ID AAT48218 standard; DNA; 25 BP.
XX
AC AAT48218;
XX
XX 20-OCT-1997 (first entry)
DT
DE attR1 core region.
XX
XX att recombination site; core region; mutation; enhance; recombination;
KW vector; subcloning; regulation; exchange; ss.
XX
XX Synthetic.
OS
XX WO9640724-A1.
XX
XX 19-DEC-1996.
XX
XX 07-JUN-1996; 96WO-US10082.
XX
XX 07-JUN-1995; 95US-0486139.
XX
XX (LIFE-) LIFE TECHNOLOGIES INC.
PA
XX Brasch MA, Hartley JL;
PI

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XX WPI; 1997-065168/06.
XX
XX Nucleic acids, vectors and methods to obtain chimeric nucleic acid -
PT using recombinant proteins and engineered recombination sites in
PT vitro or in vivo
XX
XX Claim 14; Page 55; 106pp; English.
XX
XX AAT48210-25 are att recombination site core region DNA sequences. The
CC core region has at least one engineered mutation that enhances
CC recombination in vitro in the formation of a Cointegrate or Product DNA.
CC These core regions can be incorporated into novel vector donor DNA
CC molecules. The nucleic acids, vectors and methods of the invention are
CC used to obtain chimeric nucleic acid using recombination proteins and
CC engineered recombination sites in vitro or in vivo. The improved
CC specificity, speed and yields of the invention facilitates DNA or RNA
CC subcloning, regulation or exchange useful for any related purpose, e.g.
CC in vitro recombination of DNA segments, and in vitro or in vivo insertion
CC or modification of transcribed, replicated, isolated or genomic DNA or
CC RNA.
XX
XX Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 other;
SQ
    Query Match      93.6%; Score 23.4; DB 18; Length 25;
    Best Local Similarity 96.0%; Pred. No. 0.59;
    Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
OY 1 GTTCAGCTTTCTGTACAAACTTGT 25
Db 1 GTTCAGCTTTCTGTACAAACTTGT 25
XX
RESULT 12
AAX78943
ID AAX78943 standard; DNA; 25 BP.
XX
AC AAX78943;
XX
XX 17-AUG-1999 (first entry)
DT
DE Oligonucleotide #9 for recombination and cloning method.
XX
XX Cloning; donor; recombination site; vector; chimeric; ss.
XX
XX Synthetic.
OS
XX WO9921977-A1.
XX
XX 06-MAY-1999.
PD
XX
XX 26-OCT-1998; 98WO-US22589.
XX
XX 23-OCT-1998; 98US-0177387.
XX
XX 24-OCT-1997; 97US-0065930.
XX
XX (LIFE-) LIFE TECHNOLOGIES INC.
PA
XX Brasch MA, Fox DK, Hartley JL, Temple GF;
PI
XX WPI; 1999-303011/25.
XX
XX New nucleic acid cloning methods
PT
XX
XX Disclosure; Page 161; 185pp; English.
XX
XX The invention relates to novel methods for cloning or subcloning one or
CC more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or
CC in vivo: (1) at least one insert donor molecules (IDMs) comprising one
CC or more desired nucleic acid segments flanked by at least 2
CC recombination sites which do not recombine with each other; (2) one or
CC more vector donor molecules (VDMs) comprising at least 2 recombination
CC sites which do not recombine with each other; and (3) one or more

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PD 05-DEC-2002.
 XX 30-MAY-2002; 2002WO-US17451.
 PF 30-MAY-2001; 2001US-294687P.
 XX 04-JUN-2001; 2001US-296329P.
 PR (CHRO-) CHROMOSOMAL SYSTEMS INC.
 XX (AGRI-) AGRISOMA INC.
 PA Perez C, Fabijanski SF, Perkins E;
 PI WPI; 2003-140436/13.
 XX Producing artificial chromosome by introducing a nucleic acid into
 DR plant cell, selecting artificial chromosome that has one or more repeat
 XX regions with equivalent amounts of euchromatic and heterochromatic
 XX nucleic acids
 PS Disclosure; Page 262; 269pp; English.
 XX The invention relates to a novel method for producing plant artificial
 CC chromosomes. The invention also relates to methods for targeting
 CC insertion of heterologous DNA into plant artificial chromosomes, methods
 CC for delivery of plant chromosomes to selected cells and tissues. The
 CC isolated plant artificial chromosome (PAC) is useful for producing a
 CC transgenic plant, which involves introducing the PAC into a plant cell.
 CC The PAC comprises a heterologous nucleic acid encoding a gene product
 CC such as enzymes, antisense RNA, tRNA, rDNA, structural proteins, marker
 CC proteins, ligands, receptors, ribozymes, therapeutic proteins, and
 CC biopharmaceutical proteins, vaccines, blood factors, antigens, hormones,
 CC cytokines, growth factors, antibodies, or a product that provides for
 CC resistance to diseases, insects, herbicides, or stress in a plant. The
 CC heterologous nucleic acid optionally encodes a product that provides an
 CC agronomically important trait in the plant, e.g. a product that alters
 CC nutrient use and/or improves the nutrient quality of the plant. The
 CC heterologous nucleic acid is contained within a bacterial artificial
 CC chromosome (BAC) or a yeast artificial chromosome (YAC). This
 CC polynucleotide sequence represents an oligo relating to the method for
 CC producing plant artificial chromosomes of the invention.
 XX Sequence 25 BP; 5 A; 5 C; 4 G; 11 T; 0 other;
 SQ Query Match 100.0%; Score 25; DB 25; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTCTGACAAACTGT 25
 |||||
 Db 1 GTTCAGCTTCTCTGACAAACTGT 25

RESULT 9
 AAC55546/c
 ID AAC55546 standard; DNA; 43 BP.
 XX AC AAC55546;
 XX 11-JAN-2001 (first entry)
 DT att site PCR primer attr2.
 XX Bacteriophage lambda; att; recombination site; attB; attP; attL;
 KW mutant; recombinational cloning; entry vector; destination vector;
 KW gene product targeting; fusion tag cleavage; PCR primer; ss.
 XX Bacteriophage lambda.
 OS Synthetic.
 OS WO200052027-A1.
 FN 08-SEP-2000.
 PD 08-SEP-2000.
 XX

PF 02-MAR-2000; 2000WO-US05432.
 XX 02-MAR-1999; 99US-012389.
 PR 23-MAR-1999; 99US-0126049.
 PR 28-MAY-1999; 99US-0136744.
 XX (LIFE-) LIFE TECHNOLOGIES INC.
 PA Hartley JL, Brasch MA, Temple GF, Cheo D;
 PI WPI; 2000-543948/49.
 DR Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 XX attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 PT recombinational cloning of polypeptides -
 PT Example 19; Page 142; 459pp; English.
 PS The present invention describes isolated nucleic acid molecules (I)
 XX encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
 CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity
 CC of interaction between the recombination site and a second att
 CC recombination site; and (2) an isolated nucleic acid molecule (III)
 CC comprising one or more mutated att recombination sites comprising at
 CC least one mutation in its core region that enhances the efficiency of
 CC recombination between a first nucleic acid molecule comprising the
 CC mutated att recombination site and a second nucleic acid molecule
 CC comprising a second recombination site that interacts with the mutated
 CC att recombination site. (I), (II), (III) primers, vectors and methods
 CC from the present invention are used for the recombinational cloning of
 CC nucleic acid molecules. They can be used for changing vectors, targeting
 CC gene products to intracellular locations, cleaving fusion tags from
 CC desired proteins, operably linking nucleic acid molecules of interest to
 CC regulatory genetic sequences, constructing genes for fusion proteins,
 CC changing copy number, changing replicons, cloning into phages and
 CC cloning. (I), (II), (III), host cells and vectors can be used in the
 CC production of polypeptides and antibodies. The present sequence is
 CC used in the exemplification of the present invention.
 XX Sequence 43 BP; 19 A; 5 C; 12 G; 7 T; 0 other;
 SQ Query Match 100.0%; Score 25; DB 21; Length 43;
 Best Local Similarity 100.0%; Pred. No. 0.12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTCTGACAAACTGT 25
 |||||
 Db 29 GTTCAGCTTCTCTGACAAACTGT 5

RESULT 10
 AAS06218/c
 ID AAS06218 standard; DNA; 43 BP.
 XX AC AAS06218;
 XX 12-SEP-2001 (first entry)
 DT PCR primer attR2 used to produce a population of hybrid DNA molecules.
 DE Bacteriophage lambda; recombination; att site; PCR primer; lambda Int;
 XX lambda integrase; therapeutic; ss.
 KW Bacteriophage lambda.
 OS Synthetic.
 OS WO200142509-A1.
 FN 14-JUN-2001.
 XX 11-DEC-2000; 2000WO-US33546.
 PF

PN WO200259294-A1.
XX
XX
XX 01-AUG-2002.
XX
XX
XX 24-JAN-2002; 2002WO-AU00073.
XX
XX 26-JAN-2001; 2001US-264067P.
XX 29-NOV-2001; 2001US-333743P.
XX
XX (CSR) COMMONWEALTH SCI & IND RES ORG.
XX
XX Wesley S, Waterhouse P, Helliwell C;
XX
XX WPI; 2002-682669/73.
XX
XX New vectors comprising operably linked DNA fragments having an origin
XX of replication, a selectable marker and a chimeric DNA construct,
XX PT useful for silencing target nucleic acids and for producing large
XX PT amounts of double-stranded RNA -
XX
XX
XX Disclosure; Page 14; 104pp; English.
XX
XX The present invention describes a vector (I) comprising operably linked
XX DNA fragments having: (a) origin of replication allowing replication in a
XX recipient cell, preferably in bacteria such as *Escherichia coli*;
XX (b) selectable marker region capable of being expressed in the recipient
XX cell; and (c) a chimeric DNA construct comprising: (i) promoter or
XX promoter region capable of being recognized by RNA polymerases of a
XX eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second,
XX third and fourth recombination sites; (iii) 3' transcription terminating
XX and polyadenylation region functional in the eukaryotic cell. The first
XX and fourth recombination sites, or the second and third recombination
XX sites are capable of reacting with a same recombination site, and
XX preferably are identical. The first and second recombination sites, or
XX the third and fourth recombination sites, do not recombine with each
XX other or with a same recombination site. The vector is useful for
XX producing large amounts of double-stranded RNA which can be used for
XX silencing target nucleic acid sequences. The vectors can also be used to
XX convert a DNA fragment into an inverted repeat structure. Plants
XX transformed with a vector from the present invention can be used in a
XX conventional breeding scheme to produce more plants with the same
XX characteristics or to introduce a chimeric gene for reduction of the
XX phenotypic expression of nucleic acids. The present sequence represents
XX the core sequence of recombination site attB1 which is given in the
XX exemplification of the present invention.
XX
XX Sequence 25 BP; 5 A; 5 C; 4 G; 11 T; 0 other;
XX
XX
XX Query Match 100.0%; Score 25; DB 24; Length 25;
XX Best Local Similarity 100.0%; Pred. No. 0.12;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX
XX QY 1 GTTCAGCTTCTTGTCACAACTTGT 25
XX
XX Db 1 GTTCAGCTTCTTGTCACAACTTGT 25
XX
XX
XX RESULT 7
XX ACC44659
XX ID ACC44659 standard; DNA; 25 BP.
XX
XX AC ACC44659;
XX
XX DT 29-MAY-2003 (first entry)
XX
XX DE Recombination site related oligonucleotide SEQ ID NO:50.
XX
XX XX Chromosome-based platform; artificial chromosome; eukaryotic chromosome;
XX att site; integrase; recombinase; ACes; Gene therapy; transgenic animal;
XX platform artificial chromosome expression system; PCR primer; ss.
XX
XX OS Synthetic.
XX
XX

PN WO200297059-A2.
XX
XX
XX 05-DEC-2002.
XX
XX
XX 30-MAY-2002; 2002WO-US17452.
XX
XX 30-MAY-2001; 2001US-294758P.
XX 21-MAR-2002; 2002US-366891P.
XX
XX (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
XX
XX Perkins E, Perez C, Lindenbaum M, Greene A, Leung J, Fleming E;
XX Stewart S, Shellard J;
XX
XX WPI; 2003-140461/13.
XX
XX Novel eukaryotic chromosome comprising one or many att sites which
XX permits site-directed integration in the presence of lambda-integrase,
XX PT useful for site-specific recombination-directed integration of DNA of
XX PT interest -
XX
XX
XX Claim 43; Page 143; 272pp; English.
XX
XX The present invention describes a eukaryotic chromosome (I) comprising
XX one or several att sites, where an att site is heterologous to the
XX chromosome, and permits site-directed integration in the presence of
XX lambda-integrase. Also described: (1) a platform artificial chromosome
XX expression system (ACes) (II) comprising several sites that participate
XX in recombinase catalysed recombination; and (2) a method (M1) for
XX introducing a heterologous nucleic acid into a platform artificial
XX chromosome. (I) can be used in gene therapy. (M1) is useful for
XX introducing a heterologous nucleic acid molecule into a platform
XX artificial chromosome, preferably an ACes. (II) is useful for producing a
XX transgenic animal (e.g. a fish, insect, reptile, amphibian, arachnid, or
XX mammal) by introducing (II) by cell fusion, lipid-mediated transfection
XX by a carrier system, microinjection, microcell fusion, electroporation,
XX microprojectile bombardment or direct DNA transfer into an embryonic
XX cell, preferably a stem cell or an embryo. (II) comprises a heterologous
XX nucleic acid that encodes a therapeutic product which is useful for
XX making a library of ACes comprising random portions of a genome. ACC44612
XX to ACC44732 and ABP96650 to ABP96657 represent sequences used in the
XX exemplification of the present invention.
XX
XX Sequence 25 BP; 5 A; 5 C; 4 G; 11 T; 0 other;
XX
XX
XX Query Match 100.0%; Score 25; DB 25; Length 25;
XX Best Local Similarity 100.0%; Pred. No. 0.12;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX
XX QY 1 GTTCAGCTTCTTGTCACAACTTGT 25
XX
XX Db 1 GTTCAGCTTCTTGTCACAACTTGT 25
XX
XX
XX RESULT 8
XX ABT16629
XX ID ABT16629 standard; DNA; 25 BP.
XX
XX AC ABT16629;
XX
XX DT 03-APR-2003 (first entry)
XX
XX DE Artificial plant chromosome related oligo SEQ ID NO 41.
XX
XX KW Plant artificial chromosome; PAC; transgenic plant; vaccine;
XX blood factor; herbicide; stress; agronomical; nutrient quality;
XX bacterial artificial chromosome; BAC; yeast artificial chromosome; YAC;
XX ds.
XX
XX OS Unidentified.
XX
XX PN WO200296923-A1.
XX

```
Oy 1 GTTCAGCTTCTTGACAAACTTGT 25
Db 1 GTTCAGCTTCTTGACAAACTTGT 25

RESULT 4
AAF55744
ID AAF55744 standard; DNA; 25 BP.
XX AC AAF55744;
XX DT 12-APR-2001 (first entry)
XX DE Recombination site attr2.
XX KW Recombination site; cloning; att; ss.
XX OS Unidentified.
XX PN US6171861-B1.
XX PD 09-JAN-2001.
XX PF 12-JAN-1998; 98US-0005476.
XX PR 07-JUN-1996; 96US-0663002.
XX PS 07-JUN-1995; 95US-0486139.
XX PA (LIFE-) LIFE TECHNOLOGIES INC.
XX PI Hartley JL, Brasch MA;
XX DR WPI; 2001-136877/14.
XX PT In vitro cloning of nucleic acid involves mixing vectors comprising
XX PT recombination sites and/or nucleic acid, incubating mixture to produce
XX PT chimeric molecule, contacting hosts with mixture and selecting host -
XX PS Claim 25; Column 46; 73pp; English.
XX CC The present invention relates to a method for in vitro cloning of a
XX CC nucleic acid of interest. The method involves mixing in vitro two vectors
XX CC each comprising at least one recombination site and the nucleic acid of
XX CC interest; incubating the mixture in the presence of at least one
XX CC recombination protein to result in recombination of the recombination
XX CC sites, leading to production of a chimeric nucleic acid molecule
XX CC comprising the nucleic acid of interest; contacting hosts with the
XX CC mixture; and selecting for a host comprising the chimeric nucleic acid
XX CC molecule; and selecting against a host comprising the vectors comprising
XX CC the second vector, to clone the nucleic acid. The present sequence is a
XX CC recombination site, which may be used in the method of the present
XX CC invention.
XX SQ Sequence 25 BP; 5 A; 5 C; 4 G; 11 T; 0 other;
Query Match 100.0%; Score 25; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTTCAGCTTCTTGACAAACTTGT 25
Db 1 GTTCAGCTTCTTGACAAACTTGT 25

RESULT 5
AAC87875
ID AAC87875 standard; DNA; 25 BP.
XX AC AAC87875;
XX DT 02-MAR-2001 (first entry)
XX DE Escherichia coli core region recombinant site attr2 SEQ ID NO:10.
```

```
XX Core region; recombination site; cloning; chimeric DNA;
XX characteristic; mutation; att site; lox site; ss.
XX OS Escherichia coli.
XX PN US6143557-A.
XX PD 07-NOV-2000.
XX PF 20-JAN-1999; 99US-0233493.
XX PR 07-JUN-1996; 96US-0663002.
XX PR 12-JAN-1998; 98US-0005476.
XX PR 07-JUN-1995; 95US-0486139.
XX XX (LIFE-) LIFE TECHNOLOGIES INC.
XX PI Brasch MA, Hartley JL;
XX DR WPI; 2001-049004/06.
XX PT Isolated nucleic acid molecules comprising a DNA segment having two
XX PT engineered recombination sites, derived from att or lox, which flank a
XX PT selectable marker and comprise a core region having an engineered
XX PT mutation -
XX PS Claim 1; Column 18; 73pp; English.
XX CC The present invention describes an isolated nucleic acid molecule (I)
XX CC comprising a first nucleic acid sequence having a defined sequence
XX CC (AAC87866 to AAC87881), sequences complementary to AAC87866 to AAC87881,
XX CC or an RNA sequence corresponding to AAC87866 to AAC87881. Also described
XX CC are: (1) an isolated nucleic acid molecule (II) comprising a first
XX CC mutated recombination site that removes one or more stop codons from the
XX CC recombination site or avoids hairpin formation, the recombination site
XX CC being an att or lox site; (2) an isolated nucleic acid molecule (III)
XX CC comprising a first att recombination site comprising a mutation that
XX CC enhances recombination specificity; (3) vectors (IV) comprising the
XX CC above mentioned nucleic acids; and (4) cells comprising the above
XX CC mentioned nucleic acids or (IV). The nucleic acids are used in
XX CC engineering a core region of a given recombination site to provide
XX CC mutative sites suitable for subcloning reactions. The use of nucleic
XX CC acids for obtaining engineered recombination in vitro or in vivo makes
XX CC the methods for DNA or RNA subcloning, highly specific, rapid, and
XX CC less labour intensive.
XX SQ Sequence 25 BP; 5 A; 5 C; 4 G; 11 T; 0 other;
Query Match 100.0%; Score 25; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTTCAGCTTCTTGACAAACTTGT 25
Db 1 GTTCAGCTTCTTGACAAACTTGT 25

RESULT 6
ABQ82122
ID ABQ82122 standard; DNA; 25 BP.
XX AC ABQ82122;
XX DT 11-DEC-2002 (first entry)
XX DE Core sequence of recombination site attr2 SEQ ID NO:5.
XX KW Chimeric nucleic acid construct; recombinational cloning; silencing;
XX KW recombination site; double stranded RNA; plant; ss.
XX OS Synthetic.
```

PT vitro or in vivo
 PS Claim 14; Page 55; 106pp; English.
 CC AAP48210-25 are att recombination site core region DNA sequences. The
 CC core region has at least one engineered mutation that enhances
 CC recombination in vitro in the formation of a Cointegrate or Product DNA.
 CC These core regions can be incorporated into novel vector donor DNA
 CC molecules. The nucleic acids, vectors and methods of the invention are
 CC used to obtain chimeric nucleic acid using recombination proteins and
 CC engineered recombination sites in vitro or in vivo. The improved
 CC specificity, speed and yields of the invention facilitates DNA or RNA
 CC subcloning, regulation or exchange useful for any related purpose, e.g.
 CC in vitro recombination of DNA segments, and in vitro or in vivo insertion
 CC or modification of transcribed, replicated, isolated or genomic DNA or
 CC RNA.
 XX Sequence 25 BP; 5 A; 5 C; 4 G; 11 T; 0 other;
 SQ Query Match 100.0%; Score 25; DB 18; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GTTCAGCTTCTGTGACAACTTGT 25
 Db 1 GTTCAGCTTCTGTGACAACTTGT 25
 RESULT 2
 AAX78944
 ID AAX78944 standard; DNA; 25 BP.
 AC AAX78944;
 XX 17-AUG-1999 (first entry)
 DT
 XX Oligonucleotide #10 for recombination and cloning method.
 DE Cloning; donor; recombination site; vector; chimeric; ss.
 XX Synthetic.
 OS WO9921977-A1.
 PN 06-MAY-1999.
 PD 26-OCT-1998; 98WO-US22589.
 PF 23-OCT-1998; 98US-0177387.
 PR 24-OCT-1997; 97US-0065930.
 XX (LIFE-) LIFE TECHNOLOGIES INC.
 PA Brasch MA, Fox DK, Hartley JL, Temple GF;
 PI WPI; 1999-303011/25.
 DR New nucleic acid cloning methods
 XX Disclosure; Page 161; 185pp; English.
 PS The invention relates to novel methods for cloning or subcloning one or
 CC more nucleic acid molecules (NAMS) comprising: (a) combining in vitro or
 CC in vivo: (1) at least one insert donor molecules (IDMs) comprising one
 CC or more desired nucleic acid segments flanked by at least 2
 CC recombination sites which do not recombine with each other; (2) one or
 CC more vector donor molecules (VDMs) comprising at least 2 recombination
 CC sites which do not recombine with each other; and (3) one or more
 CC site-specific recombination proteins; (b) incubating the combination to
 CC transfer one or more of the desired segments into one or more of the
 CC VDMs, thereby producing one or more desired product molecules (PMs). The
 CC methods can be used for the efficient and specific recombination of NAM
 CC segments. They can be used to generate chimeric DNA or RNA molecules that

CC have the desired characteristics and/or nucleic acid segments. The
 CC methods can also be used for changing vectors. The oligonucleotides
 CC AAX78935-X78994 are used in the method of the invention.
 XX Sequence 25 BP; 5 A; 5 C; 4 G; 11 T; 0 other;
 SQ Query Match 100.0%; Score 25; DB 20; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GTTCAGCTTCTGTGACAACTTGT 25
 Db 1 GTTCAGCTTCTGTGACAACTTGT 25
 RESULT 3
 AAD14438
 ID AAD14438 standard; DNA; 25 BP.
 XX AAD14438;
 AC AAD14438;
 XX 01-NOV-2001 (first entry)
 DT
 XX Recombination site attR2 DNA.
 DE Recombination site; copy number; replicon; recombinatorial cloning;
 XX attR2; ds.
 KW Unidentified.
 OS US6270969-B1.
 PN 07-AUG-2001.
 XX 20-JAN-1999; 99US-0233492.
 PF 07-JUN-1996; 96US-0663002.
 PR 07-JUN-1995; 95US-0486139.
 XX (INVI-) INVITROGEN CORP.
 PA Hartley JL, Brasch MA;
 PI WPI; 2001-488248/53.
 DR Methods for apposing nucleic acids comprising an expression signal and
 PT a gene/partial gene, using recombinatorial cloning by incubating the
 PT nucleic acids in the presence of a recombination protein under
 PT conditions for recombination -
 XX Claim 14; Column 18; 76pp; English.
 PS The invention relates to a method for apposing an expression signal and
 CC a gene or partial gene, using recombinatorial cloning. The method
 CC incubates nucleic acids comprising the expression signal and the gene/
 CC partial gene in the presence of a recombination protein under conditions
 CC sufficient to cause recombination and therefore appose the expression
 CC signal and the gene or partial gene. The methods are useful for apposing
 CC an expression signal and a gene or partial gene using recombinatorial
 CC cloning. The methods are also useful for changing vectors, constructing
 CC genes for fusion proteins, changing copy number, changing replicons,
 CC cloning into phages, and cloning e.g., PCR products (with an attB site
 CC at one end and a loxP site at the other end), genomic DNAs, and cDNAs.
 CC The methods are highly specific, rapid, and less labour intensive than
 CC prior art methods. The present sequence is a recombination site
 CC useful for recombination cloning.
 XX Sequence 25 BP; 5 A; 5 C; 4 G; 11 T; 0 other;
 SQ Query Match 100.0%; Score 25; DB 22; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
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Title: US-10-055-001A-5

Perfect score: 25

Sequence: 1 gttcagctttctgtacaacttgt 25

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	25	18	attR2 core region.
2	25	100.0	25	20	Oligonucleotide #1
3	25	100.0	25	22	Recombination site
4	25	100.0	25	22	Recombination site
5	25	100.0	25	22	Escherichia coli c
6	25	100.0	25	22	Core sequence of r
7	25	100.0	25	25	Recombination site
8	25	100.0	25	25	Artificial plant c

C	9	25	100.0	43	21	AAC55546	att site PCR prime
C	10	25	100.0	43	22	AAS06218	PCR primer attR2 u
	11	23.4	93.6	25	18	AAT48219	attR1 core region.
	12	23.4	93.6	25	20	AAI78943	Oligonucleotide #9
	13	23.4	93.6	25	22	AAI14437	Recombination site
	14	23.4	93.6	25	22	AAS06181	Phage-lambda recom
	15	23.4	93.6	25	22	AAF55743	Recombination site
	16	23.4	93.6	25	22	AAI87874	Escherichia coli c
	17	23.4	93.6	25	23	AAI14785	Lambda phage int x
	18	23.4	93.6	25	24	ABQ82121	Core sequence of r
	19	23.4	93.6	25	25	ACC44658	Recombination site
	20	23.4	93.6	25	25	ABZ58734	Att site nucleotid
	21	23.4	93.6	25	25	ABT16628	Artificial plant c
C	22	23.4	93.6	35	22	AAH19591	Plasmid pZC7201 c
C	23	23.4	93.6	35	24	ABL58593	Oligonucleotide MO
C	24	23.4	93.6	43	21	AAC55545	att site PCR prime
C	25	23.4	93.6	43	22	AAS06217	PCR primer attR1 u
C	26	23.4	93.6	82	21	AAC55503	Destination vector
C	27	23.4	93.6	87	21	AAC55517	Destination vector
C	28	23.4	93.6	95	21	AAC55497	Destination vector
C	29	23.4	93.6	102	21	AAC55458	GST expression cas
C	30	23.4	93.6	102	21	AAC55500	Destination vector
C	31	23.4	93.6	102	21	AAC55505	Destination vector
C	32	23.4	93.6	102	21	AAC55508	Destination vector
C	33	23.4	93.6	102	21	AAC55511	Destination vector
C	34	23.4	93.6	120	21	AAC55453	Trc expression cas
C	35	23.4	93.6	125	21	AAC55384	Recombination site
C	36	23.4	93.6	153	21	AAC55485	Destination vector
C	37	23.4	93.6	153	21	AAC55488	Destination vector
C	38	23.4	93.6	204	21	AAC55465	Destination vector
C	39	23.4	93.6	204	21	AAC55470	Destination vector
C	40	23.4	93.6	204	21	AAC55476	Destination vector
C	41	23.4	93.6	255	21	AAC55460	Hise-Trx expressio
C	42	23.4	93.6	255	21	AAC55478	Destination vector
C	43	23.4	93.6	306	21	AAC55468	Destination vector
C	44	23.4	93.6	306	21	AAC55514	Destination vector
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ALIGNMENTS

RESULT 1
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ID AAT48219 standard; DNA; 25 BP.
XX
AC AAT48219;
XX
DT 20-OCT-1997 (first entry)
XX
DE attR2 core region.
XX
DE
XX
KW att recombination site; core region; mutation; enhance; recombination;
KW vector; subcloning; regulation; exchange; ss.
XX
OS Synthetic.
XX
FN WO9640724-A1.
XX
PD 19-DEC-1996.
XX
PF 07-JUN-1996; 96WO-US10082.
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PR 07-JUN-1995; 95US-0486139.
XX
PA (LIFE-) LIFE TECHNOLOGIES INC.
XX
PI Brasch MA, Hartley JL;
DR WPI; 1997-065168/06.
XX
PT Nucleic acids, vectors and methods to obtain chimeric nucleic acid -
PT using recombinant proteins and engineered recombination sites in

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Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTGTGACAAACTTG 24
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RESULT 38
AR124528 25 bp DNA linear PAT 16-MAY-2001
LOCUS
DEFINITION Sequence 8 from patent US 6171861.
ACCESSION AR124528
VERSION AR124528.1 GI:14109889
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6171861-A 8 09-JAN-2001;
FEATURES
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BASE COUNT 6 a 7 c 3 g 9 t
ORIGIN

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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTCTGTGACAAACTTGT 25
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RESULT 39
AR163179 25 bp DNA linear PAT 17-OCT-2001
LOCUS
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ACCESSION AR163179
VERSION AR163179.1 GI:16233687
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6270969-A 8 07-AUG-2001;
FEATURES
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BASE COUNT 6 a 7 c 3 g 9 t
ORIGIN

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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
Db 4 CAGCTTCTGTGACAAACTTGT 25
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RESULT 40
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LOCUS
DEFINITION Sequence 8 from Patent EPI227147.
ACCESSION AX491647
VERSION AX491647.1 GI:22324155
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: EP 1227147-A 8 31-JUL-2002;
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ORIGIN

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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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VERSION      BD131342.1  GI:23226287
KEYWORDS     JP 2002500861-A/16.
SOURCE       unidentified
ORGANISM     unidentified.
REFERENCE    1 (bases 1 to 25)
AUTHORS     Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.
TITLE       Recombinational cloning using nucleic acids having recombination
JOURNAL     Patent: JP 2002500861-A 16 15-JAN-2002;
            LIFE TECHNOLOGIES INC
COMMENT      OS unknown
            PN JP 2002500861-A/16
            PD 15-JAN-2002
            PF 26-OCT-1998 JP 2000518069
            PR 24-OCT-1997 US 60/065930,23-OCT-1998 US 09/177387 PI
            JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DONNA K FOX PC
            C12N15/09,C12Q1/68,C12N15/00
            CC Description of Unknown Organism: recombination products FH
            Key Location/Qualifiers
            FT source 1..25
            FT Location/Qualifiers
            FT /organism='Unknown'.
            FT 1..25
            FT Location/Qualifiers
            FT /organism='unidentified'
            FT /mol_type='genomic DNA'
            FT /db_xref='taxon:32644'
            FT 5 a 4 c 6 g 10 t

BASE COUNT   5 a 4 c 6 g 10 t
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Query Match 89.6%; Score 22.4; DB 6; Length 25;
Best Local Similarity 95.8%; Pred. No. 47;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTGTGACAACTTG 24
Db 1 GTTCAGCTTCTGTGACAACTTG 24

RESULT 36
CVE311874 18691 bp DNA circular SYN 09-JUL-2002
LOCUS      Cloning vector PHELLSGATE.
DEFINITION AJ311874
ACCESSION  AJ311874.1 GI:15982218
VERSION     kanomycin resistance protein; neomycin phosphotransferase II; nptII
KEYWORDS    gene; promoter; spec gene; spectinomycin resistance protein;
            transposon Tn7.
SOURCE      Cloning vector PHELLSGATE
ORGANISM    Cloning vector PHELLSGATE
REFERENCE    1
AUTHORS      Wesley,V.S., Helliwell,C., Smith,N.A., Wang,M.B., Rouse,D., Liu,Q.,
            Gooding,ps., Singh,S.R., Abbott,D., Stoutjesdijk,A., Robinson,S.P.,
            Gleave,A.P., Green,A.G. and Waterhouse,P.M.
            Construct design for efficient, effective and high-throughput gene
            silencing in plants
JOURNAL     Plant J. 27 (6), 581-590 (2001)
MEDLINE     21461301
PUBMED      11576441
REFERENCE    2 (bases 1 to 18691)
AUTHORS      Waterhouse,P.M.
TITLE       Direct Submission
JOURNAL     Submitted (04-MAY-2001) Waterhouse P.M., Plant Industry,
            C.S.I.R.O., P.O. Box 1600, Canberra, ACT 2601, AUSTRALIA
FEATURES     Location/Qualifiers
            source 1..18691
            /organism="Cloning vector PHELLSGATE"
            /mol_type="genomic DNA"
            /db_xref="taxon:167049"
            /lab_host="Escherichia coli"
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            /notes="pHELLSGATE is a derivative of cloning vector
            PART27"

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/mol_type="genomic DNA"
/db_xref="taxon:358"
449..1442
/organism="Escherichia coli"
/mol_type="genomic DNA"
/db_xref="taxon:562"
1443..7792
/organism="Agrobacterium tumefaciens"
/mol_type="genomic DNA"
/db_xref="taxon:358"
7793..9388
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/mol_type="genomic DNA"
/db_xref="taxon:562"
9389..11673
/organism="Agrobacterium tumefaciens"
/mol_type="genomic DNA"
/db_xref="taxon:358"
11674..113019
/organism="Cauliflower mosaic virus"
/mol_type="genomic DNA"
/db_xref="taxon:10641"
14660..16258
/organism="Flaveria trinervia"
/mol_type="genomic DNA"
/db_xref="taxon:4227"
17922..18691
/organism="Agrobacterium tumefaciens"
/mol_type="genomic DNA"
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264..447
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448..1269
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/note="neomycin phosphotransferase II (nptII)"
/codon_start=1
/transl_table=11
/product="kanomycin resistance protein"
/protein_id="CAC86252.1"
/db_xref="GI:15982219"
/db_xref="REMTREMBL:CAC86252"
/transl_table="NAITLSAIFISARISAGSPAAWVERLFGYDWAQQTIGCSDA
VFRLSAQRPVLVKTDLSGALNELQDEARLSMLATGVCAAVLDVVTBGRDWLL
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LVDDDLDEHQGLAPAEFLKARMPDGLVVTGDACLPIMVNGRFSGFIDC
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/db_xref="GI:15982220"
/db_xref="REMTREMBL:CAC86253"
/transl_table="MREAVIAEVSTQLSEVVGVIERHLEPTLLAVHLYGSAVDGGLKP
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BASE COUNT      5 a      4 c      6 g      10 t
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Query Match      89.6%; Score 22.4; DB 6; Length 25;
Best Local Similarity 95.8%; Pred. No. 47;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTACAAACTTG 24
|||||
Db 1 GTTCAGCTTCTTGTACAAAGTTG 24

RESULT 31
AX491650
LOCUS      25 bp      DNA      linear      PAT 16-AUG-2002
DEFINITION Sequence 11 from Patent EP1227147.
ACCESSION  AX491650
VERSION     AX491650.1 GI:22324158
KEYWORDS
SOURCE      unidentified
ORGANISM    unidentified
REFERENCE 1
AUTHORS     Hartley,J.L. and Brasch,M.A.
TITLE       Recombinational cloning using engineered recombination sites
JOURNAL     Patent: EP 1227147-A 11 31-JUL-2002;
INVITROGEN CORPORATION (US)
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT      5 a      4 c      6 g      10 t
ORIGIN
Query Match      89.6%; Score 22.4; DB 6; Length 25;
Best Local Similarity 95.8%; Pred. No. 47;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTACAAACTTG 24
|||||
Db 1 GTTCAGCTTCTTGTACAAAGTTG 24

RESULT 32
AX491655
LOCUS      25 bp      DNA      linear      PAT 16-AUG-2002
DEFINITION Sequence 16 from Patent EP1227147.
ACCESSION  AX491655
VERSION     AX491655.1 GI:22324163
KEYWORDS
SOURCE      unidentified
ORGANISM    unidentified
REFERENCE 1
AUTHORS     Hartley,J.L. and Brasch,M.A.
TITLE       Recombinational cloning using engineered recombination sites
JOURNAL     Patent: EP 1227147-A 16 31-JUL-2002;
INVITROGEN CORPORATION (US)
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT      5 a      4 c      6 g      10 t
ORIGIN
Query Match      89.6%; Score 22.4; DB 6; Length 25;
Best Local Similarity 95.8%; Pred. No. 47;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTACAAACTTG 24
|||||
Db 1 GTTCAGCTTCTTGTACAAAGTTG 24

RESULT 33
AX498621
LOCUS      25 bp      DNA      linear      PAT 26-SEP-2002
DEFINITION Sequence 11 from Patent EP1229113.
ACCESSION  AX498621
VERSION     AX498621.1 GI:23343418
KEYWORDS
SOURCE      unidentified
ORGANISM    unidentified
REFERENCE 1
AUTHORS     Hartley,J.L. and Brasch,M.A.
TITLE       Recombinational cloning using engineered recombination sites
JOURNAL     Patent: EP 1229113-A 11 07-AUG-2002;
INVITROGEN CORPORATION (US)
FEATURES
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT      5 a      4 c      6 g      10 t
ORIGIN
Query Match      89.6%; Score 22.4; DB 6; Length 25;
Best Local Similarity 95.8%; Pred. No. 47;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTACAAACTTG 24
|||||
Db 1 GTTCAGCTTCTTGTACAAAGTTG 24

RESULT 34
AX498626
LOCUS      25 bp      DNA      linear      PAT 26-SEP-2002
DEFINITION Sequence 16 from Patent EP1229113.
ACCESSION  AX498626
VERSION     AX498626.1 GI:23343423
KEYWORDS
SOURCE      unidentified
ORGANISM    unidentified
REFERENCE 1
AUTHORS     Hartley,J.L. and Brasch,M.A.
TITLE       Recombinational cloning using engineered recombination sites
JOURNAL     Patent: EP 1229113-A 16 07-AUG-2002;
INVITROGEN CORPORATION (US)
FEATURES
source
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT      5 a      4 c      6 g      10 t
ORIGIN
Query Match      89.6%; Score 22.4; DB 6; Length 25;
Best Local Similarity 95.8%; Pred. No. 47;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTACAAACTTG 24
|||||
Db 1 GTTCAGCTTCTTGTACAAAGTTG 24

RESULT 35
BD131342
LOCUS      25 bp      DNA      linear      PAT 18-SEP-2002
DEFINITION Recombinational cloning using nucleic acids having recombination
sites.
ACCESSION  BD131342
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AR163182.1 GI:16233692
AR163182.1 GI:16233692
/note="Synthetically generated vector sequence"
/wd_xref=taxon:32830
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Best Local Similarity 96.0%; Pred. No. 5.1;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTTGTACAACTTGT 25
Db 3701 GTTCAGCTTTCTTTGTACAACTTGT 3725

RESULT 23
AX356862 13274 bp DNA linear PAT 13-FEB-2002
DEFINITION Sequence 20 from Patent WO206490.
ACCESSION AX356862
VERSION AX356862.1 GI:18674110
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Dudler,R., Schaffath,U. and Lawton,K.A.
TITLE Lipoxigenase genes, promoters, transit peptides and proteins
JOURNAL thereof
PATENT: WO 0206490-A 20 24-JAN-2002;
SYNGENTA PARTICIPATIONS AG (CH) ; Universitaet Zuerich (CH)
FEATURES
source
1. .13274
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
BASE COUNT 3343 a 3271 c 3178 g 3482 t
ORIGIN
Query Match 93.6%; Score 23.4; DB 6; Length 13274;
Best Local Similarity 96.0%; Pred. No. 5;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTTGTACAACTTGT 25
Db 4026 GTTCAGCTTTCTTTGTACAACTTGT 4050

RESULT 24
AF541939/c
LOCUS 13990 bp DNA linear SYN 01-DEC-2002
DEFINITION His-3 integration vector pJHAM007, complete sequence.
ACCESSION AF541939
VERSION AF541939.1 GI:25988997
KEYWORDS His-3 integration vector pJHAM007
SOURCE His-3 integration vector pJHAM007
ORGANISM artificial sequences; vectors.
REFERENCE 1 (bases 1 to 13990)
AUTHORS Haag,J.R., Lee,D.W. and Aramayo,R.
TITLE Description of a GATEWAY Destination Vector For High-Throughput
Construction of Neurospora crassa Histidine-3 (his-3)-Gene
Replacement Plasmids
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 13990)
AUTHORS Haag,J.R., Lee,D.W. and Aramayo,R.
TITLE Direct Submission
JOURNAL Submitted (27-AUG-2002) Biology, Texas A&M University, BSW #415,
College Station, TX 77843-3258, USA
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1. .8369
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1. .8554
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site"
8804..9463
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/protein_id="AAN76304.1"
/db_xref="GI:25988998"
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LKTVKKNKHFYPAFIHLARLMAHAFERMAKDGELVIWDSVHPCTVFEHQPTFF
SSLASEYHDDFRPLHIYSDVACVGENLAVPPKGFLENMFVSANPWVSTFSLNV
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/db_xref="GI:25988999"
/translation="MQFKVITYKRSRYLLFVDVQSDIIDTPGRMVIPLASARLLSD
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/note="attR2; Gateway; Bacteriophage Lambda recombination
site"
10419..13990
/note="his-3 right flank; his-3 target integration site"
BASE COUNT 3385 a 3549 c 3559 g 3497 t
ORIGIN
Query Match 93.6%; Score 23.4; DB 12; Length 13990;
Best Local Similarity 96.0%; Pred. No. 5;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTTGTACAACTTGT 25
Db 8454 GTTCAGCTTTCTTTGTACAACTTGT 8430

RESULT 25
BD131368 25 bp DNA linear PAT 18-SEP-2002
LOCUS Recombinational cloning using nucleic acids having recombination
DEFINITION sites.
ACCESSION BD131368
VERSION BD131368.1 GI:23226313
KEYWORDS JP 2002500861-A/42.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.
TITLE Recombinational cloning using nucleic acids having recombination
JOURNAL Patent: JP 2002500861-A 42 15-JAN-2002;
LIFE TECHNOLOGIES INC
COMMENT OS Unknown
PN JP 2002500861-A/42
PD 15-JAN-2002
PF 26-OCT-1998 JP 2000518069
PR 24-OCT-1997 US 60/065930,23-OCT-1998 US 09/177387 PI
JAMES L HARTLEY,MICHAEL A BRASCH,GARY F TEMPLE,DONNA K FOX PC
C12N15/09,C12N15/68,C12N15/00
CC Description of Unknown Organism: recombination products FH
Key Location/Qualifiers
FT source 1..25
/organism='Unknown'.
FEATURES
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1..25
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
4 a 3 c 3 g 9 t 6 others
BASE COUNT 4 a 3 c 3 g 9 t 6 others
ORIGIN
Query Match 90.4%; Score 22.6; DB 6; Length 25;

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Db      1030 GTTCAGCTTTTGTACAACTTGT 1006
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RESULT 20
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LOCUS      AY196825      12677 bp      DNA      circular SYN 26-FEB-2003
DEFINITION piggyBac transformation vector pB-UGIR w+, complete sequence.
ACCESSION  AY196825
VERSION     AY196825.1  GI:28565731
KEYWORDS
SOURCE      piggyBac transformation vector pB-UGIR w+
ORGANISM    piggyBac transformation vector pB-UGIR w+
            artificial sequences; vectors.
REFERENCE   1 (bases 1 to 12677)
AUTHORS     Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE       A toolkit for transformation and mutagenesis in Drosophila using
            piggyBac
JOURNAL     Unpublished
AUTHORS     Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE       Direct Submission
JOURNAL     Submitted (13-DEC-2002) Invertebrate Targets, Syngenta
            Biotechnology, Inc., 3054 Cornwallis Rd, Research Triangle Park, NC
            27709, USA
FEATURES   Location/Qualifiers
            source          1..12677
                        /organism="piggyBac transformation vector pB-UGIR w+"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:221642"
                        complement(11..>620)
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                        /transposon="piggyBac transposable element"
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                        /note="5x UAS hsp70 TATA signal"
            misc_feature    1003..2713
                        /note="Gateway recombination cassette A; attR1 Cmr ccdB
                        attR2"
            intron          2726..3040
                        /note="RpS5"
                        /number=3
            misc_feature    complement(3076..4788)
                        /note="Gateway recombination cassette B; attR1 Cmr ccdB
                        attR2"
            polyA_signal    4789..5246
                        /note="SV40"
            gene            5247..9369
                        /gene="w"
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                        /transposon="piggyBac transposable element"
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                        /note="Gateway recombination cassette A; attR1 Cmr ccdB
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            intron          2726..3040
                        /note="RpS5"
                        /number=3
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                        /note="Gateway recombination cassette B; attR1 Cmr ccdB
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            polyA_signal    4789..5246
                        /note="SV40"
            gene            5247..9369
                        /gene="w"
            repeat_region   complement(<9370..9819)
                        /transposon="piggyBac transposable element"
            BASE COUNT     3423 a 2924 c 2833 g 3497 t
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Query Match      93.6%; Score 23.4; DB 12; Length 12677;
Best Local Similarity 96.0%; Pred. No. 5.1;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GTTCAGCTTTCTGTACAACTTGT 25
|||||
Db      4760 GTTCAGCTTTTGTACAACTTGT 4784
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RESULT 21
AY196825/c
LOCUS      AY196825      12677 bp      DNA      circular SYN 26-FEB-2003
DEFINITION piggyBac transformation vector pB-UGIR w+, complete sequence.
ACCESSION  AY196825
VERSION     AY196825.1  GI:28565731
KEYWORDS
SOURCE      piggyBac transformation vector pB-UGIR w+
ORGANISM    piggyBac transformation vector pB-UGIR w+
            artificial sequences; vectors.
REFERENCE   1 (bases 1 to 12677)
AUTHORS     Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE       A toolkit for transformation and mutagenesis in Drosophila using
            piggyBac
JOURNAL     Unpublished
AUTHORS     Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE       Direct Submission
JOURNAL     Submitted (13-DEC-2002) Invertebrate Targets, Syngenta
            Biotechnology, Inc., 3054 Cornwallis Rd, Research Triangle Park, NC
            27709, USA
FEATURES   Location/Qualifiers
            source          1..12677
                        /organism="piggyBac transformation vector pB-UGIR w+"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:221642"
                        complement(11..>620)
            repeat_region   632..998
                        /transposon="piggyBac transposable element"
            TATA_signal     632..998
                        /note="5x UAS hsp70 TATA signal"
            misc_feature    1003..2713
                        /note="Gateway recombination cassette A; attR1 Cmr ccdB
                        attR2"
            intron          2726..3040
                        /note="RpS5"
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            gene            5247..9369
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                        /transposon="piggyBac transposable element"
            BASE COUNT     3423 a 2924 c 2833 g 3497 t
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Query Match      93.6%; Score 23.4; DB 12; Length 12677;
Best Local Similarity 96.0%; Pred. No. 5.1;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GTTCAGCTTTCTGTACAACTTGT 25
|||||
Db      4760 GTTCAGCTTTTGTACAACTTGT 4784
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RESULT 22
AX590202
LOCUS      AX590202      12789 bp      DNA      linear      PAT 24-JAN-2003
DEFINITION Sequence 9 from Patent WO02083888.
ACCESSION  AX590202
VERSION     AX590202.1  GI:27901286
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE   1
AUTHORS     Goossens,A. and Inz,D.
TITLE       The use of genes encoding membrane transporter pumps to stimulate
            the production of secondary metabolites in biological cells
            Patent: WO 02083888-A 9 24-OCT-2002;
            Vlaams Interuniversitair Instituut voor Biotechnologie vzw. (BE)
            Location/Qualifiers
            source          1..12789
                        /organism="synthetic construct"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:32630"
                        /note="vector pK7WG2D"
            BASE COUNT     3050 a 3326 c 3397 g 3015 t
            ORIGIN
Query Match      93.6%; Score 23.4; DB 6; Length 12789;

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AUTHORS     Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE       A toolkit for transformation and mutagenesis in Drosophila using
            piggyBac
JOURNAL     Unpublished
AUTHORS     Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE       Direct Submission
JOURNAL     Submitted (13-DEC-2002) Invertebrate Targets, Syngenta
            Biotechnology, Inc., 3054 Cornwallis Rd, Research Triangle Park, NC
            27709, USA
FEATURES   Location/Qualifiers
            source          1..12677
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                        /mol_type="genomic DNA"
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                        complement(11..>620)
            repeat_region   632..998
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            TATA_signal     632..998
                        /note="5x UAS hsp70 TATA signal"
            misc_feature    1003..2713
                        /note="Gateway recombination cassette A; attR1 Cmr ccdB
                        attR2"
            intron          2726..3040
                        /note="RpS5"
                        /number=3
            misc_feature    complement(3076..4788)
                        /note="Gateway recombination cassette B; attR1 Cmr ccdB
                        attR2"
            polyA_signal    4789..5246
                        /note="SV40"
            gene            5247..9369
                        /gene="w"
            repeat_region   complement(<9370..9819)
                        /transposon="piggyBac transposable element"
            BASE COUNT     3423 a 2924 c 2833 g 3497 t
            ORIGIN
Query Match      93.6%; Score 23.4; DB 12; Length 12677;
Best Local Similarity 96.0%; Pred. No. 5.1;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GTTCAGCTTTCTGTACAACTTGT 25
|||||
Db      1030 GTTCAGCTTTTGTACAACTTGT 1006
|||||
RESULT 22
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LOCUS      AX590202      12789 bp      DNA      linear      PAT 24-JAN-2003
DEFINITION Sequence 9 from Patent WO02083888.
ACCESSION  AX590202
VERSION     AX590202.1  GI:27901286
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE   1
AUTHORS     Goossens,A. and Inz,D.
TITLE       The use of genes encoding membrane transporter pumps to stimulate
            the production of secondary metabolites in biological cells
            Patent: WO 02083888-A 9 24-OCT-2002;
            Vlaams Interuniversitair Instituut voor Biotechnologie vzw. (BE)
            Location/Qualifiers
            source          1..12789
                        /organism="synthetic construct"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:32630"
                        /note="vector pK7WG2D"
            BASE COUNT     3050 a 3326 c 3397 g 3015 t
            ORIGIN
Query Match      93.6%; Score 23.4; DB 6; Length 12789;

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/genes="ccdB"
/notes="encodes a cytotoxic protein that is a potent poison
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/protein_id="AAM622303.1"
/db_xref="GI:21552740"
/translation="MQPKVYTKRSRYRLFDVDSQDIIDTGRRWVIFLASRLISD
KYSRELPPVHIGDESWMITDMASVPVSVIGSEVADLSHRENDIKNAINLMFWGI"
complement(2888..3547)
/genes="CmR"
complement(2888..3547)
/genes="CmR"
/function="confers resistance to antibiotic
chloramphenicol"
/codon_start=1
/product="CmR"
/protein_id="AAM622302.1"
/db_xref="GI:21552739"
/translation="MEKKITGVTVDISOWHRKEHPEAFQSVAAQCTYNQVOLDITAF
LTKVKNKHKVPAPFTHILARLMAHPEFRMAKQGLYIMDSVHPCTVFEHQETF
SLMSYHDDFQFLHIYSQDUCNGENLAYFKGFIENFPVSANPWVSFTSLNV
AMNDNFAPVFTMGKTYTGQDKVLMPLAIQVHHAVCDGPHVGRMLNELQQYCDQWQGG
A"
misc_feature
complement(3657..3783)
/notes="attR1 of Gateway conversion cassette frame A"
BASE COUNT 2337 a 2150 c 2185 g 2347 t
ORIGIN
Query Match 93.6%; Score 23.4; DB 12; Length 9019;
Best Local Similarity 96.0%; Pred. No. 5.4;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTACAAACTTGT 25
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Db 53 GTTCAGCTTCTTGTACAAACTTGT 29

RESULT 18
AY196824 LOCUS 11005 bp DNA circular SYN 26-FEB-2003
DEFINITION PiggyBac transformation vector pB-UGateway w+, complete sequence.
ACCESSION AY196824
VERSION AY196824.1 GI:28565716
KEYWORDS
SOURCE
ORGANISM
PiggyBac transformation vector pB-UGateway w+
artificial sequences; vectors.
REFERENCE
1 (bases 1 to 11005)
AUTHORS
Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE
A toolkit for transformation and mutagenesis in Drosophila using
PiggyBac
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 11005)
AUTHORS
Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE
Direct Submision
Submitted (13-DEC-2002) Invertebrate Targets, Syngenta
JOURNAL
Biotechnology, Inc., 3054 Cornwallis Rd, Research Triangle Park, NC
27709, USA
FEATURES
Location/Qualifiers
source
1..11005
/organism="piggyBac transformation vector pB-UGateway w+"
/mol_type="genomic DNA"
/db_xref="taxon:221641"
complement(11..3620)
repeat_region
TATA_signal
misc_feature
643..999
/notes="5x UAS hsp70 TATA signal"
1003..2713
/notes="Gateway recombination cassette A; attR1 CmR ccdB
attR2"
intron
2726..3040
/notes="RpS5"
/number=3
polyA_signal
3072..3573
/notes="SV40"
3574..7697
/genes="w"
repeat_region
complement(<7698..8147)
/notes="mini-white; derived from Drosophila"
/transposon="piggyBac transposable element"
BASE COUNT 2952 a 2528 c 2491 g 3034 t
ORIGIN
Query Match 93.6%; Score 23.4; DB 12; Length 11005;
Best Local Similarity 96.0%; Pred. No. 5.2;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTACAAACTTGT 25
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intron
2726..3040
/notes="RpS5"
/number=3
polyA_signal
3072..3573
/notes="SV40"
3574..7697
/genes="w"
repeat_region
complement(<7698..8147)
/notes="mini-white; derived from Drosophila"
/transposon="piggyBac transposable element"
BASE COUNT 2952 a 2528 c 2491 g 3034 t
ORIGIN
Query Match 93.6%; Score 23.4; DB 12; Length 11005;
Best Local Similarity 96.0%; Pred. No. 5.2;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTACAAACTTGT 25
|||||
Db 3089 GTTCAGCTTCTTGTACAAACTTGT 3113

RESULT 19
AY196824/c LOCUS 11005 bp DNA circular SYN 26-FEB-2003
DEFINITION PiggyBac transformation vector pB-UGateway w+, complete sequence.
ACCESSION AY196824
VERSION AY196824.1 GI:28565716
KEYWORDS
SOURCE
ORGANISM
PiggyBac transformation vector pB-UGateway w+
artificial sequences; vectors.
REFERENCE
1 (bases 1 to 11005)
AUTHORS
Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE
A toolkit for transformation and mutagenesis in Drosophila using
PiggyBac
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 11005)
AUTHORS
Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE
Direct Submision
Submitted (13-DEC-2002) Invertebrate Targets, Syngenta
JOURNAL
Biotechnology, Inc., 3054 Cornwallis Rd, Research Triangle Park, NC
27709, USA
FEATURES
Location/Qualifiers
source
1..11005
/organism="piggyBac transformation vector pB-UGateway w+"
/mol_type="genomic DNA"
/db_xref="taxon:221641"
complement(11..3620)
repeat_region
TATA_signal
misc_feature
643..999
/notes="5x UAS hsp70 TATA signal"
1003..2713
/notes="Gateway recombination cassette A; attR1 CmR ccdB
attR2"
intron
2726..3040
/notes="RpS5"
/number=3
polyA_signal
3072..3573
/notes="SV40"
3574..7697
/genes="w"
repeat_region
complement(<7698..8147)
/notes="mini-white; derived from Drosophila"
/transposon="piggyBac transposable element"
BASE COUNT 2952 a 2528 c 2491 g 3034 t
ORIGIN
Query Match 93.6%; Score 23.4; DB 12; Length 11005;
Best Local Similarity 96.0%; Pred. No. 5.2;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTACAAACTTGT 25
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LKTVMKHKHGFYPAFTHILARLMAHPEFRMAKDGELVINDSVHPCTYVFHQETET
SSLSEYHDDRFQFLHIYSQDVACYGENLAYFPKGFLENMFVSANPWVSFTSFDLNV
ANMNDFFAPVFTMGKIYTGQDKVLMPLAIQVHHA VCDGPHVGRMLNELQYCDWQGG
A"
gene      1263..1568
          /gene="ccdB"
CDS       1263..1568
          /gene="ccdB"
          /note="encodes a cytotoxic protein that is a potent poison
of DNA gyrase"
          /codon_start=1
          /product="CcdB"
          /protein_id="AAM62301.1"
          /db_xref="GI:21552738"
          /translation="MQFKVYTKRSRYRLFVDVQSDIIDTPGRMVIPLASARLLSD
KVSRELYPVVHIGDESWMRTTDMASVPVSVIGEEVADLSHRENDIKNAINLMFWGI"
misc_feature 1610..1736
          /note="attr2 of Gateway conversion cassette frame A"
misc_feature 1762..2048
          /note="contains intron 1 of Arabidopsis thaliana WRKY
transcription factor 33"
          /complement(2073..3783)
          /note="antisense orientation of Gateway conversion
cassette frame A containing attr1-R2 repeats, Cmr gene and
ccdB gene"
          /complement(2073..2199)
          /note="attr2 of Gateway conversion cassette frame A"
          /gene="ccdB"
          /complement(2241..2546)
          /gene="ccdB"
          /note="encodes a cytotoxic protein that is a potent poison
of DNA gyrase"
          /codon_start=1
          /product="CcdB"
          /protein_id="AAM62301.1"
          /db_xref="GI:21552740"
          /translation="MQFKVYTKRSRYRLFVDVQSDIIDTPGRMVIPLASARLLSD
KVSRELYPVVHIGDESWMRTTDMASVPVSVIGEEVADLSHRENDIKNAINLMFWGI"
          /complement(2888..3547)
          /gene="Cmr"
          /complement(2888..3547)
          /gene="Cmr"
          /function="confers resistance to antibiotic
chloramphenicol"
          /codon_start=1
          /product="Cmr"
          /protein_id="AAM62302.1"
          /db_xref="GI:21552739"
          /translation="MEKKITGYTTVDISQWHRKEHFEAFQSVQACTYNOTVQLDITAF
LKTVMKHKHGFYPAFTHILARLMAHPEFRMAKDGELVINDSVHPCTYVFHQETET
SSLSEYHDDRFQFLHIYSQDVACYGENLAYFPKGFLENMFVSANPWVSFTSFDLNV
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A"
misc_feature 3657..3783
          /note="attr1 of Gateway conversion cassette frame A"
BASE COUNT 2337 a 2150 c 2185 g 2347 t
ORIGIN

Query Match      93.6%; Score 23.4; DB 12; Length 9019;
Best local Similarity 96.0%; Pred. No. 5.4;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GTTCAGCTTTCTTGTACAACTTGT 25
      |||||
Db      3756 GTTCAGCTTTTGTACAACTTGT 3780

RESULT 17
AF408413/c
LOCUS      AF408413
DEFINITION Binary vector pJawohl8-RNAi, complete sequence.

```

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ACCESSION AF408413.1 GI:21552736
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 9019)
AUTHORS Ulker,B., Lipka,V., Rademacher,T.R. and Somssich,I.E.
TITLE pJawohl8-RNAi a binary vector for gene silencing in plants
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 9019)
AUTHORS Ulker,B., Lipka,V., Rademacher,T.R. and Somssich,I.E.
TITLE Direct Submision
JOURNAL Submitted (08-AUG-2001) Biochemistry, Max-Planck-Institut
f.Zuechtungsforschung, Carl-von-Linne Weg 10, Koeln, NRW D-50829,
Germany
FEATURES
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/organism="Binary vector pJawohl8-RNAi"
/mol_type="genomic DNA"
/db_xref="taxon:188084"
/focus
/note="binary plant gene silencing vector for one-step
cloning of inverted sequences"
3803..9019
/organism="Binary vector pJawohl8-RNAi"
/mol_type="genomic DNA"
/db_xref="taxon:176105"
26..1733
/note="sense orientation of Gateway conversion cassette
frame A containing attr1-R2 repeats, Cmr gene and ccdB
gene"
repeat_region
26..1733
/note="attr1 of Gateway conversion cassette frame A"
misc_feature 26..152
gene 262..921
CDS 262..921
/gene="Cmr"
262..921
/gene="Cmr"
/function="confers resistance to antibiotic
chloramphenicol"
/codon_start=1
/product="Cmr"
/protein_id="AAM62300.1"
/db_xref="GI:21552737"
/translation="MEKKITGYTTVDISQWHRKEHFEAFQSVQACTYNOTVQLDITAF
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SSLSEYHDDRFQFLHIYSQDVACYGENLAYFPKGFLENMFVSANPWVSFTSFDLNV
ANMNDFFAPVFTMGKIYTGQDKVLMPLAIQVHHA VCDGPHVGRMLNELQYCDWQGG
A"
gene 1263..1568
CDS 1263..1568
/gene="ccdB"
/gene="ccdB"
/note="encodes a cytotoxic protein that is a potent poison
of DNA gyrase"
/codon_start=1
/product="CcdB"
/protein_id="AAM62301.1"
/db_xref="GI:21552738"
/translation="MQFKVYTKRSRYRLFVDVQSDIIDTPGRMVIPLASARLLSD
KVSRELYPVVHIGDESWMRTTDMASVPVSVIGEEVADLSHRENDIKNAINLMFWGI"
1610..1736
/note="attr2 of Gateway conversion cassette frame A"
1762..2048
/note="contains intron 1 of Arabidopsis thaliana WRKY
transcription factor 33"
complement(2073..3783)
/note="antisense orientation of Gateway conversion
cassette frame A containing attr1-R2 repeats, Cmr gene and
ccdB gene"
complement(2073..2199)
/note="attr2 of Gateway conversion cassette frame A"
complement(2241..2546)

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/mol_type="genomic DNA"
/db_xref="taxon:225975"
31. .443
/note="358"
421. .424
/note="358"
456. 580
/note="attR1"
689. .1348
/gene="cat"
689. .1348
/gene="cat"
/codon_start=1
/product="chloramphenicol acetyl transferase"
/protein_id="CAD83080.1"
/db_xref="GI:29335743"
/translaton="MEKKITGYTVDISOWHRKEHFAFOSVAQCTYNQTVQLDITAF
LKTWKYKDDPQFLHIYHILARLMAHPEFRMAKDELVIWDSVHPCYTFHEQETTF
SSLWSEYHDDPQFLHIYHILARLMAHPEFRMAKDELVIWDSVHPCYTFHEQETTF
ANMNDPAPVPTMCKYITQSKVLMLPLAIQVHVAVCDFHVGRLNELQYCDSEWQGG
A"
1690. .1995
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1690. .1995
/gene="ccdB"
/codon_start=1
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/protein_id="CAD83081.1"
/db_xref="GI:29335744"
/translaton="MQFKVITYKRESRYLRFVDVQSDIIDTFGRRMVPLASARLLSD
KVSRLVPVHVHIGBESWRMTTDMASVPVSIGVEADLSHRENDIKNAINLFWGI"
2036. 2160
/note="attR2"
2168. .2463
/gene="nost"
2168. .2463
/gene="nost"
2606. 3466
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2606. .3466
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/db_xref="GI:29335745"
/translaton="MSIQHFRVALIPFAACLPVFAHPETLVKVKDAEDQLGARVGY
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YSPVTEKLTDTGTVRELCSAATMSDNTAANLLTTIGSPKELTAFLLNNQGHVTRL
DRWPELNEATPNDERDTMPVAMATTLRLITGLLTLLASRQQLIDWMEADKVAQPL
LRSLAPAGWFIADKSGAGERSGIIAALPGDKPSRIWITYTGSQATMDERNQIA
EIGASLIKHW"
BASE COUNT 1223 a 995 c 1065 g 1179 t
ORIGIN

Query Match 93.6%; Score 23.4; DB 12; Length 4462;
Best Local Similarity 96.0%; Pred. No. 6.2;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGACAAACTTGT 25
|||||
Db 480 GTTCAGCTTTCTTGACAAACTTGT 456

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/db_xref="GI:29335744"
/translaton="MQFKVITYKRESRYLRFVDVQSDIIDTFGRRMVPLASARLLSD
KVSRLVPVHVHIGBESWRMTTDMASVPVSIGVEADLSHRENDIKNAINLFWGI"
2036. 2160
/note="attR2"
2168. .2463
/gene="nost"
2168. .2463
/gene="nost"
2606. 3466
/gene="amp"
2606. .3466
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/codon_start=1
/product="beta lactamase"
/protein_id="CAD83082.1"
/db_xref="GI:29335745"
/translaton="MSIQHFRVALIPFAACLPVFAHPETLVKVKDAEDQLGARVGY
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YSPVTEKLTDTGTVRELCSAATMSDNTAANLLTTIGSPKELTAFLLNNQGHVTRL
DRWPELNEATPNDERDTMPVAMATTLRLITGLLTLLASRQQLIDWMEADKVAQPL
LRSLAPAGWFIADKSGAGERSGIIAALPGDKPSRIWITYTGSQATMDERNQIA
EIGASLIKHW"
BASE COUNT 1223 a 995 c 1065 g 1179 t
ORIGIN

Query Match 93.6%; Score 23.4; DB 12; Length 4462;
Best Local Similarity 96.0%; Pred. No. 6.2;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGACAAACTTGT 25
|||||
Db 480 GTTCAGCTTTCTTGACAAACTTGT 456

misc_feature
26. .152
/note="attR1 of Gateway conversion cassette frame A"
gene
262. .921
/gene="Cmr"
CDS
262. .921
/gene="Cmr"
/function="confers resistance to antibiotic chloramphenicol"
/codon_start=1
/product="Cmr"
/protein_id="AA062300.1"
/db_xref="GI:21552737"

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ORGANISM synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Plaetinck,G., Renard,J.P. and Bogaert,T.
TITLE Vector constructs
JOURNAL Patent: WO 0188121-A 10 22-NOV-2001;
Devgen NV (BE)
FEATURES
Location/Qualifiers
source 1. .5148
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/notes="Plasmid pGN39"
BASE COUNT 1359 a 1199 c 1279 g 1311 t
ORIGIN

Query Match 93.6%; Score 23.4; DB 6; Length 5148;
Best Local Similarity 96.0%; Pred. No. 6;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGACAAACTTGT 25
|||||
Db 171 GTTCAGCTTTCTTGACAAACTTGT 147

RESULT 16
AF408413 9019 bp DNA circular SYN 25-JUN-2002
LOCUS Binary vector pJawohl8-RNAi, complete sequence.
DEFINITION AF408413
ACCESSION AF408413
VERSION AF408413.1 GI:21552736
KEYWORDS
SOURCE Binary vector pJawohl8-RNAi
ORGANISM Binary vector pJawohl8-RNAi
artificial sequences; vectors.
REFERENCE
1 (bases 1 to 9019)
AUTHORS Ulker,B., Lipka,V., Rademacher,T.R. and Somssich,I.E.
TITLE pJawohl8-RNAi a binary vector for gene silencing in plants
JOURNAL Unpublished
REFERENCE
2 (bases 1 to 9019)
AUTHORS Ulker,B., Lipka,V., Rademacher,T.R. and Somssich,I.E.
TITLE Direct Submision
JOURNAL Submitted (08-AUG-2001) Biochemistry, Max-Planck-Institut
f. Zuechtungsforchung, Carl-von-Linne Weg 10, Koeln, NRW D-50829,
Germany
FEATURES
Location/Qualifiers
source 1. .9019
/organism="Binary vector pJawohl8-RNAi"
/mol_type="genomic DNA"
/db_xref="taxon:188084"
/focus
/note="binary plant gene silencing vector for one-step cloning of inverted sequences"
3803. .9019
/organism="Binary vector pJawohl3-RNAi"
/mol_type="genomic DNA"
/db_xref="taxon:176105"
26. .1733
/note="sense orientation of Gateway conversion cassette frame A containing attR1-R2 repeats, Cmr gene and ccdB gene"
misc_feature 26. .152
/note="attR1 of Gateway conversion cassette frame A"
gene 262. .921
/gene="Cmr"
CDS 262. .921
/gene="Cmr"
/function="confers resistance to antibiotic chloramphenicol"
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/product="Cmr"
/protein_id="AA062300.1"
/db_xref="GI:21552737"

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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
5 a 4 c 4 g 12 t
BASE COUNT
ORIGIN

Query Match 93.6%; Score 23.4; DB 6; Length 25;
Best Local Similarity 96.0%; Pred. No. 17;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAACTTGT 25
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 11
BD131335 25 bp DNA linear PAT 18-SEP-2002
LOCUS Recombinational cloning using nucleic acids having recombination
DEFINITION sites.
ACCESSION BD131335
VERSION JP 2002500861-A/9.
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.
TITLE Recombinational cloning using nucleic acids having recombination
JOURNAL Patent: JP 2002500861-A 9 15-JAN-2002;
LIFE TECHNOLOGIES INC
COMMENT OS Unknown
PN JP 2002500861-A/9
PD 15-JAN-2002
PF 26-OCT-1998 JP 2000518069
PR 24-OCT-1997 US 60/065930,23-OCT-1998 US 09/177387 PI
JAMES L HARTLEY,MICHAEL A BRASCH,GARY F TEMPLE,DONNA K FOX PC
C12N15/09,C12Q1/68,C12N15/00
CC Description of Unknown Organism: recombination products FH
Key source Location/Qualifiers
FT 1..25
FT /organism='Unknown'.

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source
1..25
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
5 a 4 c 4 g 12 t
BASE COUNT
ORIGIN

Query Match 93.6%; Score 23.4; DB 6; Length 25;
Best Local Similarity 96.0%; Pred. No. 17;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAACTTGT 25
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 12
AX684690/c 35 bp DNA linear PAT 29-MAR-2003
LOCUS Sequence 9 from Patent WO0224865.
DEFINITION AX684690
ACCESSION AX684690
VERSION AX684690.1 GI:29371240
KEYWORDS Escherichia coli
SOURCE Escherichia coli
ORGANISM Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
REFERENCE 1
AUTHORS Holtzman,D., Madden,K., Maxon,M. and Sherman,A.
TITLE Modulation of secondary metabolite production by zinc binuclear
Cluster proteins
Patent: WO 0224865-A 9 28-MAR-2002;
Microbia, INC. (US)
FEATURES
source
Location/Qualifiers
1..35
/organism="Escherichia coli"
/mol_type="genomic DNA"
/db_xref="taxon:562"
14 a 7 c 7 t
BASE COUNT
ORIGIN

Query Match 93.6%; Score 23.4; DB 6; Length 35;
Best Local Similarity 96.0%; Pred. No. 16;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAACTTGT 25
Db 35 GTTCAGCTTTTGTACAAACTTGT 11

RESULT 13
AX703501/c 1846 bp DNA linear PAT 03-APR-2003
LOCUS Sequence 63 from Patent WO02066653.
DEFINITION AX703501
ACCESSION AX703501
VERSION AX703501.1 GI:29538461
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Li,M. and Liu,Y.C.
TITLE Prokaryotic libraries and uses
JOURNAL Patent: WO 02066653-A 63 29-AUG-2002;
Xencor (US)
FEATURES
source
Location/Qualifiers
1..1846
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
527 a 381 c 434 g 504 t
BASE COUNT
ORIGIN

Query Match 93.6%; Score 23.4; DB 6; Length 1846;
Best Local Similarity 96.0%; Pred. No. 7.3;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAACTTGT 25
Db 25 GTTCAGCTTTTGTACAAACTTGT 1

RESULT 14
VFO551314/c 4462 bp DNA circular SYN 27-MAR-2003
LOCUS Transfection vector pBTdest.
DEFINITION AJ551314
ACCESSION AJ551314
VERSION AJ551314.1 GI:29335742
KEYWORDS amp gene; beta lactamase; cat gene; ccdB gene; chloramphenicol
acetyl transferase; control of cell death B protein.
SOURCE Transfection vector pBTdest
ORGANISM Transfection vector pBTdest
REFERENCE 1
AUTHORS Jakoby,M.J., Heim,M.A. and Weisshaar,B.
TITLE Use of a gateway compatible vector for transient plant transfection
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 4462)
AUTHORS Jakoby,M.J.
TITLE Direct Submission
JOURNAL Submitted (26-MAR-2003) Jakoby M.J., Salamini, MPI for Plant
Breeding Research, Carl-von-Linne Weg 10, 50829 Koeln, GERMANY
FEATURES
Location/Qualifiers

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QY 1 GTTCAGCTTTCTTGTACAAACTTGT 25
 Db 1 GTTCAGCTTTCTTGTACAAACTTGT 25

RESULT 6
 AR124529
 LOCUS AR124529 25 bp DNA linear PAT 16-MAY-2001
 DEFINITION Sequence 9 from patent US 6171861.
 ACCESSION AR124529
 VERSION AR124529.1 GI:14109890
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED.
 REFERENCE 1 (bases 1 to 25)
 AUTHORS Hartley,J.L. and Brasch,M.A.
 TITLE Recombinational cloning using engineered recombination sites
 JOURNAL Patent: US 6171861-A 9 09-JAN-2001;
 FEATURES
 source Location/Qualifiers
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RESULT 7
 AR163180
 LOCUS AR163180 25 bp DNA linear PAT 17-OCT-2001
 DEFINITION Sequence 9 from patent US 6270969.
 ACCESSION AR163180
 VERSION AR163180.1 GI:16233689
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED.
 REFERENCE 1 (bases 1 to 25)
 AUTHORS Hartley,J.L. and Brasch,M.A.
 TITLE Recombinational cloning using engineered recombination sites
 JOURNAL Patent: US 6270969-A 9 07-AUG-2001;
 FEATURES
 source Location/Qualifiers
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 /organism="unknown"
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BASE COUNT
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 Db 1 GTTCAGCTTTCTTGTACAAACTTGT 25

RESULT 8
 AX269136
 LOCUS AX269136 25 bp DNA linear PAT 29-OCT-2001
 DEFINITION Sequence 7 from Patent WO0174861.
 ACCESSION AX269136
 VERSION AX269136.1 GI:16542056
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.

REFERENCE 1
 AUTHORS Vile,R.G., Harrington,K., Murphy,S. and Bateman,A.
 TITLE Compositions and methods for tissue specific gene regulation therapy
 JOURNAL Patent: WO 0174861-A 7 11-OCT-2001;
 FEATURES
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 Db 1 GTTCAGCTTTCTTGTACAAACTTGT 25

RESULT 9
 AX491648
 LOCUS AX491648 25 bp DNA linear PAT 16-AUG-2002
 DEFINITION Sequence 9 from Patent EP1227147.
 ACCESSION AX491648
 VERSION AX491648.1 GI:22324156
 KEYWORDS
 SOURCE unidentified
 ORGANISM unidentified
 UNCLASSIFIED.
 REFERENCE 1
 AUTHORS Hartley,J.L. and Brasch,M.A.
 TITLE Recombinational cloning using engineered recombination sites
 JOURNAL Patent: EP 1227147-A 9 31-JUL-2002;
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 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 Db 1 GTTCAGCTTTCTTGTACAAACTTGT 25

RESULT 10
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 LOCUS AX498619 25 bp DNA linear PAT 26-SEP-2002
 DEFINITION Sequence 9 from Patent EP1229113.
 ACCESSION AX498619
 VERSION AX498619.1 GI:23343416
 KEYWORDS
 SOURCE unidentified
 ORGANISM unidentified
 UNCLASSIFIED.
 REFERENCE 1
 AUTHORS Hartley,J.L. and Brasch,M.A.
 TITLE Recombinational cloning using engineered recombination sites
 JOURNAL Patent: EP 1229113-A 9 07-AUG-2002;
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 source Location/Qualifiers
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Db 1 GTTCAGCTTCTGTACAACTTGT 25

RESULT 2
AX491649
LOCUS 25 bp DNA linear PAT 17-OCT-2001
DEFINITION
Sequence 10 from patent US 6270969.
ACCESSION AR163181
VERSION AR163181.1
KEYWORDS AR163181.1 GI:16233690
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6270969-A 10 07-AUG-2001;
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Location/Qualifiers
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BASE COUNT 5 a 5 c 4 g
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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GTTCAGCTTCTGTACAACTTGT 25

RESULT 3
AX491649
LOCUS 25 bp DNA linear PAT 16-AUG-2002
DEFINITION
Sequence 10 from Patent EP1227147.
ACCESSION AX491649
VERSION AX491649.1
KEYWORDS AR163181.1 GI:22324157
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: EP 1227147-A 10 31-JUL-2002;
FEATURES
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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTGTACAACTTGT 25
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RESULT 4
AX498620
LOCUS 25 bp DNA linear PAT 26-SEP-2002
DEFINITION
Sequence 10 from Patent EP1229113.
ACCESSION AX498620
VERSION AX498620.1
KEYWORDS AR163181.1 GI:23343417
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: EP 1229113-A 10 07-AUG-2002;
FEATURES
Location/Qualifiers
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/organism="unidentified"
/mol_type="genomic DNA"
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BASE COUNT 5 a 5 c 4 g
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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTGTACAACTTGT 25
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RESULT 5
BD131336
LOCUS 25 bp DNA linear PAT 18-SEP-2002
DEFINITION
Recombinational cloning using nucleic acids having recombination sites.
ACCESSION BD131336
VERSION BD131336.1
KEYWORDS GI:23226281
SOURCE JP 2002500861-A/10.
ORGANISM
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.
TITLE Recombinational cloning using nucleic acids having recombination sites
JOURNAL Patent: JP 2002500861-A 10 15-JAN-2002;
COMMENT LIFE TECHNOLOGIES INC
OS Unknown
PN JP 2002500861-A/10
PD 15-JAN-2002
PR 26-OCT-1998 JP 2000518069
PR 24-OCT-1997 US 60/065930, 23-OCT-1998 US 09/177387 PI
JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DONNA K FOX PC
C12N15/09, C12Q1/68, C12N15/00
CC Description of Unknown Organism: recombination products PH
Key Location/Qualifiers
FT source 1. .25
/organism='Unknown'.
FT Location/Qualifiers
1. .25
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
11 t
BASE COUNT 5 a 5 c 4 g
ORIGIN
Query Match 100.0%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTGTACAACTTGT 25
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Fri Nov 7 08:08:39 2003

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 6, 2003, 21:07:03 ; Search time 601 Seconds
(without alignments)
1701.732 Million cell updates/sec

Title: US-10-055-001A-5

Perfect score: 25
Sequence: 1 gttcagctttcttgracaacttgt 25

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Gapop 10.0 , Gapext 1.0

Searched: 2889711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 40: em.htgo.mus.*
- 41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	25	100.0	25	6	AR124530	AR124530 Sequence
2	25	100.0	25	6	AR163181	AR163181 Sequence
3	25	100.0	25	6	AX491649	AX491649 Sequence
4	25	100.0	25	6	AX498620	AX498620 Sequence
5	25	100.0	25	6	BD131336	BD131336 Recombina
6	23.4	93.6	25	6	AR124529	AR124529 Sequence
7	23.4	93.6	25	6	AR163180	AR163180 Sequence
8	23.4	93.6	25	6	AX269136	AX269136 Sequence
9	23.4	93.6	25	6	AX491648	AX491648 Sequence
10	23.4	93.6	25	6	AX498619	AX498619 Sequence
11	23.4	93.6	25	6	BD131335	BD131335 Recombina
12	23.4	93.6	35	6	AX684690	AX684690 Sequence
13	23.4	93.6	1846	6	AX703501	AX703501 Sequence
14	23.4	93.6	4462	12	VFO551314	AJ551314 Transfect
15	23.4	93.6	5148	6	AX306327	AX306327 Sequence
16	23.4	93.6	9019	12	AF408413	AF408413 Binary ve
17	23.4	93.6	9019	12	AY196824	AY196824 PiggyBac
18	23.4	93.6	11005	12	AY196824	AY196824 PiggyBac
19	23.4	93.6	11005	12	AY196825	AY196825 PiggyBac
20	23.4	93.6	12677	12	AY196825	AY196825 PiggyBac
21	23.4	93.6	12677	12	AX590202	AX590202 Sequence
22	23.4	93.6	12789	6	AX356862	AX356862 Sequence
23	23.4	93.6	13274	6	AF541939	AF541939 His-3 int
24	23.4	93.6	13990	12	BD131368	BD131368 Recombina
25	22.6	90.4	25	6	AR124531	AR124531 Sequence
26	22.4	89.6	25	6	AR124536	AR124536 Sequence
27	22.4	89.6	25	6	AR163182	AR163182 Sequence
28	22.4	89.6	25	6	AR163187	AR163187 Sequence
29	22.4	89.6	25	6	AX269137	AX269137 Sequence
30	22.4	89.6	25	6	AX491650	AX491650 Sequence
31	22.4	89.6	25	6	AX491655	AX491655 Sequence
32	22.4	89.6	25	6	AX498621	AX498621 Sequence
33	22.4	89.6	25	6	AX498626	AX498626 Sequence
34	22.4	89.6	25	6	BD131342	BD131342 Recombina
35	22.4	89.6	18691	12	CVE311874	AJ311874 Cloning v
36	22.4	89.6	18691	12	CVE311874	AJ311874 Cloning v
37	22.4	89.6	18691	12	CVE311874	AJ311874 Cloning v
38	22.4	89.6	25	6	AR124528	AR124528 Sequence
39	22.4	89.6	25	6	AR163179	AR163179 Sequence
40	22.4	89.6	25	6	AX491647	AX491647 Sequence
41	22.4	89.6	25	6	AX498618	AX498618 Sequence
42	21.8	87.2	25	6	BD131337	BD131337 Recombina
43	21.8	87.2	1846	6	AX703501	AX703501 Sequence
44	21.8	87.2	4462	12	VFO551314	AJ551314 Transfect
45	21.8	87.2	5148	6	AX306327	AX306327 Sequence

ALIGNMENTS

RESULT 1	AR124530	Sequence 10 from patent US 6171861.	25 bp	DNA	linear	PAT 16-MAY-2001
LOCUS	AR124530	Sequence 10 from patent US 6171861.				
DEFINITION	AR124530	Sequence 10 from patent US 6171861.				
ACCESSION	AR124530	Sequence 10 from patent US 6171861.				
VERSION	AR124530.1	GI:14109891				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 25)					
AUTHORS	Hartley,J.L. and Brasch,M.A.					
TITLE	Recombinational cloning using engineered recombination sites					
JOURNAL	Patent: US 6171861-A 10 09-JAN-2001;					
FEATURES	Location/Qualifiers					

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Best Local Similarity 96.0%; Pred. No. 1.4;
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Qy 1 GTTCAGCTTCTTGTACAAACTTGT 25
Db 13050 GTTCAGCTTTTGTACAAACTTGT 13026

RESULT 38
US-10-055-001A-26
; Sequence 26, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 26
; LENGTH: 17681
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE12
US-10-055-001A-26

Query Match 93.6%; Score 23.4; DB 14; Length 17681;
Best Local Similarity 96.0%; Pred. No. 1.4;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 16879 GTTCAGCTTTTGTACAAACTTGT 16903

RESULT 39
US-10-055-001A-26/c
; Sequence 26, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 26
; LENGTH: 17681
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE12
US-10-055-001A-26

Query Match 93.6%; Score 23.4; DB 14; Length 17681;
Best Local Similarity 96.0%; Pred. No. 1.4;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTTGTACAAACTTGT 25
Db 13050 GTTCAGCTTTTGTACAAACTTGT 13026

RESULT 40
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US-09-855-797A-42
; Sequence 42, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855,797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 42
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-855-797A-42

Query Match 90.4%; Score 22.6; DB 9; Length 25;
Best Local Similarity 76.0%; Pred. No. 1.1;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

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; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 17458
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE11
US-10-055-001A-25

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Best Local Similarity 96.0%; Pred. No. 1.4;
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Db 13050 GTTCAGCTTTTGTACAAACTTGT 13026

RESULT 34
US-10-385-546-7
; Sequence 7, Application US/10385546
; Publication No. US20030175783A1
; GENERAL INFORMATION:
; APPLICANT: Waterhouse, Peter
; APPLICANT: Wesley, Susan
; APPLICANT: Helliwell, Chris
; TITLE OF INVENTION: Methods and means for monitoring and modulating gene silencing
; FILE REFERENCE: COLINA-US2
; CURRENT APPLICATION NUMBER: US/10/385,546
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60363852
; PRIOR FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 17476
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: plasmid pHELLSGATE 8
US-10-385-546-7

Query Match          93.6%; Score 23.4; DB 12; Length 17476;
Best Local Similarity 96.0%; Pred. No. 1.4;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 16674 GTTCAGCTTTTGTACAAACTTGT 16698

RESULT 35
US-10-385-546-7/c
; Sequence 7, Application US/10385546
; Publication No. US20030175783A1
; GENERAL INFORMATION:
; APPLICANT: Waterhouse, Peter
; APPLICANT: Wesley, Susan
; APPLICANT: Helliwell, Chris
; TITLE OF INVENTION: Methods and means for monitoring and modulating gene silencing
; FILE REFERENCE: COLINA-US2
; CURRENT APPLICATION NUMBER: US/10/385,546
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60363852
; PRIOR FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
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; SEQ ID NO 7
; LENGTH: 17476
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: plasmid pHELLSGATE 8
US-10-385-546-7

Query Match          93.6%; Score 23.4; DB 12; Length 17476;
Best Local Similarity 96.0%; Pred. No. 1.4;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTACAAACTTGT 25
Db 13050 GTTCAGCTTTTGTACAAACTTGT 13026

RESULT 36
US-10-055-001A-24
; Sequence 24, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 17476
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE8
US-10-055-001A-24

Query Match          93.6%; Score 23.4; DB 14; Length 17476;
Best Local Similarity 96.0%; Pred. No. 1.4;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 16674 GTTCAGCTTTTGTACAAACTTGT 16698

RESULT 37
US-10-055-001A-24/c
; Sequence 24, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 17476
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE8
US-10-055-001A-24

Query Match          93.6%; Score 23.4; DB 14; Length 17476;
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; APPLICANT: Byrd, Devon R.N.
; TITLE OF INVENTION: Use of Multiple Recombination Sites with Unique Specificity in
; FILE REFERENCE: 0942.5010002
; CURRENT APPLICATION NUMBER: US/09/732,914
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/169,983
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 60/188,020
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 44
; LENGTH: 43
; TYPE: DNA
; ORGANISM: attR1 PCR Primer
US-09-732-914-44

Query Match 93.6%; Score 23.4; DB 9; Length 43;
Best Local Similarity 96.0%; Pred. No. 0.52;
Matches 24; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAACTTGT 25
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Db 29 GTTCAGCTTTTGTACAAACTTGT 5

RESULT 27
US-10-151-690-19/c
; Sequence 19, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MO
; FILE REFERENCE: 0942.5120001
; CURRENT APPLICATION NUMBER: US/10/151,690
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 120
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: plasmid pDEST1
US-10-151-690-19

Query Match 93.6%; Score 23.4; DB 14; Length 120;
Best Local Similarity 96.0%; Pred. No. 0.62;
Matches 24; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAACTTGT 25
|||
Db 118 GTTCAGCTTTTGTACAAACTTGT 94

RESULT 28
US-10-023-208-63/c
; Sequence 63, Application US/10023208
; Publication No. US20030124537A1
; GENERAL INFORMATION:
; APPLICANT: Li, Min
; APPLICANT: Liu, Yuan-Ching
; TITLE OF INVENTION: PROCAROTIC LIBRARIES AND USES
; FILE REFERENCE: A-70174-1/RET/RMS/RMK

; CURRENT APPLICATION NUMBER: US/10/023,208
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: US 60/256,163
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 1846
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-023-208-63

Query Match 93.6%; Score 23.4; DB 14; Length 1846;
Best Local Similarity 96.0%; Pred. No. 0.98;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAACTTGT 25
|||
Db 25 GTTCAGCTTTTGTACAAACTTGT 1

RESULT 29
US-10-241-596-137/c
; Sequence 137, Application US/10241596
; Publication No. US20030166238A1
; GENERAL INFORMATION:
; APPLICANT: Microbiological Research Authority
; APPLICANT: The Speywood Laboratory Limited
; TITLE OF INVENTION: Recombinant Toxin Fragments
; FILE REFERENCE: 1581.0130003
; CURRENT APPLICATION NUMBER: US/10/241,596
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 09/255,829
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: US 09/242,689
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: PCT/GB97/02273
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 08/782,893
; PRIOR FILING DATE: 1996-12-27
; PRIOR APPLICATION NUMBER: GB 9625996.5
; PRIOR FILING DATE: 1996-12-13
; PRIOR APPLICATION NUMBER: GB 9617671.4
; PRIOR FILING DATE: 1996-08-23
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 137
; LENGTH: 5558
; TYPE: DNA
; ORGANISM: Clostridium botulinum
US-10-241-596-137

Query Match 93.6%; Score 23.4; DB 12; Length 5558;
Best Local Similarity 96.0%; Pred. No. 1.2;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAACTTGT 25
|||
Db 1666 GTTCAGCTTTTGTACAAACTTGT 1642

RESULT 30
US-10-151-690-20/c
; Sequence 20, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.


```

; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-162-879-9
Query Match 93.6%; Score 23.4; DB 14; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.47;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTTGACAAACTTGT 25
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 23
US-10-161-403-49
; Sequence 49, Application US/10161403
; Publication No. US20030119104A1
; GENERAL INFORMATION:
; APPLICANT: Perkins, Edward
; APPLICANT: Perez, Carl
; APPLICANT: Lindenbaum, Michael
; APPLICANT: Greene, Amy
; APPLICANT: Leung, Josephine
; APPLICANT: Fleming, Elena
; APPLICANT: Stewart, Sandra
; APPLICANT: Shellard, Joan
; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
; FILE REFERENCE: 24601-420
; CURRENT APPLICATION NUMBER: US/10/161,403
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/294,758
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 60/366,891
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: attr1
US-10-161-403-49
Query Match 93.6%; Score 23.4; DB 14; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.47;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTTGACAAACTTGT 25
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 24
US-10-151-690-32
; Sequence 32, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MO
; FILE REFERENCE: 0942.5120001
; CURRENT APPLICATION NUMBER: US/10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 25
; TYPE: DNA
; ORGANISM: attr1
US-10-151-690-32
Query Match 93.6%; Score 23.4; DB 14; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.47;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTTGACAAACTTGT 25
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 25
US-09-974-760B-33/c
; Sequence 33, Application US/09974760B
; Publication No. US20030143705A1
; GENERAL INFORMATION:
; APPLICANT: Roberts, Shannon
; APPLICANT: Sherman, Amir
; APPLICANT: Trueheart, Joshua
; APPLICANT: Milne, G. Todd
; TITLE OF INVENTION: LOVE VARIANT REGULATOR MOLECULES
; FILE REFERENCE: 14184-009001
; CURRENT APPLICATION NUMBER: US/09/974,760B
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-974-760B-33
Query Match 93.6%; Score 23.4; DB 12; Length 35;
Best Local Similarity 96.0%; Pred. No. 0.5;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTTGACAAACTTGT 25
Db 35 GTTCAGCTTTTGTACAAACTTGT 11

RESULT 26
US-09-732-914-44/c
; Sequence 44, Application US/09732914
; Patent No. US20020007051A1
; GENERAL INFORMATION:
; APPLICANT: Cheo, David
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Hartley, James L.
```

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; CURRENT APPLICATION NUMBER: US/10/300,892
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/907,719
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
; US-10-300-892-9

Query Match          93.6%; Score 23.4; DB 12; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.47;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAACTTGT 25
   ||||| ||||| ||||| ||||| |||||
Db 1 GTTCAGCTTTTGTACAACTTGT 25

RESULT 20
US-10-055-001A-4
; Sequence 4, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; FILE REFERENCE: HELLGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: core sequence of recombination site attr1
; US-10-055-001A-4

Query Match          93.6%; Score 23.4; DB 14; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.47;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAACTTGT 25
   ||||| ||||| ||||| ||||| |||||
Db 1 GTTCAGCTTTTGTACAACTTGT 25

RESULT 21
US-10-058-292-9
; Sequence 9, Application US/10058292
; Publication No. US20030054552A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; RECOMBINATION SITES
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC

QY 1 GTTCAGCTTTCTGTACAACTTGT 25
   ||||| ||||| ||||| ||||| |||||
Db 1 GTTCAGCTTTTGTACAACTTGT 25

RESULT 22
US-10-162-879-9
; Sequence 9, Application US/10162879
; Publication No. US20030068799A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; RECOMBINATION SITES
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC

QY 1 GTTCAGCTTTCTGTACAACTTGT 25
   ||||| ||||| ||||| ||||| |||||
Db 1 GTTCAGCTTTTGTACAACTTGT 25
```

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; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/058,292
; FILING DATE: 30-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/432,085
; FILING DATE: 1999-11-02
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-Jan-1999
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-Jan-1998
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-Jun-1996
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-Jun-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-058-292-9

Query Match          93.6%; Score 23.4; DB 14; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.47;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAACTTGT 25
   ||||| ||||| ||||| ||||| |||||
Db 1 GTTCAGCTTTTGTACAACTTGT 25

RESULT 22
US-10-162-879-9
; Sequence 9, Application US/10162879
; Publication No. US20030068799A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; RECOMBINATION SITES
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC

QY 1 GTTCAGCTTTCTGTACAACTTGT 25
   ||||| ||||| ||||| ||||| |||||
Db 1 GTTCAGCTTTTGTACAACTTGT 25

RESULT 23
US-10-058-292-9
; Sequence 9, Application US/10058292
; Publication No. US20030054552A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; RECOMBINATION SITES
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC

QY 1 GTTCAGCTTTCTGTACAACTTGT 25
   ||||| ||||| ||||| ||||| |||||
Db 1 GTTCAGCTTTTGTACAACTTGT 25
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; Publication No. US20020192819A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,719
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 9
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
; US-09-907-719-9

Query Match          93.6%; Score 23.4; DB 10; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.47;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTCACAACTTGT 25
Db 1 GTTCAGCTTCTTGTCACAACTTGT 25

RESULT 17
US-09-432-085-9
; Sequence 9, Application US/09432085
; Publication No. US20030100110A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,085
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139

```

```

; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; US-09-432-085-9

Query Match          93.6%; Score 23.4; DB 11; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.47;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTCACAACTTGT 25
Db 1 GTTCAGCTTCTTGTCACAACTTGT 25

RESULT 18
US-09-985-448-9
; Sequence 9, Application US/09985448
; Publication No. US20030157716A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/985,448
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 9
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
; US-09-985-448-9

Query Match          93.6%; Score 23.4; DB 12; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.47;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTCACAACTTGT 25
Db 1 GTTCAGCTTCTTGTCACAACTTGT 25

RESULT 19
US-10-300-892-9
; Sequence 9, Application US/10300892
; Publication No. US20030175970A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004

```

; Sequence 8, Application US/09732914
; Patent No. US20020007051A1
; GENERAL INFORMATION:
; APPLICANT: Cheo, David
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Hartley, James L.
; APPLICANT: Byrd, Devon R.N.
; TITLE OF INVENTION: Use of Multiple Recombination Sites with Unique Specificity in
; TITLE OF INVENTION: Recombinational Cloning
; FILE REFERENCE: 0942.5010002
; CURRENT APPLICATION NUMBER: US/09/732,914
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/169,983
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 60/188,020
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 25
; TYPE: DNA
; ORGANISM: attr1
US-09-732-914-8

Query Match 93.6%; Score 23.4; DB 9; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.47; 1; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGACAACTTGT 25
Db 1 GTTCAGCTTTCTTGACAACTTGT 25

RESULT 13
US-09-855-797A-9
; Sequence 9, Application US/09855797A
; Patent No. US2002009457A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855,797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-855-797A-9

Query Match 93.6%; Score 23.4; DB 9; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.47; 1; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGACAACTTGT 25
Db 1 GTTCAGCTTTCTTGACAACTTGT 25

RESULT 14

US-09-822-634-7
; Sequence 7, Application US/09822634
; Patent No. US2002015056A1
; GENERAL INFORMATION:
; APPLICANT: Vile, Richard G.
; APPLICANT: Harrington, Kevin
; APPLICANT: Bateman, Andrew
; APPLICANT: Murphy, Steven
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TISSUE
; TITLE OF INVENTION: SPECIFIC GENE REGULATION THERAPY
; FILE REFERENCE: 07039-289001
; CURRENT APPLICATION NUMBER: US/09/822,634
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 60/193,977
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated vector sequence
US-09-822-634-7

Query Match 93.6%; Score 23.4; DB 10; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.47; 1; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGACAACTTGT 25
Db 1 GTTCAGCTTTCTTGACAACTTGT 25

RESULT 15
US-09-907-900-9
; Sequence 9, Application US/09907900
; Patent No. US20020172997A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,900
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
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Db 1 GTTCAGCTTTCTTGACAACTTGT 25

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; Sequence 9, Application US/09907719

us-10-055-001a-5.rnpb

Fri Nov 7 08:08:40 2003

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; Sequence 10, Application US/10162879
; Publication No. US2003006879A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; Brach, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/162,879
; FILING DATE: 06-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,085
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2540
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-162-879-10

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RESULT 10
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; Sequence 50, Application US/10161403
; Publication No. US2003011910A1
; GENERAL INFORMATION:
; APPLICANT: Perkins, Edward
; APPLICANT: Perez, Carl
; APPLICANT: Lindenbaum, Michael
; APPLICANT: Greene, Amy
; APPLICANT: Leung, Josephine
; APPLICANT: Fleming, Elena
; APPLICANT: Stewart, Sandra
; APPLICANT: Shellard, Joan
; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
; FILE REFERENCE: 24601-420
; CURRENT APPLICATION NUMBER: US/10/161,403
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/294,758
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 60/366,891
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 129
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; OTHER INFORMATION: attr2
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; Patent No. US20020007051A1
; GENERAL INFORMATION:
; APPLICANT: Cheo, David
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Hartley, James L.
; APPLICANT: Byrd, Devon R.N.
; TITLE OF INVENTION: Use of Multiple Recombination Sites with Unique Specificity in
; Recombinational Cloning
; FILE REFERENCE: 0942.5010002
; CURRENT APPLICATION NUMBER: US/09/732,914
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/169,983
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 60/188,020
; PRIOR FILING DATE: 2000-03-09
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US-09-732-914-8

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US-09-907-900-10
; Sequence 10, Application US/09907900
; Publication No. US20020172997A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/907,900
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 10
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-900-10
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Best Local Similarity 100.0%; Pred. No. 0.089;
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; Sequence 10, Application US/09907719
; Publication No. US20020192819A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT FILING DATE: 2001-07-19
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentin Ver. 2.0
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; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
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; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
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; Sequence 10, Application US/09432085
; Publication No. US20030100110A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/432,085
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-432-085-10
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; Sequence 10, Application US/09985448
; Publication No. US20030157716A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
US-09-985-448-10
Query Match 100.0%; Score 25; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.089;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GTTCAGCTTCTTGACAACTTGT 25

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US-09-432-085-10

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GenCore version 5.1.6
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Title: US-10-055-001A-5

Perfect score: 25

Sequence: 1 gttcagctttctgtacaaactgt 25

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5	25	100.0	25	12	US-09-985-448-10
6	25	100.0	25	12	US-10-300-892-10
7	25	100.0	25	14	US-10-055-001A-5
8	25	100.0	25	14	US-10-058-292-10
9	25	100.0	25	14	US-10-162-879-10
10	25	100.0	25	14	US-10-161-403-50
11	25	100.0	43	9	US-09-732-914-45
12	23.4	93.6	25	9	US-09-732-914-8
13	23.4	93.6	25	9	US-09-855-797A-9
14	23.4	93.6	25	10	US-09-822-634-7
15	23.4	93.6	25	10	US-09-907-900-9
16	23.4	93.6	25	10	US-09-907-719-9

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ALIGNMENTS

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; Sequence 10, Application US/09855797A

; Patent No. US20020094574A1

; GENERAL INFORMATION:

; APPLICANT: Hartley, James L.

; APPLICANT: Brasch, Michael A.

; APPLICANT: Temple, Gary F.

; APPLICANT: Fox, Donna K.

; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having

; TITLE OF INVENTION: Recombination Sites

; FILE REFERENCE: 0942.2850008

; CURRENT APPLICATION NUMBER: US/09/855,797A

; CURRENT FILING DATE: 2001-05-16

; PRIOR APPLICATION NUMBER: 09/296,281

; PRIOR FILING DATE: 1999-04-22

; PRIOR APPLICATION NUMBER: US 60/065,930

; PRIOR FILING DATE: 1997-10-24

; NUMBER OF SEQ ID NOS: 60

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 10

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Unknown

; FEATURE:

; OTHER INFORMATION: Description of Unknown Organism: recombination

; OTHER INFORMATION: products

US-09-855-797A-10

Query Match 100.0%; Score 25; DB 9; Length 25;

Best Local Similarity 100.0%; Pred.No. 0.089;

Mismatches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GTTCAGCTTCTGTGACAAACTGT 25

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ORGANISM     synthetic construct
             artificial sequences.
REFERENCE    1
AUTHORS      Vile,R.G., Harrington,K., Murphy,S. and Bateman,A.
TITLE        Compositions and methods for tissue specific gene regulation
             therapy
JOURNAL      Patent: WO 0174861-A 11 11-OCT-2001;
             MAYO FOUNDATION FOR MEDICAL EDUCATION AND RESEARCH (US)
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ACCESSION    AX491653
VERSION      AX491653.1 GI:22324161
KEYWORDS
SOURCE        unidentified
              unidentified
              unclassified.
REFERENCE     1
AUTHORS       Hartley,J.L. and Brasch,M.A.
TITLE         Recombinational cloning using engineered recombination sites
JOURNAL       Patent: EP 1227147-A 14 31-JUL-2002;
              INVITROGEN CORPORATION (US)
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ACCESSION    AX498624
VERSION      AX498624.1 GI:23343421
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SOURCE        unidentified
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              unclassified.
REFERENCE     1
AUTHORS       Hartley,J.L. and Brasch,M.A.
TITLE         Recombinational cloning using engineered recombination sites
JOURNAL       Patent: EP 1229113-A 14 07-AUG-2002;
              INVITROGEN CORPORATION (US)
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TITLE      Recombinational cloning using engineered recombination sites
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ACCESSION      ARI24534
VERSION      ARI24534.1 GI:14109895
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SOURCE      Unknown.
ORGANISM      Unclassified.
REFERENCE      1 (bases 1 to 25)
AUTHORS      Hartley,J.L. and Brasch,M.A.
TITLE      Recombinational cloning using engineered recombination sites
JOURNAL      Patent: US 6171861-A 14 09-JAN-2001;
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Query Match      88.0%; Score 22; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 CAGCTTTCTGTACAAAGTTG 25
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Db      4 CAGCTTTCTGTACAAAGTTG 25

RESULT 37
ARI63185
LOCUS      ARI63185
DEFINITION      Sequence 14 from patent US 6270969.
ACCESSION      ARI63185
VERSION      ARI63185.1 GI:16233697
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unclassified.
REFERENCE      1 (bases 1 to 25)
AUTHORS      Hartley,J.L. and Brasch,M.A.
TITLE      Recombinational cloning using engineered recombination sites
JOURNAL      Patent: US 6270969-A 14 07-AUG-2001;
FEATURES
      source
      Location/Qualifiers
      1..25
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BASE COUNT      6 a      6 c      5 g      8 t
ORIGIN

Query Match      88.0%; Score 22; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 CAGCTTTCTGTACAAAGTTG 25
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Db      4 CAGCTTTCTGTACAAAGTTG 25

RESULT 38
AX269140
LOCUS      AX269140
DEFINITION      Sequence 11 from Patent WO01/74861.
ACCESSION      AX269140

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632..998
/feature="5x UAS hsp70 TATA signal"
1003..2713
/notes="Gateway recombination cassette A; attR1 CmR ccdB
attR2"
2726..3040
/feature="RpS5"
/number=3
complement(3076..4788)
/notes="Gateway recombination cassette B; attR1 CmR ccdB
attR2"
4789..5246
/feature="SV40"
5247..9369
/feature="w"
/notes="mini-white; derived from Drosophila"
complement(<9370..9819)
/transposon="piggyBac transposable element"
BASE COUNT 3423 a 2924 c 2833 g 3497 t
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Best Local Similarity 95.8%; Pred. No. 4.4;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTCAGCTTCTGTGACAAAGTTG 24
|||||
Db 2686 GTTCAGCTTCTGTGACAAAGTTG 2709
|||||
RESULT 32
AY196825/c
LOCUS AY196825 12677 bp DNA circular SYN 26-FEB-2003
DEFINITION PiggyBac transformation vector pB-UGIR w+, complete sequence.
ACCESSION AY196825
VERSION AY196825.1 GI:28565731
SOURCE piggyBac transformation vector pB-UGIR w+
ORGANISM piggyBac transformation vector pB-UGIR w+
artificial sequences; vectors.
REFERENCE 1 (bases 1 to 12677)
AUTHORS Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE A toolkit for transformation and mutagenesis in Drosophila using
piggyBac
JOURNAL Unpublished
2 (bases 1 to 12677)
AUTHORS Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE Direct Submission
JOURNAL Submitted (13-DEC-2002) Invertebrate Targets, Syngenta
Biotechnology, Inc., 3054 Cornwallis Rd, Research Triangle Park, NC
27709, USA
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Location/Qualifiers
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complement(11..>620)
/transposon="piggyBac transposable element"
632..998
/feature="5x UAS hsp70 TATA signal"
1003..2713
/notes="Gateway recombination cassette A; attR1 CmR ccdB
attR2"
2726..3040
/feature="RpS5"
/number=3
complement(3076..4788)
/notes="Gateway recombination cassette B; attR1 CmR ccdB
attR2"
4789..5246
/feature="SV40"
5247..9369
/feature="w"
/notes="mini-white; derived from Drosophila"
complement(<9370..9819)
/transposon="piggyBac transposable element"
BASE COUNT 3423 a 2924 c 2833 g 3497 t
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Query Match 89.6%; Score 22.4; DB 12; Length 12677;
Best Local Similarity 95.8%; Pred. No. 4.4;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTCAGCTTCTGTGACAAAGTTG 24
|||||
Db 2686 GTTCAGCTTCTGTGACAAAGTTG 2709
|||||
RESULT 32
AY196825/c
LOCUS AY196825 12677 bp DNA circular SYN 26-FEB-2003
DEFINITION PiggyBac transformation vector pB-UGIR w+, complete sequence.
ACCESSION AY196825
VERSION AY196825.1 GI:28565731
SOURCE piggyBac transformation vector pB-UGIR w+
ORGANISM piggyBac transformation vector pB-UGIR w+
artificial sequences; vectors.
REFERENCE 1 (bases 1 to 12677)
AUTHORS Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE A toolkit for transformation and mutagenesis in Drosophila using
piggyBac
JOURNAL Unpublished
2 (bases 1 to 12677)
AUTHORS Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE Direct Submission
JOURNAL Submitted (13-DEC-2002) Invertebrate Targets, Syngenta
Biotechnology, Inc., 3054 Cornwallis Rd, Research Triangle Park, NC
27709, USA
FEATURES
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Location/Qualifiers
/organism="piggyBac transformation vector pB-UGIR w+"
/mol_type="genomic DNA"
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complement(11..>620)
/transposon="piggyBac transposable element"
632..998
/feature="5x UAS hsp70 TATA signal"
1003..2713
/notes="Gateway recombination cassette A; attR1 CmR ccdB
attR2"
2726..3040
/feature="RpS5"
/number=3
complement(3076..4788)
/notes="Gateway recombination cassette B; attR1 CmR ccdB
attR2"
4789..5246
/feature="SV40"
5247..9369
/feature="w"
/notes="mini-white; derived from Drosophila"
complement(<9370..9819)
/transposon="piggyBac transposable element"
BASE COUNT 3423 a 2924 c 2833 g 3497 t
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/feature="SV40"
5247..9369
/feature="w"
/notes="mini-white; derived from Drosophila"
complement(<9370..9819)
/transposon="piggyBac transposable element"
BASE COUNT 3423 a 2924 c 2833 g 3497 t
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Query Match 89.6%; Score 22.4; DB 12; Length 12677;
Best Local Similarity 95.8%; Pred. No. 4.4;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTCAGCTTCTGTGACAAAGTTG 24
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Db 3104 GTTCAGCTTCTGTGACAAAGTTG 3081
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RESULT 33
AX590202/c
LOCUS AX590202 12789 bp DNA linear PAT 24-JAN-2003
DEFINITION Sequence 9 from Patent WO02083888.
ACCESSION AX590202
VERSION AX590202.1 GI:27901286
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Goossens,A. and Inz,D.
TITLE The use of genes encoding membrane transporter pumps to stimulate
the production of secondary metabolites in biological cells
JOURNAL Patent: WO 02083888-A 9 24-OCT-2002;
Vlaams Interuniversitair Instituut voor Biotechnologie vzw. (BE)
FEATURES
source
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Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/feature="vector pK7WG2D"
BASE COUNT 3050 a 3326 c 3397 g 3015 t
ORIGIN
Query Match 89.6%; Score 22.4; DB 6; Length 12789;
Best Local Similarity 95.8%; Pred. No. 4.4;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTCAGCTTCTGTGACAAAGTTG 24
|||||
Db 2045 GTTCAGCTTCTGTGACAAAGTTG 2022
|||||
RESULT 34
AX356862/c
LOCUS AX356862 13274 bp DNA linear PAT 13-FEB-2002
DEFINITION Sequence 20 from Patent WO0206490.
ACCESSION AX356862
VERSION AX356862.1 GI:18674110
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Dudler,R., Schaffrath,U. and Lawton,K.A.
TITLE Lipoxigenase genes, promoters, transit peptides and proteins
thereof
JOURNAL Patent: WO 0206490-A 20 24-JAN-2002;
Syngenta Participations AG (CH); Universitaet Zuerich (CH)
FEATURES
source
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Location/Qualifiers
/organism="synthetic construct"
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of DNA gyrase"
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          /protein_id="AA062301.1"
          /db_xref="GI:21552738"
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          /note="attr2 of Gateway conversion cassette frame A"
          1762..2048
          /note="contains intron 1 of Arabidopsis thaliana WRKY
transcription factor 33"
          /complement(2073..3783)
          /note="antisense orientation of Gateway conversion
cassette frame A containing attR1-R2 repeats, Cmr gene and
ccdB gene"
          /complement(2073..2199)
          /note="attr2 of Gateway conversion cassette frame A"
          /complement(2241..2546)
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          /note="encodes a cytotoxic protein that is a potent poison
of DNA gyrase"
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          /db_xref="GI:21552740"
          /translation="MFKVYTYKREGRYRLFVDVQSDIIDTPGRRMVPIASARLLSD
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          /complement(2888..3547)
          /gene="Cmr"
          /function="confers resistance to antibiotic
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          /protein_id="AA062302.1"
          /db_xref="GI:21552739"
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A"

misc_feature      complement(3657..3783)
BASE COUNT      2337 a 2150 c 2185 g 2347 t
ORIGIN
Query Match      89.6%; Score 22.4; DB 12; Length 9019;
Best Local Similarity 95.8%; Pred. No. 4.6;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GTTCAGCTTCTGTACAAAGTTG 24
          |||
Db      2100 GTTCAGCTTCTGTACAAAGTGG 2077
          |||

RESULT 30
LOCUS      AY196824
DEFINITION PiggyBac transformation vector pB-UGateway w+, complete sequence.
ACCESSION      AY196824

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VERSION      AY196824.1 GI:28565716
KEYWORDS
SOURCE      piggyBac transformation vector pB-UGateway w+
ORGANISM      piggyBac transformation vector pB-UGateway w+
              artificial sequences; vectors.
REFERENCE      1 (bases 1 to 11005)
AUTHORS      Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE      A toolkit for transformation and mutagenesis in Drosophila using
              piggyBac
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 11005)
AUTHORS      Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE      Direct Submission
JOURNAL      Submitted (13-DEC-2002) Invertebrate Targets, Syngenta
              Biotechnology, Inc., 3054 Cornwallis Rd, Research Triangle Park, NC
              27709, USA
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            /db_xref="taxon:221641"
            /complement(11..>620)
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            TATA_signal      643..999
            misc_feature      /note="5x UAS hsp70 TATA signal"
            1003..2713
            /note="Gateway recombination cassette A; attR1 Cmr ccdB
            attR2"
            intron      2726..3040
            /note="Rps5"
            /number=3
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            gene      3574..7697
            /note="SV40"
            /gene="wt"
            repeat_region      /note="mini-white; derived from Drosophila"
            complement(<7698..8147)
            /transposon="piggyBac transposable element"
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            ORIGIN
Query Match      89.6%; Score 22.4; DB 12; Length 11005;
Best Local Similarity 95.8%; Pred. No. 4.5;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GTTCAGCTTCTGTACAAAGTTG 24
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Db      2686 GTTCAGCTTCTGTACAAAGTGG 2709
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RESULT 31
LOCUS      AY196825
DEFINITION PiggyBac transformation vector pB-UGIR w+
ACCESSION      AY196825
VERSION      AY196825.1 GI:28565731
KEYWORDS
SOURCE      piggyBac transformation vector pB-UGIR w+
ORGANISM      piggyBac transformation vector pB-UGIR w+
              artificial sequences; vectors.
REFERENCE      1 (bases 1 to 12677)
AUTHORS      Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE      A toolkit for transformation and mutagenesis in Drosophila using
              piggyBac
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 12677)
AUTHORS      Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE      Direct Submission
JOURNAL      Submitted (13-DEC-2002) Invertebrate Targets, Syngenta
              Biotechnology, Inc., 3054 Cornwallis Rd, Research Triangle Park, NC
              27709, USA
FEATURES
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FEATURES
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Location/Qualifiers
/organism="Binary vector pJawohl8-RNAi"
/mol_type="genomic DNA"
/db_xref="taxon:188084"
/focus
/notes="binary plant gene silencing vector for one-step
cloning of inverted sequences"
3803. .9019
/organism="Binary vector pJawohl3-RNAi"
/mol_type="genomic DNA"
/db_xref="taxon:176105"
26. .1733
/notes="sense orientation of Gateway conversion cassette
frame A containing attR1-R2 repeats, CmR gene and ccdB
gene"
misc_feature
26. .152
/notes="attR1 of Gateway conversion cassette frame A"
262. .921
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262. .921
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chloramphenicol"
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/db_xref="GI:21552737"
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A"
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263. .1568
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1263. .1568
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/notes="encodes a cytotoxic protein that is a potent poison
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1610. .1736
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1762. .2048
/notes="contains intron 1 of Arabidopsis thaliana WRKY
transcription factor 33"
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/notes="antisense orientation of Gateway conversion
cassette frame A containing attR1-R2 repeats, CmR gene and
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misc_feature
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A"
misc_feature
complement(3657. .3783)
/notes="attR1 of Gateway conversion cassette frame A"
BASE COUNT 2337 a 2150 c 2185 g 2347 t
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Query Match 89.6%; Score 22.4; DB 12; Length 9019;
Best Local Similarity 95.8%; Pred. No. 4.6;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTCAGCTTCTGTACAAAGTTG 24
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Db 1709 GTTCAGCTTCTGTACAAAGTTG 1732
|||||
RESULT 29
AF408413/c
LOCUS AF408413 9019 bp DNA circular SYN 25-JUN-2002
DEFINITION Binary vector pJawohl8-RNAi, complete sequence.
ACCESSION AF408413
VERSION AF408413.1 GI:21552736
KEYWORDS
SOURCE
ORGANISM
Binary vector pJawohl8-RNAi
Binary vector pJawohl8-RNAi
artificial sequences; vectors.
REFERENCE
1 (bases 1 to 9019)
AUTHORS Ulker,B., Lipka,V., Rademacher,T.R. and Somssich,I.E.
TITLE pJawohl8-RNAi a binary vector for gene silencing in plants
JOURNAL Unpublished
REFERENCE
2 (bases 1 to 9019)
AUTHORS Ulker,B., Lipka,V., Rademacher,T.R. and Somssich,I.E.
TITLE Direct Submission
JOURNAL Submitted (08-AUG-2001) Biochemistry, Max-Planck-Institut
f. Zuechtungsforchung, Carl-von-Linne Weg 10, Koeln, NRW D-50829,
Germany
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/organism="Binary vector pJawohl8-RNAi"
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/focus
/notes="binary plant gene silencing vector for one-step
cloning of inverted sequences"
3803. .9019
/organism="Binary vector pJawohl3-RNAi"
/mol_type="genomic DNA"
/db_xref="taxon:176105"
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/notes="sense orientation of Gateway conversion cassette
frame A containing attR1-R2 repeats, CmR gene and ccdB
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misc_feature
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/notes="attR1 of Gateway conversion cassette frame A"
262. .921
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262. .921
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chloramphenicol"
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/protein_id="AAM62300.1"
/db_xref="GI:21552737"
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Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTACAAAGTTG 24
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 Db 1822 GTTCAGCTTCTTGTACAAAGTTG 1845

RESULT 26
 VFO551314 4462 bp DNA circular SYN 27-MAR-2003
 LOCUS Transfection vector pBdest.
 DEFINITION AJ551314
 ACCESSION AJ551314.1 GI:29335742
 VERSION
 KEYWORDS amp gene; beta lactamase; cat gene; ccdB gene; chloramphenicol acetyl transferase; control of cell death B protein.
 SOURCE Transfection vector pBdest
 ORGANISM artificial sequences; vectors.
 REFERENCE 1
 AUTHORS Jakob, M.J., Heim, M.A. and Weishaar, B.
 TITLE Use of a gateway compatible vector for transient plant transfection
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 4462)
 AUTHORS Jakob, M.J.
 TITLE Direct Submission
 JOURNAL Submitted (26-MAR-2003) Jakob M.J., Salamini, MPI for Plant Breeding Research, Carl-von-Linne Weg 10, 50829 Koeln, GERMANY
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 /organism="Transfection vector pBdest"
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 /db_xref="taxon:225975"
 31..443
 /note="35S"
 421..424
 /note="35S"
 456..580
 /note="attR1"
 689..1348
 /gene="cat"
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 /protein_id="CAD83080.1"
 /db_xref="GI:29335743"
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 1690..1995
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 /protein_id="CAD83081.1"
 /db_xref="GI:29335744"
 /translations="MQPKVTVYKRSRYRLFVDVQSDIIDTTPGRWVPIASARLLSD KVSRELYPVVHIGDESRRWMTTDMASVPVSVIGEEVADLSHRENDKNAINLMPWGL"
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 /gene="noet"
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 2606..3466
 /gene="amp"
 2606..3466
 /gene="amp"
 /codon_start=1
 /product="beta lactamase"

/protein_id="CAD83082.1"
 /db_xref="GI:29335745"
 /translations="MSIQHPRVALIFFFAAFCLPFAHPTLVKVKDAEDQLGARVGY IEDLSNGKILSFREPRFFPMSTFKVLLCGAVLSKRIDAGQQLGRRHYHQNDLVE YSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTIGGPKELTAPLHNMGDHVTFL DRWPELNEAIPNDRDTPMPVAMATLRKLTLGELLTLASRQQLIDWEADKVGFL LRSALPAGWFIADKSGAGRGSRGIIAALPGDKPSRIVIVYTTGSAQATMDERNRQIA EIGASLIKHW"
 BASE COUNT 1223 a 995 c 1065 g 1179 t
 ORIGIN

Query Match 89.6%; Score 22.4; DB 12; Length 4462;
 Best Local Similarity 95.8%; Pred. No. 5;
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTACAAAGTTG 24
 |||||
 Db 2136 GTTCAGCTTCTTGTACAAAGTTG 2159

RESULT 27
 AX306327 5148 bp DNA linear PAT 11-DEC-2001
 LOCUS Sequence 10 from Patent WO0188121.
 DEFINITION AX306327
 ACCESSION AX306327.1 GI:17645566
 VERSION
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1
 AUTHORS Plaetinck, G., Renard, J.P. and Bogaert, T.
 TITLE Vector constructs
 JOURNAL Patent: WO 0188121-A 10 22-NOV-2001;
 Devgen NV (BE)
 FEATURES
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 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 /note="Plasmid pGN39"
 BASE COUNT 1359 a 1199 c 1279 g 1311 t
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 Best Local Similarity 95.8%; Pred. No. 4.9;
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTACAAAGTTG 24
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 Db 1827 GTTCAGCTTCTTGTACAAAGTTG 1850

RESULT 28
 AF408413 9019 bp DNA circular SYN 25-JUN-2002
 LOCUS Binary vector pJawohl8-RNAi, complete sequence.
 DEFINITION AF408413
 ACCESSION AF408413.1 GI:21552736
 VERSION
 KEYWORDS Binary vector pJawohl8-RNAi
 SOURCE Binary vector pJawohl8-RNAi
 ORGANISM artificial sequences; vectors.
 REFERENCE 1 (bases 1 to 9019)
 AUTHORS Ulker, B., Lipka, V., Rademacher, T.R. and Somsich, I.E.
 TITLE pJawohl8-RNAi a binary vector for gene silencing in plants
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 9019)
 AUTHORS Ulker, B., Lipka, V., Rademacher, T.R. and Somsich, I.E.
 TITLE Direct Submission
 JOURNAL Submitted (08-AUG-2001) Biochemistry, Max-Planck-Institut f. Zuechtungsforschung, Carl-von-Linne Weg 10, Koeln, NRW D-50829, Germany

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RESULT 22
AX498620
LOCUS
DEFINITION
Sequence 10 from Patent EP1229113.
ACCESSION
AX498620
VERSION
AX498620.1 GI:23343417
KEYWORDS
unidentified
ORGANISM
unidentified
unclassified.
REFERENCE
1
AUTHORS
Hartley,J.L. and Brasch,M.A.
TITLE
Recombinational cloning using engineered recombination sites
JOURNAL
Patent: EP 1229113-A 10 07-AUG-2002;
INVITROGEN CORPORATION (US)
FEATURES
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89.6%; Score 22.4; DB 6; Length 25;
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QY 1 GTTCAGCTTCTTGACAAAGTTG 24
Db 1 GTTCAGCTTCTTGACAAAGTTG 24

RESULT 23
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LOCUS
DEFINITION
Recombinational cloning using nucleic acids having recombination
sites.
ACCESSION
BD131336
VERSION
BD131336.1 GI:23226281
KEYWORDS
JP 2002500861-A/10.
SOURCE
unidentified
ORGANISM
unidentified
unclassified.
REFERENCE
1 (bases 1 to 25)
AUTHORS
Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.
TITLE
Recombinational cloning using nucleic acids having recombination
JOURNAL
Patent: JP 2002500861-A 10 15-JAN-2002;
LIFE TECHNOLOGIES INC
COMMENT
OS Unknown
PN JP 2002500861-A/10
PD 15-JAN-2002
PF 26-OCT-1998 US 60/065930
PR 24-OCT-1997 US 60/065930,23-OCT-1998 US 09/177387 PI
JAMES L HARTLEY,MICHAEL A BRASCH,GARY F TEMPLE,DONNA K FOX PC
C12N15/09,C12Q1/68,C12N15/00
CC Description of Unknown Organism: recombination products FH
Key Location/Qualifiers
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BASE COUNT
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QY 1 GTTCAGCTTCTTGACAAAGTTG 24
Db 1 GTTCAGCTTCTTGACAAAGTTG 24

RESULT 25
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DEFINITION
Sequence 63 from Patent WO02066653.
ACCESSION
AX703501
VERSION
AX703501.1 GI:29538461
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
artificial sequences.
REFERENCE
1
AUTHORS
Li,M. and Liu,Y.C.
TITLE
Procarvotic libraries and uses
JOURNAL
Patent: WO 02066653-A 63 29-AUG-2002;
Xencor (US)
FEATURES
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BASE COUNT
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ORIGIN

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DEFINITION
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ACCESSION
BD131337
VERSION
BD131337.1 GI:23226282
KEYWORDS
JP 2002500861-A/11.
SOURCE
unidentified
ORGANISM
unidentified
unclassified.
REFERENCE
1 (bases 1 to 25)
AUTHORS
Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.
TITLE
Recombinational cloning using nucleic acids having recombination
JOURNAL
Patent: JP 2002500861-A 11 15-JAN-2002;
LIFE TECHNOLOGIES INC
COMMENT
OS Unknown
PN JP 2002500861-A/11
PD 15-JAN-2002
PF 26-OCT-1998 JP 2000518069
PR 24-OCT-1997 US 60/065930,23-OCT-1998 US 09/177387 PI
JAMES L HARTLEY,MICHAEL A BRASCH,GARY F TEMPLE,DONNA K FOX PC
C12N15/09,C12Q1/68,C12N15/00
CC Description of Unknown Organism: recombination products FH
Key Location/Qualifiers
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BASE COUNT
5 a 4 c 6 g 10 t
ORIGIN

Query Match
89.6%; Score 22.4; DB 6; Length 25;
Best Local Similarity 95.8%; Pred. No. 9.1;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGACAAAGTTG 24
Db 1 GTTCAGCTTCTTGACAAAGTTG 24

RESULT 25
AX703501
LOCUS
DEFINITION
Sequence 63 from Patent WO02066653.
ACCESSION
AX703501
VERSION
AX703501.1 GI:29538461
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
artificial sequences.
REFERENCE
1
AUTHORS
Li,M. and Liu,Y.C.
TITLE
Procarvotic libraries and uses
JOURNAL
Patent: WO 02066653-A 63 29-AUG-2002;
Xencor (US)
FEATURES
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
527 a 381 c 434 g 504 t
BASE COUNT
527 a 381 c 434 g 504 t
ORIGIN

Query Match
89.6%; Score 22.4; DB 6; Length 1846;
Best Local Similarity 95.8%; Pred. No. 5.5;

QY 1 GTTCAGCTTCTTGACAAAGTTG 24

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BASE COUNT      5 a      3 c      6 g      11 t
ORIGIN

Query Match      93.6%; Score 23.4; DB 6; Length 25;
Best Local Similarity 96.0%; Pred. No. 3;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 18
LOCUS      BD131341      25 bp      DNA      linear      PAT 18-SEP-2002
DEFINITION Recombinational cloning using nucleic acids having recombination
sites.
ACCESSION  BD131341
VERSION    BD131341.1 GI:23226286
KEYWORDS   JP 2002500861-A/15.
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 25)
AUTHORS   Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.
TITLE     Recombinational cloning using nucleic acids having recombination
JOURNAL   Patent: JP 2002500861-A 15 15-JAN-2002;
LIFE TECHNOLOGIES INC
COMMENT    OS Unknown
          PN JP 2002500861-A/15
          PD 15-JAN-2002
          PF 26-OCT-1998 US 2000518069
          PR 24-OCT-1997 US 60/065930,23-OCT-1998 US 09/177387 PI
          C12N15/09, C12Q1/68 CL2N15/00
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Key       Location/Qualifiers
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BASE COUNT      5 a      3 c      6 g      11 t
ORIGIN

Query Match      93.6%; Score 23.4; DB 6; Length 25;
Best Local Similarity 96.0%; Pred. No. 3;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 19
LOCUS      AR124530      25 bp      DNA      linear      PAT 16-MAY-2001
DEFINITION Sequence 10 from patent US 6171861.
ACCESSION  AR124530
VERSION    AR124530.1 GI:14109891
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 25)
AUTHORS   Hartley,J.L. and Brasch,M.A.
TITLE     Recombinational cloning using engineered recombination sites
JOURNAL   Patent: US 6171861-A 10 09-JAN-2001;
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          1..25
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BASE COUNT      5 a      3 c      6 g      11 t
ORIGIN

Query Match      93.6%; Score 23.4; DB 6; Length 25;
Best Local Similarity 96.0%; Pred. No. 3;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTCTTGTACAAAGTTGG 25
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Db 1 GTTCAGCTTTCTTGTACAAAGTTGG 25
    |||||

RESULT 20
LOCUS      AR163181      25 bp      DNA      linear      PAT 17-OCT-2001
DEFINITION Sequence 10 from patent US 6270969.
ACCESSION  AR163181
VERSION    AR163181.1 GI:16233690
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 25)
AUTHORS   Hartley,J.L. and Brasch,M.A.
TITLE     Recombinational cloning using engineered recombination sites
JOURNAL   Patent: US 6270969-A 10 07-AUG-2001;
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BASE COUNT      5 a      5 c      4 g      11 t
ORIGIN

Query Match      89.8%; Score 22.4; DB 6; Length 25;
Best Local Similarity 95.8%; Pred. No. 9.1;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTCTTGTACAAAGTTG 24
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Db 1 GTTCAGCTTTCTTGTACAAACTTG 24
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RESULT 21
LOCUS      AX491649      25 bp      DNA      linear      PAT 16-AUG-2002
DEFINITION Sequence 10 from Patent EP1227147.
ACCESSION  AX491649
VERSION    AX491649.1 GI:22324157
KEYWORDS   .
SOURCE     unidentified
ORGANISM   unidentified.
REFERENCE  1
AUTHORS   Hartley,J.L. and Brasch,M.A.
TITLE     Recombinational cloning using engineered recombination sites
JOURNAL   Patent: EP 1227147-A 10 31-JUL-2002;
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          1..25
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BASE COUNT      5 a      5 c      4 g      11 t
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Query Match      89.8%; Score 22.4; DB 6; Length 25;
Best Local Similarity 95.8%; Pred. No. 9.1;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTCTTGTACAAAGTTG 24
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Db 1 GTTCAGCTTTCTTGTACAAACTTG 24
    |||||

RESULT 22
LOCUS      AX491649      25 bp      DNA      linear      PAT 16-AUG-2002
DEFINITION Sequence 10 from Patent EP1227147.
ACCESSION  AX491649
VERSION    AX491649.1 GI:22324157
KEYWORDS   .
SOURCE     unidentified
ORGANISM   unidentified.
REFERENCE  1
AUTHORS   Hartley,J.L. and Brasch,M.A.
TITLE     Recombinational cloning using engineered recombination sites
JOURNAL   Patent: EP 1227147-A 10 31-JUL-2002;
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BASE COUNT      5 a      5 c      4 g      11 t
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Query Match      89.8%; Score 22.4; DB 6; Length 25;
Best Local Similarity 95.8%; Pred. No. 9.1;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTCTTGTACAAAGTTG 24
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Db 1 GTTCAGCTTTCTTGTACAAACTTG 24
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KEYWORDS
SOURCE JP 2002500861-A/43.
ORGANISM unidentified
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.
TITLE Recombinational cloning using nucleic acids having recombination
JOURNAL Patent: JP 2002500861-A 43 15-JAN-2002;
LIFE TECHNOLOGIES INC
COMMENT OS Unknown
PN JP 2002500861-A/43
PD 15-JAN-2002
PR 26-OCT-1998 JP 2000518069
PR 24-OCT-1997 US 60/065930,23-OCT-1998 US 09/177387 PI
JAMES L HARTLEY,MICHAEL A BRASCH,GARY F TEMPLE,DONNA K FOX PC
C12N15/09,C12Q1/68,C12N15/00
CC Description of Unknown Organism: recombination products PH
Key Location/Qualifiers
FT source 1..25
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Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCAGCTTCTTGTCACAAAGTTGG 25
Db 1 GTTCAGCTTCTTGTCACAAAGTTGG 25
RESULT 14
LOCUS AR124535 25 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 15 from patent US 6171861.
ACCESSION AR124535
VERSION AR124535.1 GI:14109896
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6171861-A 15 09-JAN-2001;
LIFE TECHNOLOGIES INC
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Best Local Similarity 96.0%; Pred. No. 3;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTCAGCTTCTTGTCACAAAGTTGG 25
Db 1 GTTCAGCTTCTTGTCACAAAGTTGG 25
RESULT 15
LOCUS AR163186 25 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 15 from patent US 6270969.
ACCESSION AR163186
VERSION AR163186.1 GI:16233698
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: EP 1229113-A 15 07-AUG-2002;
INVITROGEN CORPORATION (US)
FEATURES
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Best Local Similarity 96.0%; Pred. No. 3;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 1 GTTCAGCTTCTTGTCACAAAGTTGG 25
RESULT 16
LOCUS AX491654 25 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 15 from Patent EP1227147.
ACCESSION AX491654
VERSION AX491654.1 GI:22324162
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: EP 1227147-A 15 31-JUL-2002;
INVITROGEN CORPORATION (US)
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BASE COUNT 5 a 3 c 6 g 11 t
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Query Match 93.6%; Score 23.4; DB 6; Length 25;
Best Local Similarity 96.0%; Pred. No. 3;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTCAGCTTCTTGTCACAAAGTTGG 25
Db 1 GTTCAGCTTCTTGTCACAAAGTTGG 25
RESULT 17
LOCUS AX498625 25 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 15 from Patent EP1229113.
ACCESSION AX498625
VERSION AX498625.1 GI:23343422
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: EP 1229113-A 15 07-AUG-2002;
INVITROGEN CORPORATION (US)
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RESULT 12
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LOCUS Cloning vector pHELLSGATE.
DEFINITION AJ3111874
ACCESSION AJ3111874.1 GI:15982218
VERSION kanomycin resistance protein; neomycin phosphotransferase II; nptII
KEYWORDS gene; promoter; spec gene; spectinomycin resistance protein;
transposon Tn7.
SOURCE Cloning vector pHELLSGATE
ORGANISM Cloning vector pHELLSGATE
artificial sequences; vectors.

REFERENCE
1 Wesley,V.S., Helliwell,C., Smith,N.A., Wang,M.B., Rouse,D., Liu,Q.,
Gooding,p.s., Singh,S.R., Abbott,D., Stoutjesdijk,A., Robinson,S.P.,
Gleave,A.P., Green,A.G. and Waterhouse,P.M.
Construct design for efficient, effective and high-throughput gene
silencing in plants
Plant J. 27 (6), 581-590 (2001)
21461301
11576441
REFERENCE 2 (bases 1 to 18691)
Direct Submission
Waterhouse,P.M.
TITLE Submitted (04-MAY-2001) Waterhouse P.M., Plant Industry,
C.S.I.R.O., P.O. Box 1600, Canberra, ACT 2601, AUSTRALIA
LOCATION/Qualifiers
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/organism="Cauliflower mosaic virus"
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/db_xref="taxon:10641"
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/db_xref="GI:15982219"
/translation="MAITLSATSLPISARIRAGSPAAWVERLFYDWAQQTIGCSDA
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LGVEPGDGLSSHLAPAEKVSIIMADMRLLHTLDPATCFPDHQAKHRIEARTRMBA
LVDDDDLEHQGLPAELFAULKARPEDGEDLVVPHGDACLNIAMUENGREGSGFDIC
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/transl_table=1
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/protein_id="CAC86253.1"
/db_xref="GI:15982220"
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/translation="MREAIVAEVSTQLSEVVGVIERHLEPTLLAVHLYGSADVGGKLP
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AKRELQFGEMORNDILAGIREPATIDIDLALLTKAREHSVALVGPAAELEFDPVPEO
DLFEALNETLTLWNSSPPDWAGDERNVLTLSRWYSAVTGKIAPKDVAAADWAMERUPA
QYQPVLEARQAYLQGEDRLASRADQLBEFHVHYVKGEITKVVEK"
10706..11324
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/note="right border"
11674..13019
promoter
/function="35S promoter"
14660..16258
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/number=2
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/note="octopine esynthase (ocs) terminator"
BASE COUNT 4837 a 4621 c 4607 g 4626 t
ORIGIN

Query Match 100.0%; Score 25; DB 12; Length 18691;
Best Local Similarity 100.0%; Pred.No. 0.22;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTTGACAAAGTTGG 25
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Db 16418 GTTCAGCTTCTTGACAAAGTTGG 16394
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RESULT 13
BD131369
LOCUS BD131369
DEFINITION Recombinational cloning using nucleic acids having recombination
sites.
ACCESSTION BD131369
VERSION BD131369.1 GI:23226314

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/organism="unidentified"
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Query Match      100.0%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCAGCTTCTGTGACAAAGTTGG 25
Db 1 GTTCAGCTTCTGTGACAAAGTTGG 25
RESULT 11
CV3111874
LOCUS      18691 bp      DNA      circular SYN 09-JUL-2002
DEFINITION  Cloning vector pHELLSGATE.
ACCESSION  AJ311874
VERSION    AJ311874.1 GI:15982218
KEYWORDS   kanamycin resistance protein; neomycin phosphotransferase II; nptII
SOURCE     Cloning vector pHELLSGATE
ORGANISM   artificial sequences; vectors.
REFERENCE  1
AUTHORS    Wesley,V.S., Helliwell,C., Smith,N.A., Wang,M.B., Rouse,D., Liu,Q.,
           Gooding,ps., Singh,S.R., Abbott,D., Stoutjesdijk,A., Robinson,S.P.,
           Gleave,A.P., Green,A.G. and Waterhouse,P.M.
TITLE      Construct design for efficient, effective and high-throughput gene
           silencing in plants
JOURNAL    Plant J. 27 (6), 581-590 (2001)
MEDLINE    21451301
PUBMED     11576441
REFERENCE  2 (bases 1 to 18691)
AUTHORS    Waterhouse,P.M.
TITLE      Direct Submission
JOURNAL    Submitted (04-MAY-2001) Waterhouse P.M., Plant Industry,
           C.S.I.R.O., P.O. Box 1600, Canberra, ACT 2601, AUSTRALIA
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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCAGCTTCTGTGACAAAGTTGG 25

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AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: EP 1227147-A 11 31-JUL-2002;
INVITROGEN CORPORATION (US)

FEATURES source
Location/Qualifiers
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RESULT 7

AX491655

LOCUS

AX491655 Sequence 16 from Patent EP1227147. 25 bp DNA linear PAT 16-AUG-2002

DEFINITION

AX491655

ACCESSION

VERSION

AX491655.1 GI:22324163

KEYWORDS

SOURCE

ORGANISM

unidentified

unclassified.

REFERENCE

1 Hartley,J.L. and Brasch,M.A.

AUTHORS

TITLE Recombinational cloning using engineered recombination sites

JOURNAL Patent: EP 1227147-A 11 31-JUL-2002;

INVITROGEN CORPORATION (US)

FEATURES

Location/Qualifiers

1. .25

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/db_xref="taxon:32644"

5 a 4 c 6 g 10 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

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0; Indels

0; Gaps

0; Length

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QY

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1 GTTCAGCTTTCTTGTACAAAGTTGG 25

RESULT 8

AX498621

LOCUS

AX498621 Sequence 11 from Patent EP1229113. 25 bp DNA linear PAT 26-SEP-2002

DEFINITION

AX498621

ACCESSION

VERSION

AX498621.1 GI:23343418

KEYWORDS

SOURCE

ORGANISM

unidentified

unclassified.

REFERENCE

1 Hartley,J.L. and Brasch,M.A.

AUTHORS

TITLE Recombinational cloning using engineered recombination sites

JOURNAL Patent: EP 1229113-A 11 07-AUG-2002;

INVITROGEN CORPORATION (US)

FEATURES

Location/Qualifiers

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RESULT 9

AX498626

LOCUS

AX498626 Sequence 16 from Patent EP1229113. 25 bp DNA linear PAT 26-SEP-2002

DEFINITION

AX498626

ACCESSION

VERSION

AX498626.1 GI:23343423

KEYWORDS

SOURCE

ORGANISM

unidentified

unclassified.

REFERENCE

1 Hartley,J.L. and Brasch,M.A.

AUTHORS

TITLE Recombinational cloning using engineered recombination sites

JOURNAL Patent: EP 1229113-A 16 07-AUG-2002;

INVITROGEN CORPORATION (US)

FEATURES

Location/Qualifiers

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BASE COUNT

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Best Local Similarity

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0; Indels

0; Gaps

0; Length

25;

QY

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RESULT 10

BD131342

LOCUS

BD131342 Recombinational cloning using nucleic acids having recombination sites. 25 bp DNA linear PAT 18-SEP-2002

DEFINITION

BD131342

ACCESSION

VERSION

BD131342.1 GI:23226287

KEYWORDS

SOURCE

unidentified

unclassified.

REFERENCE

1 (bases 1 to 25)

AUTHORS

TITLE Recombinational cloning using nucleic acids having recombination

JOURNAL Patent: JP 2002500861-A 16 15-JAN-2002;

LIFE TECHNOLOGIES INC

COMMENT

OS UNKNOWN

PN JP 2002500861-A/16

PD 15-JAN-2002

PF 26-OCT-1998

PR 26-OCT-1998

JP 2000518069

09/177387 PI

JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DONNA K FOX PC

CI2N15/09, CI2Q1/68, CI2N15/00

CC Description of Unknown Organism: recombination products PH

Key

Location/Qualifiers

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FT source

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Location/Qualifiers

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AR124536
LOCUS AR124536 25 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 16 from patent US 6171861.
ACCESSION AR124536
VERSION AR124536.1 GI:14109897
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 25)
Hartley,J.L. and Brasch,M.A.
Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6171861-A 16 09-JAN-2001;
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Location/Qualifiers
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BASE COUNT 5 a 4 c 6 g 10 t
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LOCUS AR163182 25 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 11 from patent US 6270969.
ACCESSION AR163182
VERSION AR163182.1 GI:162233692
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 25)
Hartley,J.L. and Brasch,M.A.
Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6270969-A 11 07-AUG-2001;
FEATURES
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Query Match
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Db 1 GTTCAGCTTCTTGTCACAAAGTTGG 25

RESULT 4
AR163187
LOCUS AR163187 25 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 16 from patent US 6270969.
ACCESSION AR163187
VERSION AR163187.1 GI:162233699
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 25)
Hartley,J.L. and Brasch,M.A.
Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6270969-A 16 07-AUG-2001;
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Location/Qualifiers
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LOCUS AX269137 25 bp DNA linear PAT 29-OCT-2001
DEFINITION Sequence 8 from Patent WO0174861.
ACCESSION AX269137
VERSION AX269137.1 GI:16542057
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
1 Ville,R.G., Harrington,K., Murphy,S. and Bateman,A.
Compositions and methods for tissue specific gene regulation
Therapy
Patent: WO 0174861-A 8 11-OCT-2001;
MAYO FOUNDATION FOR MEDICAL EDUCATION AND RESEARCH (US)
FEATURES
Location/Qualifiers
source
1. .25
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RESULT 6
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LOCUS AX491650 25 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 11 from Patent EP1227147.
ACCESSION AX491650
VERSION AX491650.1 GI:22324158
KEYWORDS
SOURCE unidentified
ORGANISM unidentified.
REFERENCE
1

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 6, 2003, 21:07:03 ; Search time 601 Seconds
(without alignments)
1701.732 Million cell updates/sec

Title: US-10-055-001A-11

Perfect score: 25
Sequence: 1 gttcagctttctgtcaaaagtgg 25

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htg_mus.*

34: em_htg_pln.*

35: em_htg_rod.*

36: em_htg_man.*

37: em_htg_vrt.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	25	100.0	25	6	AR124531 Sequence
3	25	100.0	25	6	AR124536 Sequence
4	25	100.0	25	6	AR163182 Sequence
5	25	100.0	25	6	AR163187 Sequence
6	25	100.0	25	6	AX269137 Sequence
7	25	100.0	25	6	AX491650 Sequence
8	25	100.0	25	6	AX491655 Sequence
9	25	100.0	25	6	AX498621 Sequence
10	25	100.0	25	6	AX498626 Sequence
11	25	100.0	18691	12	BD131342 Recombina
12	25	100.0	18691	12	BD131342 Cloning v
13	23.8	95.2	25	6	BD131369 Recombina
14	23.4	93.6	25	6	AR124535 Sequence
15	23.4	93.6	25	6	AR163186 Sequence
16	23.4	93.6	25	6	AX491654 Sequence
17	23.4	93.6	25	6	AX498625 Sequence
18	23.4	93.6	25	6	BD131341 Recombina
19	22.4	89.6	25	6	AR124530 Sequence
20	22.4	89.6	25	6	AR163181 Sequence
21	22.4	89.6	25	6	AX491649 Sequence
22	22.4	89.6	25	6	AX498620 Sequence
23	22.4	89.6	25	6	BD131336 Recombina
24	22.4	89.6	25	6	BD131337 Recombina
25	22.4	89.6	1846	6	AX703501 Sequence
26	22.4	89.6	4462	12	VFO551314 Transfect
27	22.4	89.6	5148	6	AX306327 Sequence
28	22.4	89.6	9019	12	AF408413 Binary ve
29	22.4	89.6	9019	12	AF408413 Binary ve
30	22.4	89.6	11005	12	AV196824 PiggyBac
31	22.4	89.6	12677	12	AV196825 PiggyBac
32	22.4	89.6	12677	12	AV196825 PiggyBac
33	22.4	89.6	12789	6	AX590202 Sequence
34	22.4	89.6	13274	6	AX356862 Sequence
35	22.4	89.6	13990	12	AF541939 His-3 int
36	22	88.0	25	6	AR124534 Sequence
37	22	88.0	25	6	AR163185 Sequence
38	22	88.0	25	6	AX269140 Sequence
39	22	88.0	25	6	AX491653 Sequence
40	22	88.0	25	6	AX498624 Sequence
41	22	88.0	25	6	BD131340 Recombina
42	22	88.0	25	6	BD131368 Recombina
43	20.8	83.2	25	6	AR124529 Sequence
44	20.8	83.2	25	6	AR163180 Sequence
45	20.8	83.2	25	6	AX269136 Sequence

ALIGNMENTS

RESULT 1
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LOCUS AR124531
DEFINITION Sequence 11 from patent US 6171861.
ACCESSION AR124531
VERSION AR124531.1 GI:114109892
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6171861-A 11 09-JAN-2001;
FEATURES Location/Qualifiers

AR124531 25 bp DNA linear PAT 16-MAY-2001

Pred. No. is the number of results predicted by chance to have a

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RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
BASE COUNT 32 a 18 c 22 g 39 t
ORIGIN

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Best Local Similarity 95.5%; Pred. No. 9.2e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCTTTTGTGACAAAGTTGG 25
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Db 45 CTGCTTTTGTGACAAAGTTGG 24
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Search completed: November 7, 2003, 00:21:00
Job time : 1096.75 secs

Query Match 81.6%; Score 20.4; DB 14; Length 111;
Best Local Similarity 95.5%; Pred. No. 9.2e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCTTTTGTGACAAAGTTGG 25
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Db 71 CAGCTTTTGTGACAAAGTTGG 92
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RESULT 40
CB395510/c
LOCUS 111 bp mRNA linear EST 15-MAY-2003
DEFINITION OSTR158A1_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION CB395510
VERSION CB395510.1 GI:30737221
KEYWORDS EST.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 111)
Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong
, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson
, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,
Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, P.P.,
Placet, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,
Doucette-Stamm, L., Hill, D.E. and Vidal, M.
C. elegans ORFeome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
expression
Nat. Genet., (2003) In press
Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc.Vidal@fci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact David Hill@fci.harvard.edu or
marc.vidal@fci.harvard.edu
POLYA=No.

FEATURES
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RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
BASE COUNT 28 a 26 c 19 g 38 t
ORIGIN

Query Match 81.6%; Score 20.4; DB 14; Length 111;

Doucette-Stamm, L., Hill, D.E. and Vidal, M.
C. elegans ORFeome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
expression
Nat. Genet., (2003) In press
Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc_Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david_hill@dfci.harvard.edu or
marc_vidal@dfci.harvard.edu
POLYA-No.

FEATURES
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Location/Qualifiers
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RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
29 a 21 c 12 g 44 t

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ORIGIN
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RESULT 38
CB388456/c
LOCUS 107 bp mRNA linear EST 15-MAY-2003
DEFINITION OSTRF099E7_1 AD-wrmcDNA Caenorhabditis elegans CDNA, mRNA sequence.
ACCESSION CB388456
VERSION CB388456.1 GI:30730166
KEYWORDS EST.
SOURCE
ORGANISM
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 107)
Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong
, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson
, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,
Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, P.P.,
Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,
Doucette-Stamm, L., Hill, D.E. and Vidal, M.
C. elegans ORFeome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
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Nat. Genet., (2003) In press
Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc_Vidal@dfci.harvard.edu

Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david_hill@dfci.harvard.edu or
marc_vidal@dfci.harvard.edu
POLYA-No.

FEATURES
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Location/Qualifiers
1. .107
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"
/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
34 a 18 c 16 g 39 t

BASE COUNT
ORIGIN
Query Match 81.6%; Score 20.4; DB 14; Length 107;
Best Local Similarity 95.5%; Pred. No. 9.2e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CAGCTTTTGTACAAAGTTGG 25
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Db 29 CAGCTTTTGTACAAAGTTGG 8
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RESULT 39
CB394444
LOCUS 111 bp mRNA linear EST 15-MAY-2003
DEFINITION OSTR137H4_1 AD-wrmcDNA Caenorhabditis elegans CDNA, mRNA sequence.
ACCESSION CB394444
VERSION CB394444.1 GI:30736155
KEYWORDS EST.
SOURCE
ORGANISM
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 111)
Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong
, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson
, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,
Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, P.P.,
Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,
Doucette-Stamm, L., Hill, D.E. and Vidal, M.
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marc_vidal@dfci.harvard.edu
POLYA-No.

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Location/Qualifiers
1. .111
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/strain="N2"
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/sex="Hermaphrodite and male"

CB396275.1 GI:30737986
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 Caenorhabditis elegans
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
 : Rhabditidae; Pelodierinae; Caenorhabditis.
 1 (bases 1 to 104)
 Reboul,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M., Armstrong
 ,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T., Hudson
 ,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.,
 Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V., Toliaas,P.P.,
 Pracek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,
 Doucette-Stamm,L., Hill,D.E. and Vidal,M.
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 Email: Marc.Vidal@dfci.harvard.edu
 Sequence tag of Gateway entry clones. The primers used were
 designed on the predicted protein encoding ORF. C. elegans ORFome
 cloning project : Contact david_hill@dfci.harvard.edu or
 marc_vidal@dfci.harvard.edu
 POLYA=No.

FEATURES
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 /strain="N2"
 /db_xref="taxon:6239"
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 /dev_stage="mixed stage"
 /clone_lib="AD-wrmcDNA"
 /note="The AD-wrmcDNA library was generated with poly(A)+
 RNA isolated from both hermaphrodite and male N2 worms of
 all larval stages, embryos, adults and dauers and the
 subsequent generation of cDNAs by poly(A) priming. The
 cDNAs were cloned into pPC86"
 30 a 20 c 15 g 39 t

BASE COUNT 30 a 20 c 15 g 39 t
 ORIGIN
 Query Match 81.6%; Score 20.4; DB 14; Length 104;
 Best Local Similarity 95.5%; Pred.No. 9.1e+02;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4 CAGCTTTTGTGACAAAGTTGG 25
 Db 39 CTGCTTTTGTGACAAAGTTGG 18

RESULT 37
 CB396817/c
 LOCUS
 OSTR17957.1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence. EST 15-MAY-2003
 DEFINITION
 CB396817
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Caenorhabditis elegans
 Caenorhabditis elegans
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
 : Rhabditidae; Pelodierinae; Caenorhabditis.
 1 (bases 1 to 106)
 Reboul,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M., Armstrong
 ,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T., Hudson
 ,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.,
 Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V., Toliaas,P.P.,
 Pracek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.

designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project : Contact david_hill@fci.harvard.edu or marc_vidal@fci.harvard.edu

POLYA=No.

FEATURES

Location/Qualifiers
1..102
/organism="Caenorhabditis elegans"
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/strain="N2"
/db_xref="taxon:6239"
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/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"
/note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"
31 a 14 c 22 g 35 t
BASE COUNT
ORIGIN

Query Match 81.6%; Score 20.4; DB 14; Length 102;
Best Local Similarity 95.5%; Pred. No. 9.1e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCTTTTGTGACAAAGTTGG 25
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Db 35 CAGCTTTTGTGACAAAGTTGG 14
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RESULT 33
CB399013/c
LOCUS CB399013 102 bp mRNA linear EST 15-MAY-2003
DEFINITION OSTR213H5_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION OSTR213H5
VERSION CB399013.1 GI:30740740
KEYWORDS EST.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromodorea; Rhabditida; Rhabditoidea
; Rhabditidae; Pelodierinae; Caenorhabditis.
1 (bases 1 to 102)
Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Endress, G.A., Jenna, S., Chevret, E., Papasotiropoulos, V., Tollas, P.P., Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H., Doucette-Stamm, L., Hill, D.E. and Vidal, M.
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Email: Marc_Vidal@fci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project : Contact david_hill@fci.harvard.edu or marc_vidal@fci.harvard.edu
POLYA=No.

Location/Qualifiers
1..102
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/strain="N2"
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/tissue_type="whole animal"

/dev stage="mixed stage"
/clone lib="AD-wrmcDNA"

/note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"
32 a 17 c 21 g 32 t
BASE COUNT
ORIGIN

Query Match 81.6%; Score 20.4; DB 14; Length 102;
Best Local Similarity 95.5%; Pred. No. 9.1e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCTTTTGTGACAAAGTTGG 25
|||||

Db 46 CTGCTTTTGTGACAAAGTTGG 25
|||||

RESULT 34

CB396276/c

LOCUS CB396276 103 bp mRNA linear EST 15-MAY-2003
DEFINITION OSTR169D10_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION CB396276
VERSION CB396276.1 GI:30737987
KEYWORDS EST.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromodorea; Rhabditida; Rhabditoidea
; Rhabditidae; Pelodierinae; Caenorhabditis.
1 (bases 1 to 103)
Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Endress, G.A., Jenna, S., Chevret, E., Papasotiropoulos, V., Tollas, P.P., Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H., Doucette-Stamm, L., Hill, D.E. and Vidal, M.
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Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc_Vidal@fci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project : Contact david_hill@fci.harvard.edu or marc_vidal@fci.harvard.edu
POLYA=No.

FEATURES

Location/Qualifiers
1..103
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/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
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/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"
/note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"
29 a 25 c 17 g 32 t
BASE COUNT
ORIGIN

Query Match 81.6%; Score 20.4; DB 14; Length 103;
Best Local Similarity 95.5%; Pred. No. 9.1e+02;

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KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
C. elegans ORFeome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
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Nat. Genet., (2003) In press
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Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
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COMMENT
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cloning project : Contact david_hill@dfci.harvard.edu or
marc_vidal@dfci.harvard.edu
POLYA=No.

FEATURES
source
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RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
BASE COUNT 31 a 22 c 14 g 33 t
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Query Match 81.6%; Score 20.4; DB 14; Length 100;
Best Local Similarity 95.5%; Pred. No. 9.1e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCTTTTGTGACAAAGTTGG 25
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Db 30 CAGCTTTTGTGACAAAGTTGG 9

RESULT 32
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LOCUS
DEFINITION OST162H10_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION CB392040
VERSION CB392040.1 GI:30733750
KEYWORDS EST.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
REFERENCE Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
AUTHORS ; Rhabditidae; Peloderinae; Caenorhabditis.
Reboul,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M., Armstrong
,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T., Hudson
,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.,
Endress,G.A., Jenna,S., Chevret,E., Papasotiropoulos,V., Tolias,P.P.
, Ptacek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,
Doucette-Stamm,L., Hill,D.E. and Vidal,M.
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Email: Marc_Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
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Sequence tag of Gateway entry clones. The primers used were
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marc_vidal@dfci.harvard.edu
POLYA=No.

TITLE
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COMMENT
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Email: Marc_Vidal@dfci.harvard.edu
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designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david_hill@dfci.harvard.edu or
marc_vidal@dfci.harvard.edu
POLYA=No.

FEATURES
source
1..100
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"
/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
BASE COUNT 31 a 22 c 23 g 24 t
ORIGIN
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Best Local Similarity 95.5%; Pred. No. 9.1e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCTTTTGTGACAAAGTTGG 25
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Db 46 CTGCTTTTGTGACAAAGTTGG 25

RESULT 31
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ACCESSION CB400512
VERSION CB400512.1 GI:30742239
KEYWORDS EST.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
REFERENCE Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
AUTHORS ; Rhabditidae; Peloderinae; Caenorhabditis.
Reboul,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M., Armstrong
,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T., Hudson
,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.,
Endress,G.A., Jenna,S., Chevret,E., Papasotiropoulos,V., Tolias,P.P.
, Ptacek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,
Doucette-Stamm,L., Hill,D.E. and Vidal,M.

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/clone lib="AD-wrmcDNA"
 /note="The AD-wrmcDNA library was generated with poly(A)+
 RNA isolated from both hermaphrodite and male N2 worms of
 all larval stages, embryos, adults and dauers and the
 subsequent generation of cDNAs by poly(A) priming. The
 cDNAs were cloned into pPC86"

BASE COUNT 24 a 22 c 20 g 32 t
 ORIGIN
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 Best Local Similarity 95.5%; Pred. No. 9.1e+02;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCTTTTGTACAAAGTTGG 25
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 Db 32 CAGCTTTTGTACAAAGTTGG 11

RESULT 28
 CB392051/c
 LOCUS 100 bp mRNA linear EST 15-MAY-2003
 DEFINITION OSTF163A3_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
 ACCESSION CB392051
 VERSION CB392051.1 GI:30733761
 KEYWORDS EST.
 SOURCE Caenorhabditis elegans
 ORGANISM Caenorhabditis elegans

REFERENCE
 AUTHORS Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
 ; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 100)
 Rebol, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong
 , C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson
 , J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,
 Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolia, P.P.,
 Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,
 Doucette-Stamm, L., Hill, D.E. and Vidal, M.
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 cloning project : Contact david_hill@dfci.harvard.edu or
 marc.vidal@dfci.harvard.edu
 POLYA=No.

FEATURES Location/Qualifiers

1..100
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 /strain="N2"
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 RNA isolated from both hermaphrodite and male N2 worms of
 all larval stages, embryos, adults and dauers and the
 subsequent generation of cDNAs by poly(A) priming. The
 cDNAs were cloned into pPC86"

32 a 24 c 18 g 26 t

BASE COUNT
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Query Match 81.6%; Score 20.4; DB 14; Length 100;
 Best Local Similarity 95.5%; Pred. No. 9.1e+02;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCTTTTGTACAAAGTTGG 25
 |||||
 Db 32 CAGCTTTTGTACAAAGTTGG 11

RESULT 29
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LOCUS 100 bp mRNA linear EST 15-MAY-2003
 DEFINITION OSTR210H4_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
 ACCESSION CB398867
 VERSION CB398867.1 GI:30740594
 KEYWORDS EST.
 SOURCE Caenorhabditis elegans
 ORGANISM Caenorhabditis elegans

REFERENCE
 AUTHORS Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
 ; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 100)
 Rebol, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong
 , C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson
 , J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,
 Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolia, P.P.,
 Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,
 Doucette-Stamm, L., Hill, D.E. and Vidal, M.
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Email: Marc.Vidal@dfci.harvard.edu
 Sequence tag of Gateway entry clones. The primers used were
 designed on the predicted protein encoding ORF. C. elegans ORFeome
 cloning project : Contact david_hill@dfci.harvard.edu or
 marc.vidal@dfci.harvard.edu
 POLYA=No.

FEATURES Location/Qualifiers

1..100
 /organism="Caenorhabditis elegans"
 /mol_type="mRNA"
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 /db_xref="taxon:6239"
 /sex="Hermaphrodite and male"
 /tissue_type="whole animal"
 /dev_stage="mixed stage"
 /clone_lib="AD-wrmcDNA"

/note="The AD-wrmcDNA library was generated with poly(A)+
 RNA isolated from both hermaphrodite and male N2 worms of
 all larval stages, embryos, adults and dauers and the
 subsequent generation of cDNAs by poly(A) priming. The
 cDNAs were cloned into pPC86"

34 a 22 c 18 g 26 t

BASE COUNT
 ORIGIN

Query Match 81.6%; Score 20.4; DB 14; Length 100;
 Best Local Similarity 95.5%; Pred. No. 9.1e+02;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCTTTTGTACAAAGTTGG 25
 |||||
 Db 39 CTGCTTTTGTACAAAGTTGG 18

RESULT 30
 CB398991/c

LOCUS 100 bp mRNA linear EST 15-MAY-2003
 DEFINITION OSTR213C9_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
 ACCESSION CB398991
 VERSION CB398991.1 GI:30740718

Query Match 81.6%; Score 20.4; DB 14; Length 100;
 Best Local Similarity 95.5%; Pred. No. 9.1e+02;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

genome annotation and resource for proteome-scale protein

JOURNAL COMMENT

Nat. Genet., (2003) In press
Contact: Vidal M

Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739

Email: Marc.Vidal@dfci.harvard.edu

Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project : Contact david_hill@dfci.harvard.edu or marc_vidal@dfci.harvard.edu

FEATURES

source

Location/Qualifiers

1..95
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"

/note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

BASE COUNT
ORIGIN

28 a 20 c 19 g 28 t

Query Match 81.6%; Score 20.4; DB 14; Length 95;

Best Local Similarity 95.5%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCTTTTGTGACAAAGTTGG 25

||||| ||||||| ||||||| |||||||

Db 29 CAGCTTTCTGTGACAAAGTTGG 8

RESULT 26

CB401179/c

LOCUS

OSTF190A5_1 AD-wrmcDNA Caenorhabditis elegans cdNA, mRNA sequence.

DEFINITION

ACCESSION

CB401179

VERSION

CB401179.1

KEYWORDS

EST.

SOURCE

ORGANISM

Caenorhabditis elegans

Caenorhabditis elegans

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea

; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 97)

REFERENCE

AUTHORS

Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong

, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson

, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,

Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolia, P.P.

, Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,

Doucette-Stamm, L., Hill, D.E. and Vidal, M.

C. elegans ORFeome version 1.1: experimental verification of the

genome annotation and resource for proteome-scale protein

expression

Nat. Genet., (2003) In press

Contact: Vidal M

Marc Vidal Laboratory

Dana Farber Cancer Institute

1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA

Tel: 617 632 5180

Fax: 617 632 5739

Email: Marc.Vidal@dfci.harvard.edu

Sequence tag of Gateway entry clones. The primers used were

designed on the predicted protein encoding ORF. C. elegans ORFeome

FEATURES

source

Location/Qualifiers

1..97
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"

/note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

BASE COUNT 30 a 17 c 16 g 34 t

ORIGIN

Query Match 81.6%; Score 20.4; DB 14; Length 97;

Best Local Similarity 95.5%; Pred. No. 9.1e+02; 1; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCTTTTGTGACAAAGTTGG 25

||||| ||||||| ||||||| |||||||

Db 32 CAGCTTTCTGTGACAAAGTTGG 11

RESULT 27

CB402581/c

LOCUS

DEFINITION

CB402581

ACCESSION

CB402581.1

VERSION

CB402581.1

KEYWORDS

EST.

SOURCE

ORGANISM

Caenorhabditis elegans

Caenorhabditis elegans

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea

; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 98)

REFERENCE

AUTHORS

Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong

, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson

, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,

Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolia, P.P.

, Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,

Doucette-Stamm, L., Hill, D.E. and Vidal, M.

C. elegans ORFeome version 1.1: experimental verification of the

genome annotation and resource for proteome-scale protein

expression

Nat. Genet., (2003) In press

Contact: Vidal M

Marc Vidal Laboratory

Dana Farber Cancer Institute

1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA

Tel: 617 632 5180

Fax: 617 632 5739

Email: Marc.Vidal@dfci.harvard.edu

Sequence tag of Gateway entry clones. The primers used were

designed on the predicted protein encoding ORF. C. elegans ORFeome

cloning project : Contact david_hill@dfci.harvard.edu or

marc_vidal@dfci.harvard.edu

POLY(A)=No.

Location/Qualifiers

1..98

/organism="Caenorhabditis elegans"

/mol_type="mRNA"

/strain="N2"

/db_xref="taxon:6239"

/sex="Hermaphrodite and male"

/tissue_type="whole animal"

/dev_stage="mixed stage"

cloning project : Contact david_hill@dfci.harvard.edu or marc_vidal@dfci.harvard.edu

POLY(A)=No.


```

marc_vidal@dfci.harvard.edu
POLYA=No.

FEATURES
    source
        1..87
            /location=Qualifiers
            /organism="Caenorhabditis elegans"
            /mol_type="mRNA"
            /strain="N2"
            /db_xref="taxon:6239"
            /sex="Hermaphrodite and male"
            /tissue_type="whole animal"
            /dev_stage="mixed stage"
            /clone_lib="AD-wrmcDNA"
        /note="The AD-wrmcDNA library was generated with poly(A)+
        RNA isolated from both hermaphrodite and male N2 worms of
        all larval stages, embryos, adults and dauers and the
        subsequent generation of cDNAs by poly(A) priming. The
        cDNAs were cloned into pPC86"
BASE COUNT      26 a 16 c 21 g 24 t
ORIGIN
Query Match      81.6%; Score 20.4; DB 14; Length 87;
Best Local Similarity 95.5%; Pred. No. 9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCTTTTGTACAAAGTTGG 25
||||| ||||| ||||| ||||| |||||
Db 27 CAGCTTTTGTACAAAGTTGG 6

RESULT 21
CB392047/c
LOCUS
DEFINITION
CB392047 90 bp mRNA linear EST 15-MAY-2003
ACCESSION
CB392047.1 GI:30733757
VERSION
CB392047.1
KEYWORDS
EST.
SOURCE
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 90)
AUTHORS
Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong
, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson
, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,
Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tollas, P.P.,
Placek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,
Doucette-Stamm, L., Hill, D.E. and Vidal, M.
C. elegans ORFeome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
expression
Nat. Genet., (2003) In press
Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc.Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david_hill@dfci.harvard.edu or
marc_vidal@dfci.harvard.edu
POLYA=No.

JOURNAL
    source
        Location/Qualifiers
        1..90
            /organism="Caenorhabditis elegans"
            /mol_type="mRNA"
            /strain="N2"
            /db_xref="taxon:6239"
            /sex="Hermaphrodite and male"
            /tissue_type="whole animal"
            /dev_stage="mixed stage"
            /clone_lib="AD-wrmcDNA"
        /note="The AD-wrmcDNA library was generated with poly(A)+
        RNA isolated from both hermaphrodite and male N2 worms of
        all larval stages, embryos, adults and dauers and the
        subsequent generation of cDNAs by poly(A) priming. The
        cDNAs were cloned into pPC86"
BASE COUNT      25 a 13 c 26 g 28 t
ORIGIN
Query Match      81.6%; Score 20.4; DB 14; Length 92;
Best Local Similarity 95.5%; Pred. No. 9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCTTTTGTACAAAGTTGG 25
||||| ||||| ||||| ||||| |||||
Db 31 CAGCTTTTGTACAAAGTTGG 10

RESULT 22
CB402537/c
LOCUS
DEFINITION
CB402537 92 bp mRNA linear EST 15-MAY-2003
ACCESSION
CB402537.1 GI:30744264
VERSION
CB402537.1
KEYWORDS
EST.
SOURCE
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 92)
AUTHORS
Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong
, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson
, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,
Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tollas, P.P.,
Placek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,
Doucette-Stamm, L., Hill, D.E. and Vidal, M.
C. elegans ORFeome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
expression
Nat. Genet., (2003) In press
Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc.Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david_hill@dfci.harvard.edu or
marc_vidal@dfci.harvard.edu
POLYA=No.

JOURNAL
    source
        Location/Qualifiers
        1..92
            /organism="Caenorhabditis elegans"
            /mol_type="mRNA"
            /strain="N2"
            /db_xref="taxon:6239"
            /sex="Hermaphrodite and male"
            /tissue_type="whole animal"
            /dev_stage="mixed stage"
            /clone_lib="AD-wrmcDNA"
        /note="The AD-wrmcDNA library was generated with poly(A)+
        RNA isolated from both hermaphrodite and male N2 worms of
        all larval stages, embryos, adults and dauers and the
        subsequent generation of cDNAs by poly(A) priming. The
        cDNAs were cloned into pPC86"
BASE COUNT      25 a 13 c 26 g 28 t
ORIGIN
Query Match      81.6%; Score 20.4; DB 14; Length 92;
Best Local Similarity 95.5%; Pred. No. 9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
|||||
Db 633 GTTCAGCTTTTATANTAAAGTTGG 609

RESULT 18
CA986810/c
LOCUS
DEFINITION
CA986810 831 bp mRNA linear EST 06-JAN-2003
AGENCOURT 11113724 NICHDXGC Embl Xenopus laevis cDNA clone
IMAGE:6863318 5', mRNA sequence.
CA986810.1 GI:27519481
EST.
Xenopus laevis (African clawed frog)
Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 831)
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Martha Rebert, Steven L. Klein, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NCI-CCGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM14482 row: e column: 13
High quality sequence stop: 477.
Location/Qualifiers
1..831
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:6863318"
/tissue_type="embryo (stage 10)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NICHDXGC Embl"
/notes="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI;
Cloned unidirectionally. Primer: Oligo dt. Average insert
size 1.55 kb. Constructed by Life Technologies. Note: This
is a Xenopus Gene Collection (XGC) library."
BASE COUNT 241 a 165 c 183 g 241 t 1 others
ORIGIN

FEATURES
source
Query Match 83.2%; Score 20.8; DB 14; Length 831;
Best Local Similarity 91.7%; Pred. No. 7.9e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTACGCTTTTGTACAAAGTTGG 25
|||||
Db 821 TCCAGCTTTTGTACAAAGTTGG 798

RESULT 19
BX430288
LOCUS
DEFINITION
BX430288 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
ClonBB0142D12 5-PRIME, mRNA sequence.
ACCESSION
BX430288
VERSION
BX430288.1 GI:30770931
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

```

REFERENCE
AUTHORS
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3874.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0BAE002ZB04_AE00123_2&cluster=3874.r.
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0BAE002ZB04_AE00123_2.
Location/Qualifiers
1..868
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="ClonBB0142D12"
/tissue_type="NEUROBLASTOMA"
/clone_lib="Homo sapiens NEUROBLASTOMA"
/notes="Vector: pCMVSPORT_6; 1st strand cDNA was primed
with a NotI-oligo(dt) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
BASE COUNT 193 a 230 c 170 g 274 t 1 others
ORIGIN

Query Match 83.2%; Score 20.8; DB 13; Length 868;
Best Local Similarity 91.7%; Pred. No. 7.8e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTCAGCTTTTGTACAAAGTTGG 25
|||||
Db 599 TCCAGCTTTTGTACAAAGTTGG 622

RESULT 20
CB400039/c
LOCUS
DEFINITION
CB400039 87 bp mRNA linear EST 15-MAY-2003
OSTF167D8_1 AD-wrncDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION
CB400039
VERSION
CB400039.1 GI:30741766
KEYWORDS
EST.
SOURCE
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 87)
Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong
, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson
, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,
Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolia, P.P.
, Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,
Doucette-Stamm, L., Hill, D.E. and Vidal, M.
C. elegans ORFeome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
expression
Nat. Genet., (2003) In press
Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc.Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david.hill@dfci.harvard.edu or

```



```

COMMENT      Contact: ffrrench-Constant RH
              Department of Biology and Biochemistry
              University of Bath
              South Building, Bath BA2 7AY, UK
              Tel: (44) 1225 826621
              Fax: (44) 1225 826779
              Email: bssrfc@bath.ac.uk
              This is one of 2,122 random reads from the M13 library. For
              annotation of identified clones (BLASTX, BLASTN and mapping to E.
              coli K12 genome) please see ffrrench-Constant et al. 2000, Nucleic
              Acids Res.
              Seq primer: M13 Forward
              Class: shotgun.

FEATURES
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        /clone_lib="Photorhabdus luminescens strain W14 M13
        library"
        /dev_stage="primary phase variant"
        /clone="PLG02205"
        /db_xref="taxon:29488"
        /dev_stage="primary phase variant"
        /clone_lib="Photorhabdus luminescens strain W14 M13
        library"
        /note="Genomic DNA from strain W14 was size selected (1-2
        kb) and then cloned into M13 Janus."
        Seq primer: M13 Forward
        Class: shotgun.

BASE COUNT   135 a 72 c 63 g 101 t 24 others
ORIGIN
  Query Match      83.2%; Score 20.8; DB 28; Length 395;
  Best Local Similarity 88.0%; Pred. No. 7.2e+02;
  Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
    |||||
Db 210 GTTCAGCTTTTGTACAAAGTTGG 186

RESULT 16
AQ991011/c
LOCUS
DEFINITION
  Photorhabdus luminescens strain W14 M13 library
  Photorhabdus luminescens genomic clone PLG01864, genomic survey
  sequence.
ACCESSION
  AQ991011.1 GI:9649605
VERSION
  GSS.
KEYWORDS
  SOURCE
  ORGANISM
    Photorhabdus luminescens
    Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
    Enterobacteriaceae; Photorhabdus.
REFERENCE
  1 (bases 1 to 664)
  ffrrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
  Daborn,P.J., Bowen,D. and Blattner,F.R.
  A genomic sample sequence of the entomopathogenic bacterium
  Photorhabdus luminescens W14: potential implications for virulence
  sequence.
JOURNAL
  MEDLINE
  PUBMED
  20378633
COMMENT
  Contact: ffrrench-Constant RH
  Department of Biology and Biochemistry
  University of Bath
  South Building, Bath BA2 7AY, UK
  Tel: (44) 1225 826621
  Fax: (44) 1225 826779
  Email: bssrfc@bath.ac.uk
  This is one of 2,122 random reads from the M13 library. For
  annotation of identified clones (BLASTX, BLASTN and mapping to E.
  coli K12 genome) please see ffrrench-Constant et al. 2000, Nucleic
  Acids Res.
  Seq primer: M13 Forward
  Class: shotgun.

FEATURES
  source
    Location/Qualifiers
      1..664
        /organism="Photorhabdus luminescens"
        /mol_type="genomic DNA"
        /strain="W14"
        /db_xref="taxon:29488"
        /clone_lib="Photorhabdus luminescens strain W14 M13
        library"
        /dev_stage="primary phase variant"
        /clone="PLG00126"
        /db_xref="taxon:29488"
        /dev_stage="primary phase variant"
        /clone_lib="Photorhabdus luminescens strain W14 M13
        library"
        /note="Genomic DNA from strain W14 was size selected (1-2
        kb) and then cloned into M13 Janus."
        Seq primer: M13 Forward
        Class: shotgun.

BASE COUNT   135 a 72 c 63 g 101 t 24 others
ORIGIN
  Query Match      83.2%; Score 20.8; DB 28; Length 395;
  Best Local Similarity 88.0%; Pred. No. 7.2e+02;
  Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
    |||||
Db 210 GTTCAGCTTTTGTACAAAGTTGG 186

RESULT 17
AQ989566/c
LOCUS
DEFINITION
  Photorhabdus luminescens strain W14 M13 library
  Photorhabdus luminescens genomic clone PLG00126, genomic survey
  sequence.
ACCESSION
  AQ989566
VERSION
  AQ989566.1 GI:9648160
KEYWORDS
  SOURCE
  ORGANISM
    Photorhabdus luminescens
    Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
    Enterobacteriaceae; Photorhabdus.
REFERENCE
  1 (bases 1 to 751)
  ffrrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
  Daborn,P.J., Bowen,D. and Blattner,F.R.
  A genomic sample sequence of the entomopathogenic bacterium
  Photorhabdus luminescens W14: potential implications for virulence
  sequence.
JOURNAL
  MEDLINE
  PUBMED
  20378633
COMMENT
  Contact: ffrrench-Constant RH
  Department of Biology and Biochemistry
  University of Bath
  South Building, Bath BA2 7AY, UK
  Tel: (44) 1225 826621
  Fax: (44) 1225 826779
  Email: bssrfc@bath.ac.uk
  This is one of 2,122 random reads from the M13 library. For
  annotation of identified clones (BLASTX, BLASTN and mapping to E.
  coli K12 genome) please see ffrrench-Constant et al. 2000, Nucleic
  Acids Res.
  Seq primer: M13 Forward
  Class: shotgun.

FEATURES
  source
    Location/Qualifiers
      1..751
        /organism="Photorhabdus luminescens"
        /mol_type="genomic DNA"
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        /db_xref="taxon:29488"
        /clone_lib="Photorhabdus luminescens strain W14 M13
        library"
        /dev_stage="primary phase variant"
        /clone="PLG00126"
        /db_xref="taxon:29488"
        /dev_stage="primary phase variant"
        /clone_lib="Photorhabdus luminescens strain W14 M13
        library"
        /note="Genomic DNA from strain W14 was size selected (1-2
        kb) and then cloned into M13 Janus."
        Seq primer: M13 Forward
        Class: shotgun.

BASE COUNT   217 a 159 c 171 g 200 t 4 others
ORIGIN
  Query Match      83.2%; Score 20.8; DB 28; Length 751;
  Best Local Similarity 88.0%; Pred. No. 7.7e+02;

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Query Match      87.2%; Score 21.8; DB 28; Length 743;
Best Local Similarity 92.0%; Pred. No. 3.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTGG 25
Db 626 GTTCAGCTTTTATACTAAGTTGG 602

RESULT 13
AQ990110/c
LOCUS
DEFINITION
Rfc00827 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG00827, genomic survey
sequence.
ACCESSION
AQ990110
VERSION
AQ990110.1 GI:9648704
KEYWORDS
GSS.
SOURCE
Photorhabdus luminescens
Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
REFERENCE
1 (bases 1 to 764)
AUTHORS
ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
Daborn,P.J., Bowen,D. and Blattner,F.R.
TITLE
A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
JOURNAL
MEDLINE
20378633
PUBMED
10919786
COMMENT
Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bsr1c@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
Acids Res.
Seq primer: M13 Forward
Class: shotgun.
FEATURES
source
Location/Qualifiers
1..764
/organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"
/db_xref="taxon:29488"
/dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
library"
/note="Genomic DNA from strain W14 was size selected (1-2
kb) and then cloned into M13 Janus."
BASE COUNT 215 a 170 c 171 g 203 t 5 others
ORIGIN
Query Match      87.2%; Score 21.8; DB 28; Length 764;
Best Local Similarity 92.0%; Pred. No. 3.2e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTGG 25
Db 721 GTTCAGCTTTTATACTAAGTTGG 697

RESULT 14
AQ990470/c
LOCUS
DEFINITION
Rfc01245 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01245, genomic survey
sequence.
ACCESSION
AQ990470
VERSION
AQ990470.1 GI:9649064
KEYWORDS
GSS.
SOURCE
Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
REFERENCE
1 (bases 1 to 769)
AUTHORS
ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
Daborn,P.J., Bowen,D. and Blattner,F.R.
TITLE
A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
JOURNAL
MEDLINE
20378633
PUBMED
10919786
COMMENT
Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bsr1c@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
Acids Res.
Seq primer: M13 Forward
Class: shotgun.
FEATURES
source
Location/Qualifiers
1..769
/organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"
/db_xref="taxon:29488"
/dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
library"
/note="Genomic DNA from strain W14 was size selected (1-2
kb) and then cloned into M13 Janus."
BASE COUNT 223 a 163 c 174 g 204 t 5 others
ORIGIN
Query Match      87.2%; Score 21.8; DB 28; Length 769;
Best Local Similarity 92.0%; Pred. No. 3.2e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTGG 25
Db 631 GTTCAGCTTTTATACTAAGTTGG 607

RESULT 15
AQ991303/c
LOCUS
DEFINITION
Rfc02205 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG02205, genomic survey
sequence.
ACCESSION
AQ991303
VERSION
AQ991303.1 GI:9649897
KEYWORDS
GSS.
SOURCE
Photorhabdus luminescens
Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
REFERENCE
1 (bases 1 to 395)
AUTHORS
ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
Daborn,P.J., Bowen,D. and Blattner,F.R.
TITLE
A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
JOURNAL
MEDLINE
20378633
PUBMED
10919786
COMMENT
Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bsr1c@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
Acids Res.
Seq primer: M13 Forward
Class: shotgun.
FEATURES
source
Location/Qualifiers
1..395
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/strain="W14"
/db_xref="taxon:29488"
/dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
library"
/note="Genomic DNA from strain W14 was size selected (1-2
kb) and then cloned into M13 Janus."
BASE COUNT 223 a 163 c 174 g 204 t 5 others
ORIGIN
Query Match      87.2%; Score 21.8; DB 28; Length 769;
Best Local Similarity 92.0%; Pred. No. 3.2e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTGG 25
Db 631 GTTCAGCTTTTATACTAAGTTGG 607

```

```

MEDLINE      20378633
PUBMED      10919786
COMMENT      Contact: ffrench-Constant RH
             Department of Biology and Biochemistry
             University of Bath
             South Building, Bath BA2 7AY, UK
             Tel: (44) 1225 826621
             Fax: (44) 1225 826779
             Email: bssrfc@bath.ac.uk
             This is one of 2,122 random reads from the M13 library. For
             annotation of identified clones (BLASTX, BLASTN and mapping to E.
             coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
             Acids Res.
             Seq primer: M13 Forward
             Class: shotgun.

FEATURES     Location/Qualifiers
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             /organism="Photorhabdus luminescens"
             /mol_type="genomic DNA"
             /strain="W14"
             /db_xref="taxon:29488"
             /clone="PLG01894"
             /dev_stage="primary phase variant"
             /clone_lib="Photorhabdus luminescens strain W14 M13
             library"
             /note="Genomic DNA from strain W14 was size selected (1-2
             kb) and then cloned into M13 Janus."
BASE COUNT   193 a 148 c 165 g 187 t
ORIGIN
1 GTTACGCTTTTGTACAAAGTTGG 25
|||||
639 GTTCAGCTTTTATCTAGTTGG 615

Query Match      87.2%; Score 21.8; DB 28; Length 695;
Best Local Similarity 92.0%; Pred. No. 3.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
|||||
Db 639 GTTCAGCTTTTATCTAGTTGG 615

RESULT 11
AQ990809/c
LOCUS
DEFINITION
Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01894, genomic survey
sequence.
ACCESSION      AQ990809
VERSION        AQ990809.1 GI:9649403
KEYWORDS       GSS.
SOURCE         Photorhabdus luminescens
ORGANISM       Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
               Enterobacteriaceae; Photorhabdus.
REFERENCE      1 (bases 1 to 712)
               ffrench-Constant R.H., Waterfield,N., Burland,V., Perna,N.T.,
               Daborn,P.J., Bowen,D. and Blattner,F.R.
               A genomic sample sequence of the entomopathogenic bacterium
               Photorhabdus luminescens strain W14 M13 library
               Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
MEDLINE        20378633
PUBMED        10919786
COMMENT        Contact: ffrench-Constant RH
               Department of Biology and Biochemistry
               University of Bath
               South Building, Bath BA2 7AY, UK
               Tel: (44) 1225 826621
               Fax: (44) 1225 826779
               Email: bssrfc@bath.ac.uk
               This is one of 2,122 random reads from the M13 library. For
               annotation of identified clones (BLASTX, BLASTN and mapping to E.
               coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
               Acids Res.
               Seq primer: M13 Forward
               Class: shotgun.

FEATURES     Location/Qualifiers
             1..712
             /organism="Photorhabdus luminescens"
             /mol_type="genomic DNA"
             /strain="W14"
             /db_xref="taxon:29488"
             /clone="PLG01638"
             /dev_stage="primary phase variant"
             /clone_lib="Photorhabdus luminescens strain W14 M13
             library"
             /note="Genomic DNA from strain W14 was size selected (1-2
             kb) and then cloned into M13 Janus."
BASE COUNT   218 a 144 c 163 g 187 t
ORIGIN
1 GTTCAGCTTTTGTACAAAGTTGG 25
|||||
453 GTTCAGCTTTTATCTAGTTGG 429

RESULT 12
AQ990346/c
LOCUS
DEFINITION
Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01106, genomic survey
sequence.
ACCESSION      AQ990346
VERSION        AQ990346.1 GI:9648940
KEYWORDS       GSS.
SOURCE         Photorhabdus luminescens
ORGANISM       Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
               Enterobacteriaceae; Photorhabdus.
REFERENCE      1 (bases 1 to 743)
               ffrench-Constant R.H., Waterfield,N., Burland,V., Perna,N.T.,
               Daborn,P.J., Bowen,D. and Blattner,F.R.
               A genomic sample sequence of the entomopathogenic bacterium
               Photorhabdus luminescens strain W14 M13 library
               Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
MEDLINE        20378633
PUBMED        10919786
COMMENT        Contact: ffrench-Constant RH
               Department of Biology and Biochemistry
               University of Bath
               South Building, Bath BA2 7AY, UK
               Tel: (44) 1225 826621
               Fax: (44) 1225 826779
               Email: bssrfc@bath.ac.uk
               This is one of 2,122 random reads from the M13 library. For
               annotation of identified clones (BLASTX, BLASTN and mapping to E.
               coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
               Acids Res.
               Seq primer: M13 Forward
               Class: shotgun.

FEATURES     Location/Qualifiers
             1..743
             /organism="Photorhabdus luminescens"
             /mol_type="genomic DNA"
             /strain="W14"
             /db_xref="taxon:29488"
             /clone="PLG01106"
             /dev_stage="primary phase variant"
             /clone_lib="Photorhabdus luminescens strain W14 M13
             library"
             /note="Genomic DNA from strain W14 was size selected (1-2
             kb) and then cloned into M13 Janus."
BASE COUNT   214 a 158 c 169 g 200 t
ORIGIN
1 GTTCAGCTTTTGTACAAAGTTGG 25
|||||
639 GTTCAGCTTTTATCTAGTTGG 615

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```

Query Match      87.2%; Score 21.8; DB 13; Length 472;
Best Local Similarity 92.0%; Pred. No. 3e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
    |||||
Db 380 GTTCAGCTTTTATATACTAAGTTGG 356

RESULT 8
BQ156404/c
LOCUS
DEFINITION
  NF092E031RUF1023 Irradiated Medicago truncatula cDNA clone
  NF092E031R 5', mRNA sequence.
ACCESSION
  BQ156404
VERSION
  BQ156404.1 GI:20293463
KEYWORDS
  Medicago truncatula (barrel medic)
SOURCE
  Medicago truncatula
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
  ; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
  Medicago.
REFERENCE
  1 (bases 1 to 473)
  Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,
  Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.
  Expressed Sequence Tags from the Samuel Roberts Noble Foundation
  Medicago truncatula irradiated library
JOURNAL
  Unpublished
COMMENT
  Contact: May GD
  Plant Biology Division
  The Samuel Roberts Noble Foundation
  2510 Sam Noble Parkway, Ardmore, OK 73402, USA
  Tel: 580 221 7391
  Fax: 580 221 7360
  Email: gdmay@noble.org
  Insert Length: 473 Std Error: 0.00
  Plate: 092 row: E column: 03
  Seq primer: TCACACAGGAACACAGCTATGAC.
  Location/Qualifiers
  FEATURES
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        /clone="NF092E031R"
        /tissue_type="seedlings"
        /dev_stage="seedling"
        /clone_lib="irradiated"
        /note="Vector: Lambda Zap; Seedlings were exposed either
        to 100 Gy gamma or 0.5, 1, 5, or 10 kJ/m2 UV irradiation.
        Gamma-irradiated samples were harvested at 6, 12, 24 and
        48 hours after treatment. UV-irradiated samples were
        harvested 24 hours post-treatment. cDNA was prepared from
        polyA+ enriched, pooled samples of equivalent amounts of
        total RNA from each sample. The cDNA was directionally
        ligated into the Uni-Zap XR vector (Stratagene) and
        packaged using the Gigapack III Gold packaging extracts.
        Phagemids containing cDNA inserts were in vivo excised
        from the recombinant Uni-Zap XR vector using EXAssist
        helper phage and the E. coli strain XL1-Blue MRF'
        (Stratagene). Excised plasmids were plated using SOLR
        cells."
BASE COUNT      162 a 90 c 95 g 126 t
ORIGIN
Query Match      87.2%; Score 21.8; DB 13; Length 473;
Best Local Similarity 92.0%; Pred. No. 3e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
    |||||
Db 381 GTTCAGCTTTTATATACTAAGTTGG 357

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RESULT 9
B1422679/c
LOCUS
DEFINITION
  B1422679 tomato callus, TAMU Lycopersicon esculentum cDNA clone
  c1EC7182 5' end, mRNA sequence.
ACCESSION
  B1422679
VERSION
  B1422679.1 GI:15197297
KEYWORDS
  EST.
SOURCE
  Lycopersicon esculentum (tomato)
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE
  1 (bases 1 to 597)
  Alcalá, J., Vrebalov, J., White, R., Matern, A.L., Vision, T., Holt, I.E.,
  Liang, F., Upton, J., Craven, M.B., Bowman, C.L., Ahn, S., Ronning
  , C.M., Fraser, C.M., Martin, G.B., Tankley, S.D. and Giovannoni, J.
  Generation of ESTs from tomato callus tissue
JOURNAL
  Unpublished
COMMENT
  Contact: CUGI
  Clemson University Genomics Institute
  Clemson University
  100 Jordan Hall, Clemson, SC 29634, USA
  Email: http://www.genome.clemson.edu/orders/index.html.
  Location/Qualifiers
  FEATURES
    source
      1..597
        /organism="Lycopersicon esculentum"
        /mol_type="mRNA"
        /cultivar="TA496"
        /db_xref="taxon:4081"
        /clone="c1EC71G2"
        /tissue_type="callus"
        /dev_stage="25-40 days old"
        /lab_host="XL1-Blue MRF"
        /clone_lib="tomato callus, TAMU"
        /note="Vector: pBlueScript SK(-); Site_1: EcoRI; Site_2:
        XhoI; supplier: Giovannoni laboratory; c1EC - Cotyledons
        of seedlings 7-10 days post-germination were excised, cut
        at both ends and placed on MS medium with no selection.
        Mixed callus was harvested at 25 and 40 days and included
        undifferentiated masses. Tomato Callus EST Library"
BASE COUNT      193 a 109 c 131 g 164 t
ORIGIN
Query Match      87.2%; Score 21.8; DB 12; Length 597;
Best Local Similarity 92.0%; Pred. No. 3.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
    |||||
Db 552 GTTCAGCTTTTATATACTAAGTTGG 528

RESULT 10
AQ991039/c
LOCUS
DEFINITION
  AQ991039 Photorhabdus luminescens strain W14 M13 library
  Rf01894 Photorhabdus luminescens genomic clone PLG01894, genomic survey
  sequence.
ACCESSION
  AQ991039
VERSION
  AQ991039.1 GI:9649633
KEYWORDS
  GSS.
SOURCE
  Photorhabdus luminescens
ORGANISM
  Photorhabdus luminescens
  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
  Enterobacteriaceae; Photorhabdus.
REFERENCE
  1 (bases 1 to 695)
  french-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
  Daborn, P.J., Bowen, D. and Blattner, F.R.
  A genomic sample sequence of the entomopathogenic bacterium
  Photorhabdus luminescens W14: potential implications for virulence
  Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
JOURNAL

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus; 1 (bases 1 to 299)

REFERENCE
AUTHORS
 Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Niki, I., Ootaru, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tonaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojohori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, D.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bratt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazier, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirakawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawai, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Sempke, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.

TITLE
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL
 Nature 420, 563-573 (2002)

MEDLINE
 22354683

PUBMED
 12456851

COMMENT
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suenhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@sc.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/
 Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES
 Location/Qualifiers
 1..229
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"

BASE COUNT 162 a 89 c 95 g 126 t
ORIGIN

/clone="I430040C03"
 /tissue_type="whole body"
 /dev_stage="18 days embryo"
 /clone_lib="RIKEN full-length enriched, 18 days embryo whole body"
 85 a 50 c 54 g 110 t

BASE COUNT 85 a 50 c 54 g 110 t
ORIGIN

Query Match 87.2%; Score 21.8; DB 13; Length 299;
 Best Local Similarity 92.0%; Pred. No. 2.9e+02;
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
 |||||
Db 246 GTTCAGCTTTTGTACTAAGTTGG 270

RESULT 7
 BQ157398/c
 BQ157398/1

LOCUS
 DEFINITION
 NF104D07IR1F062 Irradiated Medicago truncatula cDNA clone
 NF104D07IR 5', mRNA sequence.

ACCESSION
 BQ157398
VERSION
 BQ157398.1 GI:20294457

KEYWORDS
 EST.
 Medicago truncatula (barrel medic)
ORGANISM
 Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
 Medicago.

REFERENCE
 1 (bases 1 to 472)
 Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.
 Expressed Sequence Tags from the Samuel Roberts Noble Foundation
 Medicago truncatula irradiated library
 Unpublished
 Contact: May GD
 Plant Biology Division
 The Samuel Roberts Noble Foundation
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA
 Tel: 580 221 7391
 Fax: 580 221 7380
 Email: gdmay@noble.org
 Insert Length: 472 Std Error: 0.00
 Plate: 104 row: D column: 07
 Seq primer: TCACACAGGAAACAGCATGAC.

FEATURES
 Location/Qualifiers
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 /clone="NF104D07IR"
 /tissue_type="seedlings"
 /dev_stage="seedling"
 /clone_lib="irradiated"
 /note="Vector: Lambda Zap; Seedlings were exposed either to 100 Gy gamma or 0.5, 1, 5, or 10 kJ/m2 UV irradiation. Gamma-irradiated samples were harvested at 6, 12, 24 and 48 hours after treatment. UV-irradiated samples were harvested 24 hours post-treatment. cDNA was prepared from polyA+ enriched, pooled samples of equivalent amounts of total RNA from each sample. The cDNA was directionally ligated into the Uni-Zap XR vector (Stratagene) and packaged using the Gigapack III Gold packaging extracts. Phagemids containing cDNA inserts were in vivo excised from the recombinant Uni-Zap XR vector using ExAssist helper phage and the E. coli strain XL1-Blue MRF' (Stratagene). Excised plasmids were plated using SOLR cells."

BASE COUNT 162 a 89 c 95 g 126 t
ORIGIN

Query Match 88.0%; Score 22; DB 14; Length 121;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CAGCTTTTGTACAAAGTTGG 25
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 Db 41 CAGCTTTTGTACAAAGTTGG 20

RESULT 4
 CB388073/c

LOCUS CB388073 141 bp mRNA linear EST 15-MAY-2003
 DEFINITION OSTF091E12_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
 ACCESSION CB388073
 VERSION CB388073.1 GI:30729783
 KEYWORDS EST
 ORGANISM Caenorhabditis elegans

REFERENCE 1 (bases 1 to 141)
 AUTHORS Rebol, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Hartley, O.L., Brasch, M.A., Vandenhoute, J., Boulton, S., Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolia, P.P., Ptacek, J.J., Snyder, M., Huang, R., Chance, M.R., Lee, H., Doucette-Stamm, L., Hill, D.E. and Vidal, M.
 TITLE C. elegans ORFeome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein expression

JOURNAL Nat. Genet., (2003) In press
 COMMENT Contact: Vidal M
 Marc Vidal Laboratory
 Dana Farber Cancer Institute
 1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
 Tel: 617 632 5180
 Fax: 617 632 5739
 Email: Marc.Vidal@dfci.harvard.edu
 Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project; Contact david_hill@dfci.harvard.edu or marc_vidal@dfci.harvard.edu
 POLYA-No.

FEATURES
 source Location/Qualifiers
 1..141
 /organism="Caenorhabditis elegans"
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 /strain="N2"
 /db_xref="taxon:6239"
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 /dev_stage="mixed stage"
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 /note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"
 40 a 32 c 23 g 46 t

BASE COUNT 40 a 32 c 23 g 46 t
 ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CAGCTTTTGTACAAAGTTGG 25
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 Db 74 CAGCTTTTGTACAAAGTTGG 53

RESULT 5
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LOCUS BQ156416 206 bp mRNA linear EST 24-APR-2002
 DEFINITION NF092F02IR1F1027 Irradiated Medicago truncatula cDNA clone NF092F02IR 5', mRNA sequence.
 ACCESSION BQ156416
 VERSION BQ156416.1 GI:20293475
 KEYWORDS EST
 SOURCE Medicago truncatula (barrel medic)
 ORGANISM Medicago truncatula

REFERENCE 1 (bases 1 to 206)
 AUTHORS Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Iman, J.T., Weller, J.W. and May, G.D.
 TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula irradiated library
 JOURNAL Unpublished
 COMMENT Contact: May GD
 Plant Biology Division
 The Samuel Roberts Noble Foundation
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA
 Tel: 580 221 7391
 Fax: 580 221 7380
 Email: gdmay@noble.org
 Insert Length: 206 Std Error: 0.00
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 Seq primer: TCACACAGGAACAGCTATGAC.

FEATURES
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 /note="Vector: Lambda Zap; Seedlings were exposed either to 100 Gy gamma or 0.5, 1, 5, or 10 kJ/m2 UV irradiation. Gamma-irradiated samples were harvested at 6, 12, 24 and 48 hours after treatment. UV-irradiated samples were harvested 24 hours post-treatment. cDNA was prepared from polyA+ enriched, pooled samples of equivalent amounts of total RNA from each sample. The cDNA was directionally ligated into the Uni-Zap XR vector (Stratagene) and packaged using the Gigapack III Gold packaging extracts. Phagemids containing cDNA inserts were in vivo excised from the recombinant Uni-Zap XR vector using Exassist helper phage and the E. coli strain XL1-Blue MRF' (Stratagene). Excised plasmids were plated using SOUR cells."
 81 a 27 c 39 g 59 t

BASE COUNT 81 a 27 c 39 g 59 t
 ORIGIN

Query Match 87.2%; Score 21.8; DB 13; Length 206;
 Best Local Similarity 92.0%; Pred. No. 2.8e+02;
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTGG 25
 |||
 Db 167 GTTCAGCTTTTGTACAAAGTTGG 143

RESULT 6
 BY115594

LOCUS BY115594 299 bp mRNA linear EST 08-DEC-2002
 DEFINITION BY115594 RIKEN full-length enriched, 18 days embryo whole body Mus musculus cDNA clone L430040C03 5', mRNA sequence.
 ACCESSION BY115594
 VERSION BY115594.1 GI:26226695
 KEYWORDS EST
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

Fax: 617 632 5739
 Email: Marc.Vidal@fci.harvard.edu
 Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project : Contact david_hill@fci.harvard.edu or marc.vidal@fci.harvard.edu
 POLYA=No.

FEATURES

Location/Qualifiers

1..95
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 /strain="N2"
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 /note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

BASE COUNT

24 a 20 c 25 g 26 t

ORIGIN

Query Match 88.0%; Score 22; DB 14; Length 95;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTTTGTACAAAGTTGG 25

Db 30 CAGCTTTTGTACAAAGTTGG 9

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 LOCUS 108 bp mRNA linear EST 15-MAY-2003
 DEFINITION OSTR212B7_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
 ACCESSION CB398919
 VERSION CB398919.1 GI:30740646
 KEYWORDS EST.
 SOURCE Caenorhabditis elegans
 ORGANISM Caenorhabditis elegans
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
 ; Rhabditidae; Peloderinae; Caenorhabditis.
 1 (bases 1 to 108)
 Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong
 , C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson
 , J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,
 Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tollas, P.P.,
 Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,
 Doucette-Stamm, L., Hill, D.E. and Vidal, M.
 C. elegans ORFeome version 1.1: experimental verification of the
 genome annotation and resource for proteome-scale protein
 expression

JOURNAL

Nat. Genet., (2003) In press
 Contact: Vidal M
 Marc Vidal Laboratory
 Dana Farber Cancer Institute
 1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
 Tel: 617 632 5180
 Fax: 617 632 5739

Email: Marc.Vidal@fci.harvard.edu
 Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project : Contact david_hill@fci.harvard.edu or marc.vidal@fci.harvard.edu
 POLYA=No.

FEATURES

Location/Qualifiers

1..108
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 /strain="N2"

/db_xref="taxon:6239"
 /sex="Hermaphrodite and male"
 /tissue_type="whole animal"
 /dev_stage="mixed stage"
 /clone_lib="AD-wrmcDNA"
 /note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

BASE COUNT

27 a 23 c 18 g 40 t

ORIGIN

Query Match 88.0%; Score 22; DB 14; Length 108;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTTTGTACAAAGTTGG 25

Db 45 CAGCTTTTGTACAAAGTTGG 24

RESULT 3

CB392422/c
 LOCUS 121 bp mRNA linear EST 15-MAY-2003
 DEFINITION OSTR099E7_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
 ACCESSION CB392422
 VERSION CB392422.1 GI:30734133
 KEYWORDS EST.
 SOURCE Caenorhabditis elegans
 ORGANISM Caenorhabditis elegans
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
 ; Rhabditidae; Peloderinae; Caenorhabditis.
 1 (bases 1 to 121)
 Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong
 , C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson
 , J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,
 Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tollas, P.P.,
 Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,
 Doucette-Stamm, L., Hill, D.E. and Vidal, M.
 C. elegans ORFeome version 1.1: experimental verification of the
 genome annotation and resource for proteome-scale protein
 expression

TITLE

C. elegans ORFeome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein expression

JOURNAL

Nat. Genet., (2003) In press
 Contact: Vidal M
 Marc Vidal Laboratory
 Dana Farber Cancer Institute
 1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
 Tel: 617 632 5180
 Fax: 617 632 5739

Email: Marc.Vidal@fci.harvard.edu
 Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project : Contact david_hill@fci.harvard.edu or marc.vidal@fci.harvard.edu
 POLYA=No.

FEATURES

source

1..121
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 /tissue_type="whole animal"
 /dev_stage="mixed stage"
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 /note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

BASE COUNT

41 a 22 c 22 g 36 t

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 6, 2003, 22:08:13 ; Search time 1093.75 Seconds
(without alignments)
555.531 Million cell updates/sec

Title: US-10-055-001A-10
Perfect score: 25
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: em_estum:*
3: em_estin:*
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6: em_estpl:*
7: em_estro:*
8: em_htc:*
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10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
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21: em_gss_fun:*
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23: em_gss_mus:*
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26: em_gss_phg:*
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28: gb_gssl:*
29: gb_gss2:*

SUMMARIES

Result No.	Score	Match	Length	ID	Description
C 1	22	88.0	95	14	CB402238 OSTF209B3
C 2	22	88.0	108	14	CB398919 OSTF212B7
C 3	22	88.0	121	14	CB392422 OSTF099E7
C 4	22	88.0	141	14	CB388073 OSTF091E1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

C	5	21.8	87.2	206	13	BQ156416
C	6	21.8	87.2	299	13	BY115594
C	7	21.8	87.2	472	13	BQ157398
C	8	21.8	87.2	473	13	BQ156404
C	9	21.8	87.2	597	12	BI422679
C	10	21.8	87.2	695	28	AQ991039
C	11	21.8	87.2	712	28	AQ990809
C	12	21.8	87.2	743	28	AQ990346
C	13	21.8	87.2	764	28	AQ990110
C	14	21.8	87.2	769	28	AQ990470
C	15	20.8	83.2	395	28	AQ991303
C	16	20.8	83.2	664	28	AQ991011
C	17	20.8	83.2	751	28	AQ989566
C	18	20.8	83.2	831	14	CA986810
C	19	20.8	83.2	868	13	EX430288
C	20	20.4	81.6	87	14	CB400039
C	21	20.4	81.6	90	14	CB392047
C	22	20.4	81.6	92	14	CB402537
C	23	20.4	81.6	94	14	CB402408
C	24	20.4	81.6	95	14	CB400591
C	25	20.4	81.6	97	14	CB401751
C	26	20.4	81.6	97	14	CB401179
C	27	20.4	81.6	98	14	CB402581
C	28	20.4	81.6	100	14	CB392051
C	29	20.4	81.6	100	14	CB398867
C	30	20.4	81.6	100	14	CB398991
C	31	20.4	81.6	100	14	CB400512
C	32	20.4	81.6	102	14	CB392040
C	33	20.4	81.6	102	14	CB399013
C	34	20.4	81.6	103	14	CB396276
C	35	20.4	81.6	103	14	CB401874
C	36	20.4	81.6	106	14	CB396275
C	37	20.4	81.6	106	14	CB396817
C	38	20.4	81.6	107	14	CB388456
C	39	20.4	81.6	111	14	CB394444
C	40	20.4	81.6	111	14	CB395510
C	41	20.4	81.6	112	14	CB396297
C	42	20.4	81.6	112	14	CB397516
C	43	20.4	81.6	112	14	CB398322
C	44	20.4	81.6	114	14	CB402012
C	45	20.4	81.6	118	14	CB396745

ALIGNMENTS

RESULT 1
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LOCUS CB402238 95 bp mRNA linear EST 15-MAY-2003
DEFINITION OSTF209B3_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION CB402238
VERSION CB402238.1 GI:30743965
KEYWORDS EST.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Pelodierinae; Caenorhabditis.
REFERENCE 1 (bases 1 to 95)
AUTHORS Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Hartley, J.L., Brach, M.A., Vandenhaute, J., Boulton, S., Andres, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, P.P., Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H., Doucette-Stamm, L., Hill, D.E. and Vidal, M.
C. elegans ORFome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein expression
Nat. Genet., (2003) In press
Contact: Vidal M

JOURNAL COMMENT

Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180

; TITLE OF INVENTION: Use of Multiple Recombination Sites with Unique Specificity in

; FILE REFERENCE: 0942.5010002

; CURRENT APPLICATION NUMBER: US/09/732,914

; CURRENT FILING DATE: 2000-12-11

; PRIOR APPLICATION NUMBER: US 60/169,983

; PRIOR FILING DATE: 1999-12-10

; PRIOR APPLICATION NUMBER: US 60/188,020

; PRIOR FILING DATE: 2000-03-09

; NUMBER OF SEQ ID NOS: 140

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 10

; LENGTH: 27

; TYPE: DNA

; ORGANISM: attP2

US-09-732-914-10

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Best Local Similarity 96.0%; Pred. No. 1.1;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 GTTCAGCTTTTGTACAAAGTTGG 25

Search completed: November 7, 2003, 02:22:26
Job time : 102.25 secs

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; Publication No. US20030068799A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
;           Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
;           Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/162,879
; FILING DATE: 06-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,085
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-162-879-16

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Best Local Similarity 96.0%; Pred. No. 1.1;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 38
US-10-161-403-51
; Sequence 51, Application US/10161403
; Publication No. US20030119104A1
; GENERAL INFORMATION:
; APPLICANT: Perkins, Edward
; APPLICANT: Lindenbaum, Michael
; APPLICANT: Greene, Amy
; APPLICANT: Leung, Josephine
; APPLICANT: Fleming, Elena
; APPLICANT: Stewart, Sandra
; APPLICANT: Shellard, Joan
; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
; FILE REFERENCE: 24601-420
; CURRENT APPLICATION NUMBER: US/10/161,403
; PRIOR FILING DATE: 2002-05-30
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
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US-10-162-879-16

Query Match          93.6%; Score 23.4; DB 14; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.1;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

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US-10-161-403-56
; Sequence 56, Application US/10161403
; Publication No. US20030119104A1
; GENERAL INFORMATION:
; APPLICANT: Perkins, Edward
; APPLICANT: Lindenbaum, Michael
; APPLICANT: Greene, Amy
; APPLICANT: Leung, Josephine
; APPLICANT: Fleming, Elena
; APPLICANT: Stewart, Sandra
; APPLICANT: Shellard, Joan
; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
; FILE REFERENCE: 24601-420
; CURRENT APPLICATION NUMBER: US/10/161,403
; PRIOR FILING DATE: 2002-05-30
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-162-879-16

Query Match          93.6%; Score 23.4; DB 14; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.1;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 40
US-09-732-914-10
; Sequence 10, Application US/09732914
; Patent No. US20020007051A1
; GENERAL INFORMATION:
; APPLICANT: Cheo, David
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Hartley, James L.
; APPLICANT: Byrd, Devon R.N.
```

```
; PRIOR APPLICATION NUMBER: 60/294,758
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 60/366,891
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: attR3
US-10-161-403-51

Query Match          93.6%; Score 23.4; DB 14; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.1;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 39
US-10-161-403-56
; Sequence 56, Application US/10161403
; Publication No. US20030119104A1
; GENERAL INFORMATION:
; APPLICANT: Perkins, Edward
; APPLICANT: Lindenbaum, Michael
; APPLICANT: Greene, Amy
; APPLICANT: Leung, Josephine
; APPLICANT: Fleming, Elena
; APPLICANT: Stewart, Sandra
; APPLICANT: Shellard, Joan
; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
; FILE REFERENCE: 24601-420
; CURRENT APPLICATION NUMBER: US/10/161,403
; PRIOR FILING DATE: 2002-05-30
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: attP2,P3
US-10-161-403-56

Query Match          93.6%; Score 23.4; DB 14; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.1;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 40
US-09-732-914-10
; Sequence 10, Application US/09732914
; Patent No. US20020007051A1
; GENERAL INFORMATION:
; APPLICANT: Cheo, David
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Hartley, James L.
; APPLICANT: Byrd, Devon R.N.
```

us-10-055-001a-10.rnpb

Fri Nov 7 08:08:37 2003

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US-10-058-292-11
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-058-292-11
; Query Match 93.6%; Score 23.4; DB 14; Length 25;
; Best Local Similarity 96.0%; Pred. No. 1.1;
; Mismatches 0; Gaps 0;
; Indels 1;
; Matches 24; Conservative 0;
;
QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
| | | | | | | | | | | | | | | | | | | | |
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25
| | | | | | | | | | | | | | | | | | | | |
;
RESULT 35
US-10-162-879-11
; Sequence 11, Application US/10162879
; Publication No. US2003006879A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/162,879
; FILING DATE: 06-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,085
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-162-879-11
; Query Match 93.6%; Score 23.4; DB 14; Length 25;
; Best Local Similarity 96.0%; Pred. No. 1.1;
; Mismatches 0; Gaps 0;
; Indels 1;
; Matches 24; Conservative 0;
;
QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
| | | | | | | | | | | | | | | | | | | | |
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25
| | | | | | | | | | | | | | | | | | | | |
;
RESULT 37
US-10-162-879-16
; Sequence 16, Application US/10162879
```

Fri Nov 7 08:08:37 2003

Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 93.6%; Score 23.4; DB 12; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.1;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
|||||
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 31

US-10-300-892-16
; Sequence 16, Application US/10300892
; Publication No. US20030175970A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.285004
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/907,719
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-10-300-892-16

Query Match 93.6%; Score 23.4; DB 12; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.1;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
|||||
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 32

US-10-055-001A-6
; Sequence 6, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: core sequence of recombination site attR3
US-10-055-001A-6

Query Match 93.6%; Score 23.4; DB 14; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.1;

Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
|||||
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 33

US-10-055-001A-11
; Sequence 11, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: core sequence of recombination site attP2, P3
US-10-055-001A-11

Query Match 93.6%; Score 23.4; DB 14; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.1;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
|||||
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 34

US-10-058-292-11
; Sequence 11, Application US/10058292
; Publication No. US20030054552A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; RECOMBINATION SITES
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/058,292
; FILING DATE: 30-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/432,085
; FILING DATE: 1999-11-02
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; APPLICATION NUMBER: 08/663,002

```

; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/432,085
; APPLICATION NUMBER: US/09/432,085
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; MISMATCHES: 0; Mismatches 0; Indels 1; Gaps 0;
US-09-432-085-11

Query Match 93.6%; Score 23.4; DB 11; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.1;
Matches 24; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTCTGTACAAAGTTGG 25

RESULT 29
US-09-432-085-16
; Sequence 16, Application US/09432085
; Publication No. US20030100110A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09432085
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-985-448-16
```

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/432,085
; APPLICATION NUMBER: US/09/432,085
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; MISMATCHES: 0; Mismatches 1; Indels 0; Gaps 0;
US-09-432-085-16

Query Match 93.6%; Score 23.4; DB 11; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.1;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTCTGTACAAAGTTGG 25

RESULT 30
US-09-985-448-16
; Sequence 16, Application US/09985448
; Publication No. US20030157716A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/985,448
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-985-448-16
```

```
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855,797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-855-797A-16

Query Match          93.6%; Score 23.4; DB 9; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.1;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
   |||||||
Db 1 GTTCAGCTTCTGTACAAAGTTGG 25

RESULT 25
US-09-822-634-8
; Sequence 8, Application US/09822634
; Patent No. US20020150556A1
; GENERAL INFORMATION:
; APPLICANT: Vile, Richard G.
; APPLICANT: Harrington, Kevin
; APPLICANT: Bateman, Andrew
; APPLICANT: Murphy, Steven
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TISSUE
; FILE REFERENCE: 07039-289001
; CURRENT APPLICATION NUMBER: US/09/822,634
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 60/193,977
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated vector sequence
US-09-822-634-8

Query Match          93.6%; Score 23.4; DB 10; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.1;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
   |||||||
Db 1 GTTCAGCTTCTGTACAAAGTTGG 25

RESULT 26
US-09-907-900-16
; Sequence 16, Application US/09907900
; Patent No. US20020172997A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
```

```
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,900
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-900-16

Query Match          93.6%; Score 23.4; DB 10; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.1;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
   |||||||
Db 1 GTTCAGCTTCTGTACAAAGTTGG 25

RESULT 27
US-09-907-719-16
; Sequence 16, Application US/09907719
; Publication No. US20020192819A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,719
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-719-16

Query Match          93.6%; Score 23.4; DB 10; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.1;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
   |||||||
Db 1 GTTCAGCTTCTGTACAAAGTTGG 25

RESULT 28
US-09-432-085-11
; Sequence 11, Application US/09432085
; Publication No. US20030100110A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
```

US-03-985-448-43
 ; Sequence 43, Application US/09985448
 ; Publication No. US20030157716A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hartley, James L.
 ; APPLICANT: Brasch, Michael A.
 ; APPLICANT: Temple, Gary F.
 ; APPLICANT: Fox, Donna K.
 ; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having

US-09-855-797A-16
; Sequence 16, Application US/09855797A
; Patent No. US2002009457A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.

Db 17792 GTTCAGCTTTTGTACAAAGTTGG 17816

RESULT 18

US-10-055-001A-13/c

; Sequence 13, Application US/10055001A

; Publication No. US20030049835A1

; GENERAL INFORMATION:

; APPLICANT: Wesley, Susan V.

; APPLICANT: Waterhouse, Peter

; APPLICANT: Helliwell, Christopher A.

; TITLE OF INVENTION: Method and means for producing efficient silencing constructs

; TITLE OF INVENTION: using recombinational cloning

; FILE REFERENCE: HELIGA

; CURRENT APPLICATION NUMBER: US/10/055,001A

; CURRENT FILING DATE: 2002-06-11

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 13

; LENGTH: 18691

; TYPE: DNA

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: acceptor vector pHELLSGATE

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (7922)..(9985)

; OTHER INFORMATION: spectinomycin resistance

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (10706)..(11324)

; OTHER INFORMATION: right T-DNA border fragment

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (11674)..(13019)

; OTHER INFORMATION: CamV35S promoter fragment

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (17890)..(17659)

; OTHER INFORMATION: attP1 recombination site (complement)

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (17610)..(16835)

; OTHER INFORMATION: ccdB selection marker (complement)

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (16351)..(16319)

; OTHER INFORMATION: attP2 recombination site (complement)

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (14660)..(16258)

; OTHER INFORMATION: pdk2 intron 2

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (15002)..(15661)

; OTHER INFORMATION: chloramphenicol resistance gene

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (14387)..(14619)

; OTHER INFORMATION: attP2 recombination site

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (13675)..(13980)

; OTHER INFORMATION: ccdB selection marker (complement)

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (13048)..(13279)

; OTHER INFORMATION: attP1 recombination site

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (17922)..(18687)

; OTHER INFORMATION: octopine synthase gene terminator region

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (264)..(496)

; OTHER INFORMATION: nopaline synthase gene promoter

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (497)..(1442)

; OTHER INFORMATION: nptII coding region

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1443)..(2148)

; OTHER INFORMATION: nopaline synthase gene terminator

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (2149)..(2706)

; OTHER INFORMATION: a left T-DNA border region

US-10-055-001A-13

Query Match 100.0%; Score 25; DB 14; Length 18691;

Best Local Similarity 100.0%; Pred. No. 0.74; 0; Indels 0; Gaps 0;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25

|||||

Db 13146 GTTCAGCTTTTGTACAAAGTTGG 13122

|||||

RESULT 19

US-09-855-797A-43

; Sequence 43, Application US/09855797A

; Patent No. US20020094574A1

; GENERAL INFORMATION:

; APPLICANT: Hartley, James L.

; APPLICANT: Brasch, Michael A.

; APPLICANT: Temple, Gary F.

; APPLICANT: Fox, Donna K.

; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having

; TITLE OF INVENTION: Recombination Sites

; FILE REFERENCE: 0942.2850008

; CURRENT APPLICATION NUMBER: US/09/855,797A

; CURRENT FILING DATE: 2001-05-16

; PRIOR APPLICATION NUMBER: 09/296,281

; PRIOR FILING DATE: 1999-04-22

; PRIOR APPLICATION NUMBER: US 60/065,930

; PRIOR FILING DATE: 1997-10-24

; NUMBER OF SEQ ID NOS: 60

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 43

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Unknown

; FEATURE:

; OTHER INFORMATION: Description of Unknown Organism: recombination

; OTHER INFORMATION: products

US-09-855-797A-43

Query Match 95.2%; Score 23.8; DB 9; Length 25;

Best Local Similarity 88.0%; Pred. No. 0.73;

Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25

|||||

Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

|||||

RESULT 20

US-09-907-900-43

; Sequence 43, Application US/09907900

; Patent No. US2002017299A1

; GENERAL INFORMATION:

; APPLICANT: Hartley, James L.

; APPLICANT: Brasch, Michael A.

; APPLICANT: Temple, Gary F.

; APPLICANT: Fox, Donna K.

us-10-055-001a-10.rnpb

Fri Nov 7 08:08:37 2003

; CURRENT APPLICATION NUMBER: US/10/055,001A
 ; CURRENT FILING DATE: 2002-06-11
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 23
 ; LENGTH: 17862
 ; TYPE: DNA
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: acceptor vector pHELLSGATE4
 ;
 ; US-10-055-001A-23

Query Match 100.0%; Score 25; DB 14; Length 17862;
 Best Local Similarity 100.0%; Pred. No. 0.73; 0; Indels 0; Gaps 0;
 Matches 25; Conservative 0; Mismatches 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTGG 25
 Db 16963 GTTCAGCTTTTGTACAAAGTTGG 16987
 |||||

RESULT 16
 US-10-055-001A-23/c
 ; Sequence 23, Application US/10055001A
 ; Publication No. US20030049835A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wesley, Susan V.
 ; APPLICANT: Waterhouse, Peter
 ; APPLICANT: Helliwell, Christopher A.
 ; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
 ; TITLE OF INVENTION: using recombinational cloning
 ; FILE REFERENCE: HELIGA
 ; CURRENT APPLICATION NUMBER: US/10/055,001A
 ; CURRENT FILING DATE: 2002-06-11
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 23
 ; LENGTH: 17862
 ; TYPE: DNA
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: acceptor vector pHELLSGATE4
 ;
 ; US-10-055-001A-23

Query Match 100.0%; Score 25; DB 14; Length 17862;
 Best Local Similarity 100.0%; Pred. No. 0.73; 0; Indels 0; Gaps 0;
 Matches 25; Conservative 0; Mismatches 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTGG 25
 Db 13146 GTTCAGCTTTTGTACAAAGTTGG 13122
 |||||

RESULT 17
 US-10-055-001A-13
 ; Sequence 13, Application US/10055001A
 ; Publication No. US20030049835A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wesley, Susan V.
 ; APPLICANT: Waterhouse, Peter
 ; APPLICANT: Helliwell, Christopher A.
 ; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
 ; TITLE OF INVENTION: using recombinational cloning
 ; FILE REFERENCE: HELIGA
 ; CURRENT APPLICATION NUMBER: US/10/055,001A
 ; CURRENT FILING DATE: 2002-06-11
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 13
 ; LENGTH: 18691
 ; TYPE: DNA
 ; ORGANISM: Artificial sequence
 ; FEATURE:

; OTHER INFORMATION: acceptor vector pHELLSGATE
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (7922)..(9985)
 ; OTHER INFORMATION: spectinomycin resistance
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (10706)..(11324)
 ; OTHER INFORMATION: right T-DNA border fragment
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (11674)..(13019)
 ; OTHER INFORMATION: CamV35S promoter fragment
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (17890)..(17659)
 ; OTHER INFORMATION: attP1 recombination site (complement)
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (17610)..(16855)
 ; OTHER INFORMATION: ccdB selection marker (complement)
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (16551)..(16319)
 ; OTHER INFORMATION: attP2 recombination site (complement)
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (14660)..(16258)
 ; OTHER INFORMATION: pdk2 intron 2
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (15002)..(15661)
 ; OTHER INFORMATION: chloramphenicol resistance gene
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (14387)..(14619)
 ; OTHER INFORMATION: attP2 recombination site
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (13048)..(13279)
 ; OTHER INFORMATION: attP1 recombination site
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (13675)..(13980)
 ; OTHER INFORMATION: ccdB selection marker (complement)
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (17922)..(18687)
 ; OTHER INFORMATION: octopine synthase gene terminator region
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (264)..(496)
 ; OTHER INFORMATION: nopaline synthase gene promoter
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (497)..(1442)
 ; OTHER INFORMATION: nptII coding region
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1443)..(2148)
 ; OTHER INFORMATION: nopaline synthase gene terminator
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (2149)..(2706)
 ; OTHER INFORMATION: a left T-DNA border region
 ; US-10-055-001A-13

Query Match 100.0%; Score 25; DB 14; Length 18691;
 Best Local Similarity 100.0%; Pred. No. 0.74; 0; Indels 0; Gaps 0;
 Matches 25; Conservative 0; Mismatches 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTGG 25
 |||||

us-10-055-001a-10.rnpb

Fri Nov 7 08:08:37 2003

```

; Sequence 30, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MO
; FILE REFERENCE: 0942.5120001
; CURRENT APPLICATION NUMBER: US/10/151,690
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 27
; TYPE: DNA
; ORGANISM: attP1
; US-10-151-690-30

Query Match 100.0%; Score 25; DB 14; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.22; 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
|||
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 13
US-10-151-690-21/c
; Sequence 21, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MO
; FILE REFERENCE: 0942.5120001
; CURRENT APPLICATION NUMBER: US/10/151,690
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 4470
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: plasmid pDONR201

NAME/KEY: gene
LOCATION: (29)..(260)
OTHER INFORMATION: attP1
FEATURE:
NAME/KEY: gene
LOCATION: (656)..(961)
OTHER INFORMATION: ccdb
FEATURE:
NAME/KEY: gene
LOCATION: (1099)..(1184)
OTHER INFORMATION: ccda
FEATURE:
NAME/KEY: gene

; Sequence 30, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MO
; FILE REFERENCE: 0942.5120001
; CURRENT APPLICATION NUMBER: US/10/151,690
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 4470
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: plasmid pDONR201

NAME/KEY: gene
LOCATION: (29)..(260)
OTHER INFORMATION: attP1
FEATURE:
NAME/KEY: gene
LOCATION: (656)..(961)
OTHER INFORMATION: ccdb
FEATURE:
NAME/KEY: gene
LOCATION: (1099)..(1184)
OTHER INFORMATION: ccda
FEATURE:
NAME/KEY: gene

; LOCATION: (1303)..(1962)
; OTHER INFORMATION: Cmr
; FEATURE:
; NAME/KEY: gene
; LOCATION: (2210)..(2442)
; OTHER INFORMATION: attP2
; FEATURE:
; NAME/KEY: gene
; LOCATION: (2565)..(3374)
; OTHER INFORMATION: Cmr
; FEATURE:
; NAME/KEY: gene
; LOCATION: (3495)..(4134)
; OTHER INFORMATION: ori
; US-10-151-690-21

Query Match 100.0%; Score 25; DB 14; Length 4470;
Best Local Similarity 100.0%; Pred. No. 0.57; 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
|||
Db 127 GTTCAGCTTTTGTACAAAGTTGG 103

RESULT 14
US-10-151-690-61
; Sequence 61, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MO
; FILE REFERENCE: 0942.5120001
; CURRENT APPLICATION NUMBER: US/10/151,690
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
; LENGTH: 5584
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: plasmid pDONR207
; US-10-151-690-61

Query Match 100.0%; Score 25; DB 14; Length 5584;
Best Local Similarity 100.0%; Pred. No. 0.59; 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
|||
Db 5458 GTTCAGCTTTTGTACAAAGTTGG 5482

RESULT 15
US-10-055-001A-23
; Sequence 23, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELIGA

```

```
Query Match      100.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.22; 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 9
US-10-162-879-15
; Sequence 15, Application US/10162879
; Publication No. US20030068799A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/162,879
; FILING DATE: 06-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,085
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-162-879-15

Query Match      100.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.22; 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 10
US-10-161-403-55
; Sequence 55, Application US/10161403
; Publication No. US2003019104A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Perkins, Edward
; APPLICANT: Perez, Carl
; APPLICANT: Lindenbaum, Michael
; APPLICANT: Greene, Amy
; APPLICANT: Leung, Josephine
; APPLICANT: Fleming, Elena
; APPLICANT: Stewart, Sandra
; APPLICANT: Shellard, Joan
; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
; FILE REFERENCE: 24601-420
; CURRENT APPLICATION NUMBER: US/10/161,403
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/294,758
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 60/366,891
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: attp1
US-10-161-403-55

Query Match      100.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.22; 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 11
US-09-732-914-6
; Sequence 6, Application US/09732914
; Patent No. US20020007051A1
; GENERAL INFORMATION:
; APPLICANT: Cheo, David
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Hartley, James L.
; APPLICANT: Byrd, Devon R.N.
; TITLE OF INVENTION: Use of Multiple Recombination Sites with Unique Specificity in
; Recombinational Cloning
; FILE REFERENCE: 0942.5010002
; CURRENT APPLICATION NUMBER: US/09/732,914
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/169,983
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 60/188,020
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 27
; TYPE: DNA
; ORGANISM: attp1
US-09-732-914-6

Query Match      100.0%; Score 25; DB 9; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.22; 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 12
US-10-151-690-30
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```
; CURRENT APPLICATION NUMBER: US/09/985,448
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-985-448-15

Query Match      100.0%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 6
US-10-300-892-15
; Sequence 15, Application US/10300892
; Publication No. US20030175970A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/10/300,892
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/907,719
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-10-300-892-15

Query Match      100.0%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 7
US-10-055-001A-10
; Sequence 10, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
```

```
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELLGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: core sequence of recombination site attp1
US-10-055-001A-10

Query Match      100.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 8
US-10-058-292-15
; Sequence 15, Application US/10058292
; Publication No. US20030054552A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; FILE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/058,292
; FILING DATE: 30-Jan-2002
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/432,085
; FILING DATE: 1999-11-02
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-058-292-15
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US-09-907-900-15
; Sequence 15, Application US/09907900
; Patent No. US20020172997A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,900
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-900-15
Query Match 100.0%; Score 25; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
DB 1 GTTCAGCTTTTGTACAAAGTTGG 25
RESULT 3
US-09-907-719-15
; Sequence 15, Application US/09907719
; Patent No. US20020192819A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,719
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-719-15
Query Match 100.0%; Score 25; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
DB 1 GTTCAGCTTTTGTACAAAGTTGG 25
```

```
; Sequence 15, Application US/09432085
; Publication No. US20030100110A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,085
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; US-09-432-085-15
Query Match 100.0%; Score 25; DB 11; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
DB 1 GTTCAGCTTTTGTACAAAGTTGG 25
RESULT 5
US-09-985-448-15
; Sequence 15, Application US/09985448
; Publication No. US20030157716A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
```



```

XX
SQ Sequence 27 BP; 6 A; 5 C; 6 G; 10 T; 0 other;
    Query Match 93.6%; Score 23.4; DB 25; Length 27;
    Best Local Similarity 96.0%; Pred. No. 1.2;
    Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAAGTTGG 25
   |||||
Db 1 GTTCAGCTTTTGTACAAAAGTTGG 25

Search completed: November 6, 2003, 22:26:29
Job time : 111.5 secs

```

CC The invention relates to a novel method for producing plant artificial
 CC chromosomes. The invention also relates to methods for targeting
 CC insertion of heterologous DNA into plant artificial chromosomes, methods
 CC for delivery of plant chromosomes to selected cells and tissues. The
 CC isolated plant artificial chromosome (PAC) is useful for producing a
 CC transgenic plant, which involves introducing the PAC into a plant cell.
 CC The PAC comprises a heterologous nucleic acid encoding a gene product
 CC such as enzymes, antisense RNA, tRNA, rDNA, structural proteins, marker
 CC proteins, ligands, receptors, ribozymes, therapeutic proteins, and
 CC biopharmaceutical proteins, vaccines, blood factors, antigens, hormones,
 CC cytokines, growth factors, antibodies, or a product that provides for
 CC resistance to diseases, insects, herbicides, or stress in a plant. The
 CC heterologous nucleic acid optionally encodes a product that provides an
 CC agronomically important trait in the plant, e.g. a product that alters
 CC nutrient use and/or improves the nutrient quality of the plant. The
 CC heterologous nucleic acid is contained within a bacterial artificial
 CC chromosome (BAC) or a yeast artificial chromosome (YAC). This
 CC polynucleotide sequence represents an oligo relating to the method for
 CC producing plant artificial chromosomes of the invention.

XX Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;

Query Match 93.6%; Score 23.4; DB 25; Length 25;
 Best Local Similarity 96.0%; Pred. No. 1.2;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTGG 25
 |||||
 Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 39
 AAS06183
 ID AAS06183 standard; DNA; 27 BP.

XX AAS06183;

DT 12-SEP-2001 (first entry)

DE Phage-lambda recombination site attP2.

KW Bacteriophage lambda; recombination; att site; PCR primer; lambda Int;
 KW lambda integrase; therapeutic; ss.

OS Bacteriophage lambda.

XX WO200142509-A1.

XX 14-JUN-2001.

XX 11-DEC-2000; 2000WO-US33546.

XX 10-DEC-1999; 99US-0169983.

XX 09-MAR-2000; 2000US-0188020.

XX (CHEO/) CHEO D.

XX (BRAS/) BRASCH M A.

XX (TEMP/) TEMPLE G F.

XX (HART/) HARTLEY J L.

XX (BYRD/) BYRD D R N.

XX Cheo D, Brasch MA, Temple GF, Hartley JL, Byrd DRN;

XX WPI; 2001-356174/37.

XX Producing hybrid nucleic acids, useful for expressing novel therapeutic
 PT polypeptides, by mixing the same or different nucleic acids having one
 PT or more recombination sites in the presence of recombination proteins,
 PT e.g. Cre -

XX Disclosure; Fig 24A; 357pp; English.

XX AAS06174-AAS06322 represent Bacteriophage lambda att recombination

CC site nucleic acid sequences, and PCR primers of the invention. The
 CC att sequences are recognised by the recombination protein lambda
 CC integrase (Int). The invention is a new method of producing a population
 CC of hybrid nucleic acids comprising mixing at least a first population of
 CC nucleic acids comprising one or more recombination sites with at least
 CC one target nucleic acid comprising one or more recombination sites and
 CC causing some or all of the nucleic acids to recombine with all or some of
 CC the target nucleic acids. The method is useful for producing a population
 CC of hybrid nucleic acids which may be the same or different. The nucleic
 CC acids may be used to express therapeutic proteins or peptides and they
 CC may also be used to create novel fusion proteins by expressing different
 CC sequences linked to each other. The method allows simultaneous cloning of
 CC two or more different nucleic acids.

XX Sequence 27 BP; 6 A; 5 C; 6 G; 10 T; 0 other;

Query Match 93.6%; Score 23.4; DB 22; Length 27;
 Best Local Similarity 96.0%; Pred. No. 1.2;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTGG 25
 |||||
 Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 40

ABZ58736

ID ABZ58736 standard; DNA; 27 BP.

XX AC ABZ58736;

XX 01-MAY-2003 (first entry)

DE Att site nucleotide sequence attP2.

KW Nucleic acid insertion; recombination; nucleic acid selection;

KW nucleic acid isolation; att; ds.

OS Synthetic.

XX WO200295055-A2.

XX 28-NOV-2002.

XX 21-MAY-2002; 2002WO-US15947.

XX 21-MAY-2001; 2001US-291973P.

XX (INVI-) INVITROGEN CORP.

XX Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN;

XX WPI; 2003-129436/12.

XX Inserting a population of nucleic acids into a second target molecule
 for selecting and isolating nucleic acid molecules by mixing the second
 population of nucleic acid with a second target nucleic acid -

XX Disclosure; Fig 13A; 273pp; English.

XX The invention relates to inserting a population of nucleic acids into a
 CC second target molecule. The method involves (a) mixing a first population
 CC of nucleic acid comprising one or more recombination sites with a target
 CC nucleic acid; (b) causing some or all of the nucleic acid molecules of
 CC the first population to recombine with the first target nucleic acid
 CC molecules to form a second population; (c) mixing the second population
 CC of nucleic acid with a second target nucleic acid; and (d) causing some
 CC or all of the nucleic acid molecules of the second population to
 CC recombine with some or all of the second target nucleic acid molecules to
 CC form a third population of nucleic acid. The method is useful for
 CC selecting and isolating nucleic acid molecules. Sequences ABZ58727-762
 CC represent att recombination site sequences used in the method of the
 CC invention.

PT interest -

PS Claim 43; Page 143; 272pp; English.

XX The present invention describes a eukaryotic chromosome (I) comprising one or several att sites, where an att site is heterologous to the chromosome, and permits site-directed integration in the presence of a lambda-integrase. Also described: (1) a platform artificial chromosome expression system (ACes) (II) comprising several sites that participate in recombinase catalysed recombination; and (2) a method (M1) for introducing a heterologous nucleic acid into a platform artificial chromosome. (I) can be used in gene therapy. (M1) is useful for introducing a heterologous nucleic acid molecule into a platform artificial chromosome, preferably an ACes. (II) is useful for producing a transgenic animal (e.g. a fish, insect, reptile, amphibian, arachnid, or mammal) by introducing (II) by cell fusion, lipid-mediated transfection by a carrier system, microinjection, microcell fusion, electroporation, microprojectile bombardment or direct DNA transfer into an embryonic cell, preferably a stem cell or an embryo. (II) comprises a heterologous nucleic acid that encodes a therapeutic product which is useful for making a library of ACes comprising random portions of a genome. ACC44612 to ACC44732 and ABP96650 to ABP96657 represent sequences used in the exemplification of the present invention.

XX SQ Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;

Query Match 93.6%; Score 23.4; DB 25; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.2;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
|||||
Db 1 GTTCAGCTTCTGTACAAAGTTGG 25

RESULT 37

ABT16630

ID ABT16630 standard; DNA; 25 BP.

XX AC ABT16630;

XX AC ABT16630;

XX DT 03-APR-2003 (first entry)

XX DE Artificial plant chromosome related oligo SEQ ID No 42.

XX Plant artificial chromosome; PAC; transgenic plant; vaccine;
KW blood factor; herbicide; stress; agronomical; nutrient quality;
KW bacterial artificial chromosome; BAC; yeast artificial chromosome; YAC;
KW ds.

XX OS Unidentified.

XX OS WO200296923-A1.

XX PN WO200296923-A1.

XX PD 05-DEC-2002.

XX PF 30-MAY-2002; 2002WO-US17451.

XX PF 30-MAY-2001; 2001US-294687P.

XX PR 04-JUN-2001; 2001US-296329P.

XX PA (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.

XX PA (AGRI-) AGRISOMA INC.

XX PI Perez C, Fabijanski SF, Perkins E;

XX DR WPI; 2003-140436/13.

XX PT Producing artificial chromosome by introducing a nucleic acid into plant cell, selecting artificial chromosome that has one or more repeat regions with equivalent amounts of euchromatic and heterochromatic nucleic acids -

PS Disclosure; Page 263; 269pp; English.

XX The invention relates to a novel method for producing plant artificial chromosomes. The invention also relates to methods for targeting insertion of heterologous DNA into plant artificial chromosomes, methods for delivery of plant chromosomes to selected cells and tissues. The isolated plant artificial chromosome (PAC) is useful for producing a transgenic plant, which involves introducing the PAC into a plant cell. The PAC comprises a heterologous nucleic acid encoding a gene product such as enzymes, antisense RNA, cRNA, rDNA, structural proteins, marker proteins, ligands, receptors, ribozymes, blood factors, antigens, hormones, biopharmaceutical proteins, vaccines, antibodies, or a product that provides for cytokines, growth factors, insects, herbicides, or stress in a plant. The heterologous nucleic acid optionally encodes a product that provides an agronomically important trait in the plant, e.g. a product that alters nutrient use and/or improves the nutrient quality of the plant. The heterologous nucleic acid is contained within a bacterial artificial chromosome (BAC) or a yeast artificial chromosome (YAC). This polynucleotide sequence represents an oligo relating to the method for producing plant artificial chromosomes of the invention.

XX SQ Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;

Query Match 93.6%; Score 23.4; DB 25; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.2;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
|||||
Db 1 GTTCAGCTTCTGTACAAAGTTGG 25

RESULT 38

ABT16635

ID ABT16635 standard; DNA; 25 BP.

XX AC ABT16635;

XX AC ABT16635;

XX DT 03-APR-2003 (first entry)

XX DE Artificial plant chromosome related oligo SEQ ID No 47.

XX Plant artificial chromosome; PAC; transgenic plant; vaccine;
KW blood factor; herbicide; stress; agronomical; nutrient quality;
KW bacterial artificial chromosome; BAC; yeast artificial chromosome; YAC;
KW ds.

XX OS Unidentified.

XX OS WO200296923-A1.

XX PN WO200296923-A1.

XX PD 05-DEC-2002.

XX PF 30-MAY-2002; 2002WO-US17451.

XX PF 30-MAY-2001; 2001US-294687P.

XX PR 04-JUN-2001; 2001US-296329P.

XX PA (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.

XX PA (AGRI-) AGRISOMA INC.

XX PI Perez C, Fabijanski SF, Perkins E;

XX DR WPI; 2003-140436/13.

XX PT Producing artificial chromosome by introducing a nucleic acid into plant cell, selecting artificial chromosome that has one or more repeat regions with equivalent amounts of euchromatic and heterochromatic nucleic acids -

XX PS Disclosure; Page 263; 269pp; English.

PT of replication, a selectable marker and a chimeric DNA construct,
 PT useful for silencing target nucleic acids and for producing large
 PT amounts of double-stranded RNA

XX
 XX
 PS Claim 12; Page 15; 104pp; English.

XX The present invention describes a vector (I) comprising operably linked
 CC DNA fragments having: (a) origin of replication allowing replication in a
 CC recipient cell, preferably in bacteria such as *Escherichia coli*;
 CC (b) selectable marker region capable of being expressed in the recipient
 CC cell; and (c) a chimeric DNA construct comprising: (i) promoter or
 CC promoter region capable of being recognized by RNA polymerases of a
 CC eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second,
 CC third and fourth recombination sites; (iii) 3' transcription terminating
 CC and polyadenylation region functional in the eukaryotic cell. The first
 CC and fourth recombination sites, or the second and third recombination
 CC sites are capable of reacting with a same recombination site, and
 CC preferably are identical. The first and second recombination sites, or
 CC the third and fourth recombination sites, do not recombine with each
 CC other or with a same recombination site. The vector is useful for
 CC producing large amounts of double-stranded RNA which can be used for
 CC silencing target nucleic acid sequences. The vectors can also be used to
 CC convert a DNA fragment into an inverted repeat structure. Plants
 CC transformed with a vector from the present invention can be used in a
 CC conventional breeding scheme to produce more plants with the same
 CC characteristics or to introduce a chimeric gene for reduction of the
 CC phenotypic expression of nucleic acids. The present sequence represents
 CC the core sequence of recombination site attB1 which is given in the
 CC exemplification of the present invention.

XX Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;

SQ Query Match 93.6%; Score 23.4; DB 24; Length 25;

Best Local Similarity 96.0%; Pred. No. 1.2;

Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25

Db 1 GTTCAGCTTCTGTACAAAGTTGG 25

RESULT 35

ACC44660

ID ACC44660 standard; DNA; 25 BP.

XX ACC44660;

XX 29-MAY-2003 (first entry)

XX Recombination site related oligonucleotide SEQ ID NO:51.

XX Chromosome-based platform; artificial chromosome; eukaryotic chromosome;

XX att site; integrase; recombinase; ACes; gene therapy; transgenic animal;

XX platform artificial chromosome expression system; PCR primer; ss.

XX Synthetic.

XX WO200297059-A2.

XX 05-DEC-2002.

XX 30-MAY-2002; 2002WO-US17452.

XX 30-MAY-2001; 2001US-294758P.

XX 21-MAR-2002; 2002US-366891P.

XX (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.

XX Perkins E, Perez C, Lindenbaum M, Greene A, Leung J, Fleming E;

XX Stewart S, Shellard J;

XX WPI; 2003-140461/13.

XX Novel eukaryotic chromosome comprising one or many att sites which

XX permits site-directed integration in the presence of lambda-integrase,

XX useful for site-specific recombination-directed integration of DNA of

PT Novel eukaryotic chromosome comprising one or many att sites which
 PT permits site-directed integration in the presence of lambda-integrase,
 PT useful for site-specific recombination-directed integration of DNA of
 PT interest

XX Claim 43; Page 143; 272pp; English.

XX The present invention describes a eukaryotic chromosome (I) comprising
 CC one or several att sites, where an att site is heterologous to the
 CC chromosome, and permits site-directed integration in the presence of
 CC lambda-integrase. Also described: (1) a platform artificial chromosome
 CC expression system (ACes) (II) comprising several sites that participate
 CC in recombinase catalysed recombination; and (2) a method (M1) for
 CC introducing a heterologous nucleic acid into a platform artificial
 CC chromosome. (I) can be used in gene therapy. (M1) is useful for
 CC introducing a heterologous nucleic acid molecule into a platform
 CC artificial chromosome, preferably an ACes. (II) is useful for producing a
 CC transgenic animal (e.g. a fish, insect, reptile, amphibian, arachnid, or
 CC mammal) by introducing (II) by cell fusion, lipid-mediated transfection
 CC by a carrier system, microinjection, microcell fusion, electroporation,
 CC microprojectile bombardment or direct DNA transfer into an embryonic
 CC cell, preferably a stem cell or an embryo. (II) comprises a heterologous
 CC nucleic acid that encodes a therapeutic product which is useful for
 CC making a library of ACes comprising random portions of a genome. ACC44612
 CC to ACC44732 and ABP96650 to ABP96657 represent sequences used in the
 CC exemplification of the present invention.

XX Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;

SQ Query Match 93.6%; Score 23.4; DB 25; Length 25;

Best Local Similarity 96.0%; Pred. No. 1.2;

Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25

Db 1 GTTCAGCTTCTGTACAAAGTTGG 25

RESULT 36

ACC44665

ID ACC44665 standard; DNA; 25 BP.

XX ACC44665;

XX 29-MAY-2003 (first entry)

XX Recombination site related oligonucleotide SEQ ID NO:56.

XX Chromosome-based platform; artificial chromosome; eukaryotic chromosome;

XX att site; integrase; recombinase; ACes; gene therapy; transgenic animal;

XX platform artificial chromosome expression system; PCR primer; ss.

XX Synthetic.

XX WO200297059-A2.

XX 05-DEC-2002.

XX 30-MAY-2002; 2002WO-US17452.

XX 30-MAY-2001; 2001US-294758P.

XX 21-MAR-2002; 2002US-366891P.

XX (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.

XX Perkins E, Perez C, Lindenbaum M, Greene A, Leung J, Fleming E;

XX Stewart S, Shellard J;

XX WPI; 2003-140461/13.

XX Novel eukaryotic chromosome comprising one or many att sites which

XX permits site-directed integration in the presence of lambda-integrase,

XX useful for site-specific recombination-directed integration of DNA of

PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
PI Vile RG, Harrington K, Murphy S, Bateman A;
XX WPI; 2001-656985/75.
XX
XX Recombinant nucleic acid vector for reducing tumour size, has expression
PT cassette comprises a promoter linked to nucleic acid sequence encoding
PT a syncytium-inducing polypeptide and flanked on either side by
PT recombination -
XX
XX Disclosure; Page 42; 84pp; English.
XX
XX The invention relates to a recombinant nucleic acid vector comprising a
CC first expression cassette, comprising a first promoter operably linked to
CC a nucleic acid sequence encoding a syncytium-inducing polypeptide (such
CC as a fusogenic membrane glycoprotein) and flanked on either side by a
CC sequence recognised by a recombinase, and/or a second expression cassette
CC comprising a tumour-specific promoter operably linked to a nucleic acid
CC sequence encoding a recombinase. The nucleic acid of the first expression
CC cassette may be linked to a hypoxic response element (HRE), the second
CC expression cassette may contain a promoter linked to a nucleic acid
CC encoding a cytokine, and a third cassette may contain a tumour specific
CC promoter linked to the nucleic acid encoding the recombinase. The tumour
CC specific promoter is, for example, a carcinoembryonic antigen (CEA)
CC promoter or a tyrosinase promoter and the recombinase is, for example,
CC Cre recombinase or FLP recombinase. The invention is useful for reducing
CC tumour size by administering the compositions as retroviral vectors, or
CC in a cell containing the vector, to an individual in need of treatment
CC for a disease caused by malignant cells. This sequence represents an int
CC recombinase site core region attR3, required for excisive recombination.
XX
XX Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;
SQ
Query Match 93.6%; Score 23.4; DB 23; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.2;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTTCTGTACAAAGTTGG 25
Db 1 GTTCAGCTTTTCTGTACAAAGTTGG 25
RESULT 33
ABQ82123
ID ABQ82123 standard; DNA; 25 BP.
XX
XX ABQ82123;
AC
XX
XX 11-DEC-2002 (first entry)
DT
DE Core sequence of recombination site attR3 SEQ ID NO:6.
DE
XX Chimeric nucleic acid construct; recombinational cloning; silencing;
XX recombination site; double stranded RNA; plant; ss.
XX
XX Synthetic.
XX
XX WO200259294-A1.
PN
XX
XX 01-AUG-2002.
PD
XX
XX 24-JAN-2002; 2002WO-AU00073.
PF
XX
XX 26-JAN-2001; 2001US-264067P.
PR
XX
XX 29-NOV-2001; 2001US-333743P.
PR
XX
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
PA
XX
XX Wesley S, Waterhouse P, Helliwell C;
PI
XX
XX WPI; 2002-682669/73.
DR
XX
XX New vectors comprising operably linked DNA fragments having an origin

PT New vectors comprising operably linked DNA fragments having an origin
PT of replication, a selectable marker and a chimeric DNA construct,
PT useful for silencing target nucleic acids and for producing large
PT amounts of double-stranded RNA -
XX
XX Disclosure; Page 15; 104pp; English.
XX
XX The present invention describes a vector (I) comprising operably linked
CC DNA fragments having: (a) origin of replication allowing replication in a
CC recipient cell, preferably in bacteria such as Escherichia coli;
CC (b) selectable marker region capable of being expressed in the recipient
CC cell; and (c) a chimeric DNA construct comprising: (i) promoter or
CC promoter region capable of being recognized by RNA polymerases of a
CC eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second,
CC third and fourth recombination sites; (iii) 3' transcription terminating
CC and polyadenylation region functional in the eukaryotic cell. The first
CC and fourth recombination sites, or the second and third recombination
CC sites are capable of reacting with a same recombination site, and
CC preferably are identical. The first and second recombination sites, or
CC the third and fourth recombination sites, do not recombine with each
CC other or with a same recombination site. The vector is useful for
CC producing large amounts of double-stranded RNA which can be used for
CC silencing target nucleic acid sequences. The vectors can also be used to
CC convert a DNA fragment into an inverted repeat structure. Plants
CC transformed with a vector from the present invention can be used in a
CC conventional breeding scheme to produce more plants with the same
CC characteristics or to introduce a chimeric gene for reduction of the
CC phenotypic expression of nucleic acids. The present sequence represents
CC the core sequence of recombination site attB1 which is given in the
CC exemplification of the present invention.
XX
XX Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;
SQ
Query Match 93.6%; Score 23.4; DB 24; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.2;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTTCTGTACAAAGTTGG 25
Db 1 GTTCAGCTTTTCTGTACAAAGTTGG 25
RESULT 34
ABQ82128
ID ABQ82128 standard; DNA; 25 BP.
XX
XX ABQ82128;
AC
XX
XX 11-DEC-2002 (first entry)
DT
DE Core sequence of recombination site attP2,P3 SEQ ID NO:11.
DE
XX Chimeric nucleic acid construct; recombinational cloning; silencing;
XX recombination site; double stranded RNA; plant; ss.
XX
XX Synthetic.
XX
XX WO200259294-A1.
PN
XX
XX 01-AUG-2002.
PD
XX
XX 24-JAN-2002; 2002WO-AU00073.
PF
XX
XX 26-JAN-2001; 2001US-264067P.
PR
XX
XX 29-NOV-2001; 2001US-333743P.
PR
XX
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
PA
XX
XX Wesley S, Waterhouse P, Helliwell C;
PI
XX
XX WPI; 2002-682669/73.
DR
XX
XX New vectors comprising operably linked DNA fragments having an origin

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PN US6143557-A.
XX 07-NOV-2000.
XX 20-JAN-1999; 99US-0233493.
XX 07-JUN-1996; 96US-0663002.
PR 12-JAN-1998; 98US-0005476.
PR 07-JUN-1995; 95US-0486139.
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX Brasch MA, Hartley JL;
XX WPI; 2001-049004/06.
XX Isolated nucleic acid molecules comprising a DNA segment having two
XX engineered recombination sites, derived from att or lox, which flank a
XX selectable marker and comprise a core region having an engineered
XX mutation -
XX Claim 1; Column 18; 73pp; English.
XX The present invention describes an isolated nucleic acid molecule (I)
XX comprising a first nucleic acid sequence having a defined sequence
XX (AAC87866 to AAC87881), sequences complementary to AAC87866 to AAC87881,
XX or an RNA sequence corresponding to AAC87866 to AAC87881. Also described
XX are: (1) an isolated nucleic acid molecule (II) comprising a first
XX recombination site that removes one or more stop codons from the
XX mutated recombination site; (2) an isolated nucleic acid molecule (III)
XX being an att or lox site; (3) an isolated nucleic acid molecule (IV)
XX comprising a first att recombination site comprising a mutation that
XX enhances recombination specificity; (4) cells comprising the above
XX mentioned nucleic acids or (IV). The nucleic acids are used in
XX engineering a core region of a given recombination site to provide
XX mutative sites suitable for subcloning reactions. The use of nucleic
XX acids for obtaining engineered recombination in vitro or in vivo makes
XX the methods for DNA or RNA subcloning, highly specific, rapid, and
XX less labour intensive.
XX Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;
XX SQ
Query Match 93.6%; Score 23.4; DB 22; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.2;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTCTACAAAGTTGG 25
Db 1 GTTCAGCTTTTCTACAAAGTTGG 25

RESULT 31
AAC87881
ID AAC87881 standard; DNA; 25 BP.
XX AC AAC87881;
XX 02-MAR-2001 (first entry)
XX Escherichia coli core region recombinant site attB2, F3 SEQ ID NO:16.
XX Core region; recombination site; cloning; chimeric DNA;
XX characteristic; mutation; att site; lox site; ss.
XX Escherichia coli.
XX OS US6143557-A.
XX PN 07-NOV-2000.
XX PD 20-JAN-1999; 99US-0233493.
XX PF 20-JAN-1999; 99US-0233493.
XX FR 20-JAN-1999; 99US-0233493.
XX XX

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PR 07-JUN-1996; 96US-0663002.
PR 12-JAN-1998; 98US-0005476.
PR 07-JUN-1995; 95US-0486139.
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX Brasch MA, Hartley JL;
XX WPI; 2001-049004/06.
XX Isolated nucleic acid molecules comprising a DNA segment having two
XX engineered recombination sites, derived from att or lox, which flank a
XX selectable marker and comprise a core region having an engineered
XX mutation -
XX Claim 1; Column 18; 73pp; English.
XX The present invention describes an isolated nucleic acid molecule (I)
XX comprising a first nucleic acid sequence having a defined sequence
XX (AAC87866 to AAC87881), sequences complementary to AAC87866 to AAC87881,
XX or an RNA sequence corresponding to AAC87866 to AAC87881. Also described
XX are: (1) an isolated nucleic acid molecule (II) comprising a first
XX recombination site that removes one or more stop codons from the
XX mutated recombination site; (2) an isolated nucleic acid molecule (III)
XX being an att or lox site; (3) an isolated nucleic acid molecule (IV)
XX comprising a first att recombination site comprising a mutation that
XX enhances recombination specificity; (4) cells comprising the above
XX mentioned nucleic acids or (IV). The nucleic acids are used in
XX engineering a core region of a given recombination site to provide
XX mutative sites suitable for subcloning reactions. The use of nucleic
XX acids for obtaining engineered recombination in vitro or in vivo makes
XX the methods for DNA or RNA subcloning, highly specific, rapid, and
XX less labour intensive.
XX Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;
XX SQ
Query Match 93.6%; Score 23.4; DB 22; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.2;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTCTACAAAGTTGG 25
Db 1 GTTCAGCTTTTCTACAAAGTTGG 25

RESULT 32
AAC87886
ID AAS14786 standard; DNA; 25 BP.
XX AC AAS14786;
XX 27-FEB-2002 (first entry)
XX Lambda phage Int recombinase site core region DNA sequence attR3.
XX Recombinant nucleic acid vector; carcinoembryonic antigen; CEA; cytokine;
XX syncytium-inducing polypeptide; fusogenic membrane glycoprotein; tumour;
XX recombinase; tumour-specific promoter; hypoxic response element; HRE; ss;
XX tyrosinase promoter; cre; FLP; retroviral vector; malignant cell; cancer;
XX cytosstatic; gene therapy; Int recombinase site core region; attR3;
XX exclusive recombination.
XX Bacteriophage lambda.
XX OS WO200174861-A2.
XX PN 11-OCT-2001.
XX PD 30-MAR-2001; 2001WO-US10250.
XX PF 31-MAR-2000; 2000US-193977P.
XX FR 31-MAR-2000; 2000US-193977P.
XX XX

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CC useful for recombination cloning.
XX
SQ Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;

Query Match          93.6%; Score 23.4; DB 22; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.2;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTGACAAAGTTGG 25
   |||||
Db 1 GTTCAGCTTCTGTACAAAGTTGG 25

RESULT 28
AAF55745
ID AAF55745 standard; DNA; 25 BP.
XX
AC AAF55745;
XX
XX 12-APR-2001 (first entry)
XX Recombination site attR3.
XX Recombination site; cloning; att; ss.
XX Unidentified.
XX
XX US6171861-B1.
XX 09-JAN-2001.
XX
XX 12-JAN-1998; 98US-0005476.
XX
XX 07-JUN-1996; 96US-0663002.
XX 07-JUN-1995; 95US-0486139.
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX Hartley JL, Brasch MA;
XX WPI; 2001-136877/14.
XX
XX In vitro cloning of nucleic acid involves mixing vectors comprising
XX recombination sites and/or nucleic acid, incubating mixture to produce
XX chimeric molecule, contacting hosts with mixture and selecting host -
XX
XX Claim 25; Column 46; 73pp; English.
XX
XX The present invention relates to a method for in vitro cloning of a
XX nucleic acid of interest. The method involves mixing in vitro two vectors
XX each comprising at least one recombination site and the nucleic acid of
XX interest; incubating the mixture in the presence of at least one
XX recombination protein to result in recombination of the recombination
XX sites, leading to production of a chimeric nucleic acid molecule
XX comprising the nucleic acid of interest; contacting hosts with the
XX mixture; and selecting for a host comprising the chimeric nucleic acid
XX molecule, and selecting against a host comprising the vectors comprising
XX the second vector, to clone the nucleic acid. The present sequence is a
XX recombination site, which may be used in the method of the present
XX invention.
XX
XX Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;

Query Match          93.6%; Score 23.4; DB 22; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.2;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTGACAAAGTTGG 25
   |||||
Db 1 GTTCAGCTTCTGTACAAAGTTGG 25

RESULT 30
AAC87876
ID AAC87876 standard; DNA; 25 BP.
XX
AC AAC87876;
XX
XX 02-MAR-2001 (first entry)
XX
XX Escherichia coli core region recombinant site attR3 SEQ ID NO:11.
XX Core region; recombination site; cloning; chimeric DNA;
XX characteristic; mutation; att site; lox site; ss.
XX
XX Escherichia coli.
XX

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DR WPI; 1999-303011/25.
 XX
 PT New nucleic acid cloning methods
 XX
 PS Disclosure; Page 163; 185pp; English.
 CC
 CC The invention relates to novel methods for cloning or subcloning one or
 CC more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or
 CC in vivo: (1) at least one insert donor molecules (IDMs) comprising one
 CC or more desired nucleic acid segments flanked by at least 2
 CC recombination sites which do not recombine with each other; (2) one or
 CC more vector donor molecules (VDMs) comprising at least 2 recombination
 CC sites which do not recombine with each other; and (3) one or more
 CC site-specific recombination proteins; (b) incubating the combination to
 CC transfer one or more of the desired segments into one or more of the
 CC VDMs, thereby producing one or more desired product molecules (PMs). The
 CC methods can be used for the efficient and specific recombination of NAM
 CC segments. They can be used to generate chimeric DNA or RNA molecules that
 CC have the desired characteristics and/or nucleic acid segments. The
 CC methods can also be used for changing vectors. The oligonucleotides
 CC AAX78935-X78994 are used in the method of the invention.
 XX
 SQ Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;
 Query Match 93.6%; Score 23.4; DB 20; Length 25;
 Best Local Similarity 96.0%; Pred. No. 1.2;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
 |||||
 DB 1 GTTCAGCTTTTGTACAAAGTTGG 25
 |||||
 RESULT 26
 AAD14439
 ID AAD14439 standard; DNA; 25 BP.
 AC AAD14439;
 XX
 DT 01-NOV-2001 (first entry)
 XX
 DE Recombination site attR3 DNA.
 XX
 KW Recombination site; copy number; replicon; recombinatorial cloning;
 KW attR3; ds.
 XX
 OS Unidentified.
 OS
 XX US6270969-B1.
 FN
 PD 07-AUG-2001.
 XX
 PF 20-JAN-1999; 99US-0233492.
 XX
 PR 07-JUN-1996; 96US-0663002.
 PR 07-JUN-1995; 95US-0486139.
 XX
 PA (INVI-) INVITROGEN CORP.
 XX
 PI Hartley JL, Brasch MA;
 XX
 DR WPI; 2001-488248/53.
 CC
 CC Methods for apposing nucleic acids comprising an expression signal and
 PT a gene/partial gene, using recombinatorial cloning by incubating the
 PT nucleic acids in the presence of a recombination protein under
 PT conditions for recombination -
 XX
 PS Claim 14; Column 18; 76pp; English.
 XX
 CC The invention relates to a method for apposing an expression signal and
 CC a gene or partial gene, using recombinatorial cloning. The method
 CC incubates nucleic acids comprising the expression signal and the gene/
 PT partial gene in the presence of a recombination protein under conditions
 PT sufficient to cause recombination and therefore appose the expression
 PT signal and the gene or partial gene. The methods are useful for apposing
 PT an expression signal and a gene or partial gene using recombinatorial
 CC cloning. The methods are also useful for changing vectors, constructing
 CC genes for fusion proteins, changing copy number, changing replicons,
 CC cloning into phages, and cloning e.g., PCR products (with an attB site
 CC at one end and a loxP site at the other end), genomic DNAs, and cDNAs.
 CC The methods are highly specific, rapid, and less labour intensive than
 CC prior art methods. The present sequence is a recombination site

CC partial gene in the presence of a recombination protein under conditions
 CC sufficient to cause recombination and therefore appose the expression
 CC signal and the gene or partial gene. The methods are useful for apposing
 CC an expression signal and a gene or partial gene using recombinatorial
 CC cloning. The methods are also useful for changing vectors, constructing
 CC genes for fusion proteins, changing copy number, changing replicons,
 CC cloning into phages, and cloning e.g., PCR products (with an attB site
 CC at one end and a loxP site at the other end), genomic DNAs, and cDNAs.
 CC The methods are highly specific, rapid, and less labour intensive than
 CC prior art methods. The present sequence is a recombination site
 XX
 SQ Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;
 Query Match 93.6%; Score 23.4; DB 22; Length 25;
 Best Local Similarity 96.0%; Pred. No. 1.2;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
 |||||
 DB 1 GTTCAGCTTTTGTACAAAGTTGG 25
 |||||
 RESULT 27
 AAD14444
 ID AAD14444 standard; DNA; 25 BP.
 AC AAD14444;
 XX
 DT 01-NOV-2001 (first entry)
 XX
 DE Recombination site attP2,P3 DNA.
 XX
 KW Recombination site; copy number; replicon; recombinatorial cloning;
 KW attP2,P3; ds.
 XX
 OS Unidentified.
 OS
 XX US6270969-B1.
 FN
 PD 07-AUG-2001.
 XX
 PF 20-JAN-1999; 99US-0233492.
 XX
 PR 07-JUN-1996; 96US-0663002.
 PR 07-JUN-1995; 95US-0486139.
 XX
 PA (INVI-) INVITROGEN CORP.
 XX
 PI Hartley JL, Brasch MA;
 XX
 DR WPI; 2001-488248/53.
 CC
 CC Methods for apposing nucleic acids comprising an expression signal and
 PT a gene/partial gene, using recombinatorial cloning by incubating the
 PT nucleic acids in the presence of a recombination protein under
 PT conditions for recombination -
 XX
 PS Claim 14; Column 18; 76pp; English.
 XX
 CC The invention relates to a method for apposing an expression signal and
 CC a gene or partial gene, using recombinatorial cloning. The method
 CC incubates nucleic acids comprising the expression signal and the gene/
 PT partial gene in the presence of a recombination protein under conditions
 PT sufficient to cause recombination and therefore appose the expression
 PT signal and the gene or partial gene. The methods are useful for apposing
 PT an expression signal and a gene or partial gene using recombinatorial
 CC cloning. The methods are also useful for changing vectors, constructing
 CC genes for fusion proteins, changing copy number, changing replicons,
 CC cloning into phages, and cloning e.g., PCR products (with an attB site
 CC at one end and a loxP site at the other end), genomic DNAs, and cDNAs.
 CC The methods are highly specific, rapid, and less labour intensive than
 CC prior art methods. The present sequence is a recombination site

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RESULT 23
AAx78977
ID AAX78977 standard; DNA; 25 BP.
XX
XX
AC AAX78977;
XX
XX 17-AUG-1999 (first entry)
XX
XX Oligonucleotide #43 for recombination and cloning method.
DE
XX
XX Cloning; donor; recombination site; vector; chimeric; ss.
XX
XX Synthetic.
XX
XX WO9921977-A1.
XX
XX 06-MAY-1999.
XX
XX 26-OCT-1998; 98WO-US22589.
XX
XX 23-OCT-1998; 98US-0177387.
XX
XX 24-OCT-1997; 97US-0065930.
XX
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX
XX Brasch MA, Fox DK, Hartley JL, Temple GF;
XX
XX WPI; 1999-303011/25.
XX
XX New nucleic acid cloning methods
XX
XX Disclosure; Page 171; 185pp; English.
XX
XX The invention relates to novel methods for cloning or subcloning one or
XX more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or
XX in vivo: (1) at least one insert donor molecules (IDMs) comprising one
XX or more desired nucleic acid segments flanked by at least 2
XX recombination sites which do not recombine with each other; (2) one or
XX more vector donor molecules (VDMs) comprising at least 2 recombination
XX sites which do not recombine with each other; and (3) one or more
XX site-specific recombination proteins; (b) incubating the combination to
XX transfer one or more of the desired segments into one or more of the
XX VDMs, thereby producing one or more desired product molecules (PMs). The
XX methods can be used for the efficient and specific recombination of NAM
XX segments. They can be used to generate chimeric DNA or RNA molecules that
XX have the desired characteristics and/or nucleic acid segments. The
XX methods can also be used for changing vectors. The oligonucleotides
XX AAX78935-X78994 are used in the method of the invention.
XX
XX SQ Sequence 25 BP; 4 A; 3 C; 5 G; 10 T; 3 other;
XX
XX Query Match 95.2%; Score 23.8; DB 20; Length 25;
XX Best Local Similarity 88.0%; Pred. No. 0.81;
XX Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GTTCAGCTTTTGTCTACAAAGTTGG 25
XX |||||
XX Db 1 GTTCAGCTTTTGTCTACAAAGTTGG 25
XX
XX RESULT 24
AAT48225
ID AAT48225 standard; DNA; 25 BP.
XX
XX AAT48225;
XX
XX 20-OCT-1997 (first entry)
XX
XX attp2,P3 core region.
XX
XX att recombination site; core region; mutation; enhance; recombination;
XX vector; subcloning; regulation; exchange; ss.
XX

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OS Synthetic.
XX
XX WO9640724-A1.
XX
XX 19-DEC-1996.
XX
XX 07-JUN-1996; 96WO-US10082.
XX
XX 07-JUN-1995; 95US-0486139.
XX
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX
XX Brasch MA, Hartley JL;
XX
XX WPI; 1997-065168/06.
XX
XX Nucleic acids, vectors and methods to obtain chimeric nucleic acid -
XX using recombinant proteins and engineered recombination sites in
XX vitro or in vivo
XX
XX Claim 14; Page 56; 106pp; English.
XX
XX AAT48210-25 are att recombination site core region DNA sequences. The
XX core region has at least one engineered mutation that enhances
XX recombination in vitro in the formation of a Co-integrate or Product DNA.
XX These core regions can be incorporated into novel vector donor DNA
XX molecules. The nucleic acids, vectors and methods of the invention are
XX used to obtain chimeric nucleic acid using recombination proteins and
XX engineered recombination sites in vitro or in vivo. The improved
XX specificity, speed and yields of the invention facilitates DNA or RNA
XX subcloning, regulation or exchange useful for any related purpose, e.g.
XX in vitro recombination of DNA segments, and in vitro or in vivo insertion
XX or modification of transcribed, replicated, isolated or genomic DNA or
XX RNA.
XX
XX SQ Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;
XX
XX Query Match 93.6%; Score 23.4; DB 18; Length 25;
XX Best Local Similarity 96.0%; Pred. No. 1.2;
XX Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 GTTCAGCTTTTGTCTACAAAGTTGG 25
XX |||||
XX Db 1 GTTCAGCTTTTGTCTACAAAGTTGG 25
XX
XX RESULT 25
AAX78950
ID AAX78950 standard; DNA; 25 BP.
XX
XX AAX78950;
XX
XX 17-AUG-1999 (first entry)
XX
XX Oligonucleotide #16 for recombination and cloning method.
XX
XX Cloning; donor; recombination site; vector; chimeric; ss.
XX
XX Synthetic.
XX
XX WO9921977-A1.
XX
XX 06-MAY-1999.
XX
XX 26-OCT-1998; 98WO-US22589.
XX
XX 23-OCT-1998; 98US-0177387.
XX
XX 24-OCT-1997; 97US-0065930.
XX
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX
XX Brasch MA, Fox DK, Hartley JL, Temple GF;
XX
XX

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Db 5458 GTTCAGCTTTTGTACAAAGTTGG 5482
|||||

RESULT 21
ABQ82130
ID ABQ82130 standard; DNA; 18691 BP.

XX AC ABQ82130;

XX DT 11-DEC-2002 (first entry)

XX DE Acceptor vector PHELLSGATE nucleotide sequence SEQ ID NO:13.

XX KW Chimeric nucleic acid construct; recombinational cloning; silencing;
XX KM recombination site; double stranded RNA; plant; ds.

XX OS Synthetic.

XX PN WO200259294-A1.

XX PD 01-AUG-2002.

XX PF 24-JAN-2002; 2002WO-AU00073.

XX PR 26-JAN-2001; 2001US-264067P.

XX PR 29-NOV-2001; 2001US-333743P.

XX PA (CSIR) COMMONWEALTH SCI & IND RES ORG.

XX PI Wesley S, Waterhouse P, Helliwell C;

XX DR WPI; 2002-682669/73.

XX PT New vectors comprising operably linked DNA fragments having an origin
XX PT of replication, a selectable marker and a chimeric DNA construct,
XX PT useful for silencing target nucleic acids and for producing large
XX PT amounts of double-stranded RNA -

XX PS Claim 13; Page 62-72; 104pp; English.

XX CC The present invention describes a vector (I) comprising operably linked
XX CC DNA fragments having: (a) origin of replication allowing replication in a
XX CC recipient cell, preferably in bacteria such as Escherichia coli;
XX CC (b) selectable marker region capable of being expressed in the recipient
XX CC cell; and (c) a chimeric DNA construct comprising: (i) promoter or
XX CC promoter region capable of being recognized by RNA polymerases of a
XX CC eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second,
XX CC third and fourth recombination sites; (iii) 3' transcription terminating
XX CC and polyadenylation region functional in the eukaryotic cell. The first
XX CC sites are capable of reacting with a same recombination site, and
XX CC the third and fourth recombination sites, do not recombine with each
XX CC other or with a same recombination site. The vector is useful for
XX CC producing large amounts of double-stranded RNA which can be used to
XX CC silence target nucleic acid sequences. The vectors can also be used to
XX CC convert a DNA fragment into an inverted repeat structure. Plants
XX CC transformed with a vector from the present invention can be used in a
XX CC conventional breeding scheme to produce more plants with the same
XX CC characteristics or to introduce a chimeric gene for reduction of the
XX CC phenotypic expression of nucleic acids. The present sequence represents
XX CC an acceptor vector nucleotide sequence from the present invention.

XX SQ Sequence 18691 BP; 4837 A; 4621 C; 4607 G; 4626 T; 0 other;

Query Match 100.0%; Score 25; DB 24; Length 18691;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTTCAGCTTTTGTACAAAGTTGG 25

Db 17792 GTTCAGCTTTTGTACAAAGTTGG 17816
|||||

RESULT 22
ABQ82130/c

ID ABQ82130 standard; DNA; 18691 BP.

XX AC ABQ82130;

XX DT 11-DEC-2002 (first entry)

XX DE Acceptor vector PHELLSGATE nucleotide sequence SEQ ID NO:13.

XX KW Chimeric nucleic acid construct; recombinational cloning; silencing;
XX KM recombination site; double stranded RNA; plant; ds.

XX OS Synthetic.

XX PN WO200259294-A1.

XX PD 01-AUG-2002.

XX PF 24-JAN-2002; 2002WO-AU00073.

XX PR 26-JAN-2001; 2001US-264067P.

XX PR 29-NOV-2001; 2001US-333743P.

XX PA (CSIR) COMMONWEALTH SCI & IND RES ORG.

XX PI Wesley S, Waterhouse P, Helliwell C;

XX DR WPI; 2002-682669/73.

XX PT New vectors comprising operably linked DNA fragments having an origin
XX PT of replication, a selectable marker and a chimeric DNA construct,
XX PT useful for silencing target nucleic acids and for producing large
XX PT amounts of double-stranded RNA -

XX PS Claim 13; Page 62-72; 104pp; English.

XX CC The present invention describes a vector (I) comprising operably linked
XX CC DNA fragments having: (a) origin of replication allowing replication in a
XX CC recipient cell, preferably in bacteria such as Escherichia coli;
XX CC (b) selectable marker region capable of being expressed in the recipient
XX CC cell; and (c) a chimeric DNA construct comprising: (i) promoter or
XX CC promoter region capable of being recognized by RNA polymerases of a
XX CC eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second,
XX CC third and fourth recombination sites; (iii) 3' transcription terminating
XX CC and polyadenylation region functional in the eukaryotic cell. The first
XX CC sites are capable of reacting with a same recombination site, and
XX CC the third and fourth recombination sites, do not recombine with each
XX CC other or with a same recombination site. The vector is useful for
XX CC producing large amounts of double-stranded RNA which can be used to
XX CC silence target nucleic acid sequences. The vectors can also be used to
XX CC convert a DNA fragment into an inverted repeat structure. Plants
XX CC transformed with a vector from the present invention can be used in a
XX CC conventional breeding scheme to produce more plants with the same
XX CC characteristics or to introduce a chimeric gene for reduction of the
XX CC phenotypic expression of nucleic acids. The present sequence represents
XX CC an acceptor vector nucleotide sequence from the present invention.

XX SQ Sequence 18691 BP; 4837 A; 4621 C; 4607 G; 4626 T; 0 other;

Query Match 100.0%; Score 25; DB 24; Length 18691;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTTCAGCTTTTGTACAAAGTTGG 25

Db 13146 GTTCAGCTTTTGTACAAAGTTGG 13122
|||||

CC desired proteins, operably linking nucleic acid molecules of interest to
CC regulatory genetic sequences, constructing genes for fusion proteins,
CC changing copy number, changing replicons, cloning into phages and
CC cloning (I), (II), (III), host cells and vectors can be used in the
CC production of polypeptides and antibodies. The present sequence is
CC used in the exemplification of the present invention.
XX

SQ Sequence 5156 BP; 1413 A; 1183 C; 1216 G; 1342 T; 2 other;

Query Match 100.0%; Score 25; DB 21; Length 5156;
Best Local Similarity 100.0%; Pred. No. 0.38; Mismatches 0; Indels 0; Gaps 0;
Matches 25; Conservative 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
|||
Db 212 GTTCAGCTTTTGTACAAAGTTGG 236
|||

RESULT 19

AAC55632
ID AAC55632 standard; DNA; 5584 BP.

AC AAC55632;

DT 11-JAN-2001 (first entry)

DE Donor plasmid pDONR207 nucleotide sequence.

KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
KW mutant; recombinational cloning; entry vector; destination vector;
KW gene product targeting; fusion tag cleavage; ds.

OS Bacteriophage lambda.

OS Synthetic.

PN WO200052027-A1.

PD 08-SEP-2000.

PF 02-MAR-2000; 2000WO-US05432.

PR 02-MAR-1999; 99US-0122389.

PR 23-MAR-1999; 99US-0126049.

PR 28-MAY-1999; 99US-0136744.

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Hartley JL, Brasch MA, Temple GF, Cheo D;

DR WPI; 2000-543948/49.

PT Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,

PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the

PT recombinational cloning of polypeptides -

XX Disclosure; Fig 97; 459pp; English.

XX The present invention describes isolated nucleic acid molecules (I)
CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
CC molecule (II) comprising one or more att recombination sites comprising
CC at least one mutation in its core region that increases the specificity
CC of interaction between the recombination site and a second att
CC recombination site; and (2) an isolated nucleic acid molecule (III)
CC comprising one or more mutated att recombination sites comprising at
CC least one mutation in its core region that enhances the efficiency of
CC recombination between a first nucleic acid molecule comprising the
CC mutated att recombination site and a second nucleic acid molecule
CC comprising a second recombination site that interacts with the mutated
CC att recombination site. (I), (II), (III), primers, vectors and methods
CC from the present invention are used for the recombinational cloning of
CC nucleic acid molecules. They can be used for changing vectors, targeting
CC gene products to intracellular locations, cleaving fusion tags from

CC desired proteins, operably linking nucleic acid molecules of interest to
CC regulatory genetic sequences, constructing genes for fusion proteins,
CC changing copy number, changing replicons, cloning into phages and
CC cloning (I), (II), (III), host cells and vectors can be used in the
CC production of polypeptides and antibodies. The present sequence is
CC used in the exemplification of the present invention.
XX

SQ Sequence 5584 BP; 1521 A; 1294 C; 1341 G; 1428 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 5584;
Best Local Similarity 100.0%; Pred. No. 0.39; Mismatches 0; Indels 0; Gaps 0;
Matches 25; Conservative 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
|||
Db 5458 GTTCAGCTTTTGTACAAAGTTGG 5482
|||

RESULT 20

ABZ58766

ID ABZ58766 standard; DNA; 5584 BP.

AC ABZ58766;

DT 01-MAY-2003 (first entry)

DE Donor plasmid pDONR207 nucleotide sequence.

KW Nucleic acid insertion; recombination; nucleic acid selection;
KW nucleic acid isolation; ds.

OS Synthetic.

PN WO200295055-A2.

PD 28-NOV-2002.

PF 21-MAY-2002; 2002WO-US15947.

PR 21-MAY-2001; 2001US-291973P.

XX (INVI-) INVITROGEN CORP.

XX Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN;

XX WPI; 2003-129436/12.

XX Inserting a population of nucleic acids into a second target molecule
PT for selecting and isolating nucleic acid molecules by mixing the second
PT population of nucleic acid with a second target nucleic acid -

PS Disclosure; Fig 18B-C; 273pp; English.

XX The invention relates to inserting a population of nucleic acids into a
CC second target molecule. The method involves (a) mixing a first population
CC of nucleic acid comprising one or more recombination sites with a target
CC nucleic acid; (b) causing some or all of the nucleic acid molecules of
CC the first population to recombine with the first target nucleic acid
CC molecules to form a second population; (c) mixing the second population
CC of nucleic acid with a second target nucleic acid; and (d) causing some
CC or all of the nucleic acid molecules of the second population to
CC recombine with some or all of the second target nucleic acid molecules to
CC form a third population of nucleic acid. The method is useful for
CC selecting and isolating nucleic acid molecules. The present sequence
CC represents the donor plasmid pDONR207 nucleotide sequence.

SQ Sequence 5584 BP; 1521 A; 1294 C; 1341 G; 1428 T; 0 other;

Query Match 100.0%; Score 25; DB 25; Length 5584;
Best Local Similarity 100.0%; Pred. No. 0.39; Mismatches 0; Indels 0; Gaps 0;
Matches 25; Conservative 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25

CC of nucleic acid with a second target nucleic acid; and (d) causing some
CC or all of the nucleic acid molecules of the second population to
CC recombine with some or all of the second target nucleic acid molecules to
CC form a third population of nucleic acid. The method is useful for
CC selecting and isolating nucleic acid molecules. The present sequence
CC represents the destination plasmid pDONR201 nucleotide sequence.

XX
SQ Sequence 4470 BP; 1193 A; 1037 C; 977 G; 1263 T; 0 other;
Query Match 100.0%; Score 25; DB 25; Length 4470;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
Db 127 GTTCAGCTTTTGTACAAAGTTGG 103

RESULT 17
AAC5525/c
ID AAC5525 standard; DNA; 4939 BP.
XX
AC AAC5525;
XX
DT 11-JAN-2001 (first entry)
XX
DE Donor plasmid pDONR205 nucleotide sequence.
XX
KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
KW mutant; recombinational cloning; entry vector; destination vector;
KW gene product targeting; fusion tag cleavage; ds.
XX
OS Bacteriophage lambda.
OS Synthetic.
XX
PN WC200052027-A1.
XX
PD 08-SEP-2000.
XX
PF 02-MAR-2000; 2000WO-US05432.
XX
PR 02-MAR-1999; 99US-0122389.
PR 23-MAR-1999; 99US-0126049.
PR 28-MAY-1999; 99US-0136744.
XX
PA (LIFE-) LIFE TECHNOLOGIES INC.
XX
PI Hartley JL, Brasch MA, Temple GF, Cheo D;
XX
DR WPI; 2000-543948/49.
XX
PT Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
PT recombinational cloning of polypeptides -
XX
PS Example 10; Fig 53; 459pp; English.

XX
CC The present invention describes isolated nucleic acid molecules (I)
CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
CC molecule (II) comprising one or more att recombination sites comprising
CC at least one mutation in its core region that increases the specificity
CC of interaction between the recombination site and a second att
CC recombination site; and (2) an isolated nucleic acid molecule (III)
CC comprising one or more mutated att recombination sites comprising at
CC least one mutation in its core region that enhances the efficiency of
CC recombination between a first nucleic acid molecule comprising the
CC mutated att recombination site and a second nucleic acid molecule
CC comprising a second recombination site that interacts with the mutated
CC att recombination site. (I), (II), (III), primers, vectors and methods
CC from the present invention are used for the recombinational cloning of
CC nucleic acid molecules. They can be used for changing vectors, targeting
CC gene products to intracellular locations, cleaving fusion tags from

CC desired proteins, operably linking nucleic acid molecules of interest to
CC regulatory genetic sequences, constructing genes for fusion proteins,
CC changing copy number, changing replicons, cloning into phages and
CC cloning. (I), (II), (III), host cells and vectors can be used in the
CC production of polypeptides and antibodies. The present sequence is
CC used in the exemplification of the present invention.

XX
SQ Sequence 4939 BP; 1193 A; 1285 C; 1152 G; 1309 T; 0 other;
Query Match 100.0%; Score 25; DB 21; Length 4939;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
Db 3661 GTTCAGCTTTTGTACAAAGTTGG 3637

RESULT 18
AAC5526
ID AAC5526 standard; DNA; 5156 BP.
XX
AC AAC5526;
XX
DT 11-JAN-2001 (first entry)
XX
DE Donor plasmid pDONR206 nucleotide sequence.
XX
KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
KW mutant; recombinational cloning; entry vector; destination vector;
KW gene product targeting; fusion tag cleavage; ds.
XX
OS Bacteriophage lambda.
OS Synthetic.
XX
PN WC200052027-A1.
XX
PD 08-SEP-2000.
XX
PF 02-MAR-2000; 2000WO-US05432.
XX
PR 02-MAR-1999; 99US-0122389.
PR 23-MAR-1999; 99US-0126049.
PR 28-MAY-1999; 99US-0136744.
XX
PA (LIFE-) LIFE TECHNOLOGIES INC.
XX
PI Hartley JL, Brasch MA, Temple GF, Cheo D;
XX
DR WPI; 2000-543948/49.
XX
PT Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
PT recombinational cloning of polypeptides -
XX
PS Example 9; Fig 54; 459pp; English.

XX
CC The present invention describes isolated nucleic acid molecules (I)
CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
CC molecule (II) comprising one or more att recombination sites comprising
CC at least one mutation in its core region that increases the specificity
CC of interaction between the recombination site and a second att
CC recombination site; and (2) an isolated nucleic acid molecule (III)
CC comprising one or more mutated att recombination sites comprising at
CC least one mutation in its core region that enhances the efficiency of
CC recombination between a first nucleic acid molecule comprising the
CC mutated att recombination site and a second nucleic acid molecule
CC comprising a second recombination site that interacts with the mutated
CC att recombination site. (I), (II), (III), primers, vectors and methods
CC from the present invention are used for the recombinational cloning of
CC nucleic acid molecules. They can be used for changing vectors, targeting
CC gene products to intracellular locations, cleaving fusion tags from

CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity
 CC of interaction between the recombination site and a second att
 CC recombination site; and (2) an isolated nucleic acid molecule (III)
 CC comprising one or more mutated att recombination sites comprising at
 CC least one mutation in its core region that enhances the efficiency of
 CC recombination between a first nucleic acid molecule comprising the
 CC mutated att recombination site and a second nucleic acid molecule
 CC comprising a second recombination site that interacts with the mutated
 CC att recombination site. (I), (II), (III), primers, vectors and methods
 CC from the present invention are used for the recombinational cloning of
 CC nucleic acid molecules. They can be used for changing vectors, targeting
 CC gene products to intracellular locations, cleaving fusion tags from
 CC desired proteins, operably linking nucleic acid molecules of interest to
 CC regulatory genetic sequences, constructing genes for fusion proteins,
 CC changing copy number, changing replicons, cloning into phages and
 CC cloning. (I), (II), (III), host cells and vectors can be used in the
 CC production of polypeptides and antibodies. The present sequence is
 CC used in the exemplification of the present invention.

XX
 SQ Sequence 4208 BP; 1172 A; 997 C; 875 G; 1164 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 4208;
 Best Local Similarity 100.0%; Pred. No. 0.38;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
 |||||
 Db 3283 GTTCAGCTTTTGTACAAAGTTGG 3259

RESULT 15
 AAC5521/c
 ID AAC5521 standard; DNA; 4470 BP.

AC AAC5521;
 XX
 DT 11-JAN-2001 (first entry)
 XX
 DE Donor plasmid pDONR201 nucleotide sequence.

XX Bacteriophage lambda: att; recombination site; attB; attP; attL;
 KW mutant; recombinational cloning; entry vector; destination vector;
 KW Gene product targeting; fusion tag cleavage; ds.

XX Bacteriophage lambda.
 OS Synthetic.

XX WO200052027-A1.

PD 08-SEP-2000.

XX 02-MAR-2000; 2000WO-US05432.

PR 02-MAR-1999; 99US-0122389.

PR 23-MAR-1999; 99US-0126049.

PR 28-MAY-1999; 99US-0136744.

XX (LIFE-) LIFE TECHNOLOGIES INC.
 XX
 XX Hartley JL, Brasch MA, Temple GF, Cheo D;
 XX WPI; 2000-543948/49.

XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 PT recombinational cloning of polypeptides -
 XX Example 9; Fig 49; 459pp; English.

XX The present invention describes isolated nucleic acid molecules (I)
 CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2

CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity
 CC of interaction between the recombination site and a second att
 CC recombination site; and (2) an isolated nucleic acid molecule (III)
 CC comprising one or more mutated att recombination sites comprising at
 CC least one mutation in its core region that enhances the efficiency of
 CC recombination between a first nucleic acid molecule comprising the
 CC mutated att recombination site and a second nucleic acid molecule
 CC comprising a second recombination site that interacts with the mutated
 CC att recombination site. (I), (II), (III), primers, vectors and methods
 CC from the present invention are used for the recombinational cloning of
 CC nucleic acid molecules. They can be used for changing vectors, targeting
 CC gene products to intracellular locations, cleaving fusion tags from
 CC desired proteins, operably linking nucleic acid molecules of interest to
 CC regulatory genetic sequences, constructing genes for fusion proteins,
 CC changing copy number, changing replicons, cloning into phages and
 CC cloning. (I), (II), (III), host cells and vectors can be used in the
 CC production of polypeptides and antibodies. The present sequence is
 CC used in the exemplification of the present invention.

XX
 SQ Sequence 4470 BP; 1193 A; 1037 C; 977 G; 1263 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 4470;
 Best Local Similarity 100.0%; Pred. No. 0.38;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
 |||||
 Db 127 GTTCAGCTTTTGTACAAAGTTGG 103

RESULT 16
 ABZ58767/c

ID ABZ58767 standard; DNA; 4470 BP.

AC ABZ58767;

XX
 DT 01-MAY-2003 (first entry)

XX Destination plasmid pDONR201 nucleotide sequence.

XX Nucleic acid insertion; recombination; nucleic acid selection;
 KW nucleic acid isolation; ds.

XX Synthetic.

XX WO200295055-A2.

PD 28-NOV-2002.

XX 21-MAY-2002; 2002WO-US15947.

PR 21-MAY-2001; 2001US-291973P.

XX (INVI-) INVITROGEN CORP.

PI Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN;
 XX WPI; 2003-129436/12.

XX Inserting a population of nucleic acids into a second target molecule
 PT for selecting and isolating nucleic acid molecules by mixing the second
 PT population of nucleic acid with a second target nucleic acid -
 XX Disclosure; Fig 26B-C; 273pp; English.

XX The invention relates to inserting a population of nucleic acids into a
 CC second target molecule. The method involves (a) mixing a first population
 CC of nucleic acid comprising one or more recombination sites with a target
 CC nucleic acid; (b) causing some or all of the nucleic acid molecules of
 CC the first population to recombine with the first target nucleic acid
 CC molecules to form a second population; (c) mixing the second population

CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity
 CC of interaction between the recombination site and a second att
 CC recombination site; and (2) an isolated nucleic acid molecule (III)
 CC comprising one or more mutated att recombination sites comprising at
 CC least one mutation in its core region that enhances the efficiency of
 CC recombination between a first nucleic acid molecule comprising the
 CC mutated att recombination site and a second nucleic acid molecule
 CC comprising a second recombination site that interacts with the mutated
 CC att recombination site. (I), (II), (III), primers, vectors and methods
 CC from the present invention are used for the recombinational cloning of
 CC nucleic acid molecules. They can be used for changing vectors, targeting
 CC gene products to intracellular locations, cleaving fusion tags from
 CC desired proteins, operably linking nucleic acid molecules of interest to
 CC regulatory genetic sequences, constructing genes for fusion proteins,
 CC changing copy number, changing replicons, cloning into phages and
 CC cloning. (I), (II), (III), host cells and vectors can be used in the
 CC production of polypeptides and antibodies. The present sequence is
 CC used in the exemplification of the present invention.

XX
 SQ Sequence 4165 BP; 1117 A; 926 C; 925 G; 1196 T; 1 other;

Query Match 100.0%; Score 25; DB 21; Length 4165;
 Best Local Similarity 100.0%; Pred. No. 0.38; 0; Indels 0; Gaps 0;
 Matches 25; Conservative 0; Mismatches 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
 |||||
 Db 212 GTTCAGCTTTTGTACAAAGTTGG 236

RESULT 13

AAC55522
 ID AAC55522 standard; DNA; 4204 BP.

AC AAC55522;

XX 11-JAN-2001 (first entry)

XX Donor plasmid pDONR202 nucleotide sequence.

XX Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
 KW mutant; recombinational cloning; entry vector; destination vector;
 KW gene product targeting; fusion tag cleavage; ds.

XX Bacteriophage lambda.

OS Synthetic.

XX WO200052027-A1.

XX 08-SEP-2000.

XX 02-MAR-2000; 2000WO-US05432.

XX 02-MAR-1999; 99US-0122389.

PR 23-MAR-1999; 99US-0126049.

PR 28-MAY-1999; 99US-0136744.

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Hartley JL, Brasch MA, Temple GF, Cheo D;

XX WPI; 2000-543948/49.

XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 PT recombinational cloning of polypeptides -

XX Example 9; Fig 50; 459pp; English.

XX The present invention describes isolated nucleic acid molecules (I)
 CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2

CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity
 CC of interaction between the recombination site and a second att
 CC recombination site; and (2) an isolated nucleic acid molecule (III)
 CC comprising one or more mutated att recombination sites comprising at
 CC least one mutation in its core region that enhances the efficiency of
 CC recombination between a first nucleic acid molecule comprising the
 CC mutated att recombination site and a second nucleic acid molecule
 CC comprising a second recombination site that interacts with the mutated
 CC att recombination site. (I), (II), (III), primers, vectors and methods
 CC from the present invention are used for the recombinational cloning of
 CC nucleic acid molecules. They can be used for changing vectors, targeting
 CC gene products to intracellular locations, cleaving fusion tags from
 CC desired proteins, operably linking nucleic acid molecules of interest to
 CC regulatory genetic sequences, constructing genes for fusion proteins,
 CC changing copy number, changing replicons, cloning into phages and
 CC cloning. (I), (II), (III), host cells and vectors can be used in the
 CC production of polypeptides and antibodies. The present sequence is
 CC used in the exemplification of the present invention.

XX
 SQ Sequence 4204 BP; 1198 A; 912 C; 959 G; 1135 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 4204;
 Best Local Similarity 100.0%; Pred. No. 0.38; 0; Indels 0; Gaps 0;
 Matches 25; Conservative 0; Mismatches 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
 |||||
 Db 260 GTTCAGCTTTTGTACAAAGTTGG 284

RESULT 14

AAC55523/c

ID AAC55523 standard; DNA; 4208 BP.

AC AAC55523;

XX 11-JAN-2001 (first entry)

XX Donor plasmid pDONR203 nucleotide sequence.

XX Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
 KW mutant; recombinational cloning; entry vector; destination vector;
 KW gene product targeting; fusion tag cleavage; ds.

XX Bacteriophage lambda.

OS Synthetic.

XX WO200052027-A1.

XX 08-SEP-2000.

XX 02-MAR-2000; 2000WO-US05432.

XX 02-MAR-1999; 99US-0122389.

PR 23-MAR-1999; 99US-0126049.

PR 28-MAY-1999; 99US-0136744.

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Hartley JL, Brasch MA, Temple GF, Cheo D;

XX WPI; 2000-543948/49.

XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 PT recombinational cloning of polypeptides -

XX Example 9; Fig 51; 459pp; English.

XX The present invention describes isolated nucleic acid molecules (I)
 CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2

DR WPI; 2003-129436/12.
 XX
 PT Inserting a population of nucleic acids into a second target molecule
 PT for selecting and isolating nucleic acid molecules by mixing the second
 PT population of nucleic acid with a second target nucleic acid -
 XX
 PS Disclosure; Fig 13A; 273pp; English.
 XX
 CC The invention relates to inserting a population of nucleic acids into a
 CC second target molecule. The method involves (a) mixing a first population
 CC of nucleic acid comprising one or more recombination sites with a target
 CC nucleic acid; (b) causing some or all of the nucleic acid molecules of
 CC the first population to recombine with the first target nucleic acid
 CC molecules to form a second population; (c) mixing the second population
 CC of nucleic acid with a second target nucleic acid; and (d) causing some
 CC or all of the nucleic acid molecules of the second population to
 CC recombine with some or all of the second target nucleic acid molecules to
 CC form a third population of nucleic acid. The method is useful for
 CC selecting and isolating nucleic acid molecules. Sequences AB258727-762
 CC represent att recombination site sequences used in the method of the
 CC invention.
 XX
 SQ Sequence 27 BP; 6 A; 4 C; 6 G; 11 T; 0 other;
 Query Match 100.0%; Score 25; DB 25; Length 27;
 Best Local Similarity 100.0%; Pred. No. 0.25;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
 DB 1 GTTCAGCTTTTGTACAAAGTTGG 25
 RESULT 11
 AAC55382
 ID AAC55382 standard; DNA; 233 BP.
 XX
 AC AAC55382;
 XX
 DT 11-JAN-2001 (first entry)
 XX
 DE Recombination site nucleotide sequence attP1.
 XX
 KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
 KW mutant; recombinational cloning; entry vector; destination vector;
 KW gene product targeting; fusion tag cleavage; ds.
 XX
 OS Bacteriophage lambda.
 XX
 PN WO200052027-A1.
 XX
 PD 08-SEP-2000.
 XX
 PF 02-MAR-2000; 2000WO-US05432.
 XX
 PR 02-MAR-1999; 99US-0122389.
 PR 23-MAR-1999; 99US-0126049.
 PR 28-MAY-1999; 99US-0136744.
 XX
 PA (LIFE-) LIFE TECHNOLOGIES INC.
 XX
 PI Hartley JL, Brasch WA, Temple GF, Cheo D;
 XX
 DR WPI; 2000-543948/49.
 XX
 PT Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 PT recombinational cloning of polypeptides -
 XX
 PS Claim 1; Fig 9; 459pp; English.
 XX
 CC The present invention describes isolated nucleic acid molecules (I)
 CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2

CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity
 CC of interaction between the recombination site and a second att
 CC recombination site; and (2) an isolated nucleic acid molecule (III)
 CC comprising one or more mutated att recombination sites comprising at
 CC least one mutation in its core region that enhances the efficiency of
 CC recombination between a first nucleic acid molecule comprising the
 CC mutated att recombination site and a second nucleic acid molecule
 CC comprising a second recombination site that interacts with the mutated
 CC att recombination site. (I), (II), (III), primers, vectors and methods
 CC from the present invention are used for the recombinational cloning of
 CC nucleic acid molecules. They can be used for changing fusion tags, targeting
 CC gene products to intracellular locations, cleaving fusion tags from
 CC desired proteins, operably linking nucleic acid molecules of interest to
 CC regulatory genetic sequences, constructing genes for fusion proteins,
 CC changing copy number, changing replicons, cloning into phages and
 CC cloning. (i), (ii), (iii), host cells and vectors can be used in the
 CC production of polypeptides and antibodies. The present sequence is
 CC used in the exemplification of the present invention.
 XX
 SQ Sequence 233 BP; 73 A; 32 C; 34 G; 94 T; 0 other;
 Query Match 100.0%; Score 25; DB 21; Length 233;
 Best Local Similarity 100.0%; Pred. No. 0.3;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
 DB 134 GTTCAGCTTTTGTACAAAGTTGG 158
 RESULT 12
 AAC55524
 ID AAC55524 standard; DNA; 4165 BP.
 XX
 AC AAC55524;
 XX
 DT 11-JAN-2001 (first entry)
 XX
 DE Donor plasmid pDONR204 nucleotide sequence.
 XX
 KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
 KW mutant; recombinational cloning; entry vector; destination vector;
 KW gene product targeting; fusion tag cleavage; ds.
 XX
 OS Bacteriophage lambda.
 OS Synthetic.
 XX
 PN WO200052027-A1.
 XX
 PD 08-SEP-2000.
 XX
 PF 02-MAR-2000; 2000WO-US05432.
 XX
 PR 02-MAR-1999; 99US-0122389.
 PR 23-MAR-1999; 99US-0126049.
 PR 28-MAY-1999; 99US-0136744.
 XX
 PA (LIFE-) LIFE TECHNOLOGIES INC.
 XX
 PI Hartley JL, Brasch WA, Temple GF, Cheo D;
 XX
 DR WPI; 2000-543948/49.
 XX
 PT Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 PT recombinational cloning of polypeptides -
 XX
 PS Example 9; Fig 52; 459pp; English.
 XX
 CC The present invention describes isolated nucleic acid molecules (I)
 CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2

PD 05-DEC-2002.
 XX 30-MAY-2002; 2002WO-US17451.
 XX 30-MAY-2001; 2001US-294687P.
 PR 04-JUN-2001; 2001US-296329P.
 XX (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
 PA (AGRI-) AGRISOMA INC.
 XX Perez C, Rabijsanski SF, Perkins E;
 XX WPI; 2003-140436/13.
 XX
 PT Producing artificial chromosome by introducing a nucleic acid into
 PT plant cell, selecting artificial chromosome that has one or more repeat
 PT regions with equivalent amounts of euchromatic and heterochromatic
 PT nucleic acids -
 XX
 PS Disclosure; Page 263; 269pp; English.
 XX
 CC The invention relates to a novel method for producing plant artificial
 CC chromosomes. The invention also relates to methods for targeting
 CC insertion of heterologous DNA into plant artificial chromosomes, methods
 CC for delivery of plant chromosomes to selected cells and tissues. The
 CC isolated plant artificial chromosome (PAC) is useful for producing a
 CC transgenic plant, which involves introducing the PAC into a plant cell.
 CC The PAC comprises a heterologous nucleic acid encoding a gene product
 CC such as enzymes, antisense RNA, rDNA, structural proteins, marker
 CC proteins, ligands, receptors, ribozymes, therapeutic proteins, and
 CC biopharmaceutical proteins, vaccines, blood factors, antigens, hormones,
 CC cytokines, growth factors, antibodies, or a product that provides for
 CC resistance to diseases, insects, herbicides, or stress in a plant. The
 CC heterologous nucleic acid optionally encodes a product that provides an
 CC agronomically important trait in the plant, e.g. a product that alters
 CC nutrient use and/or improves the nutrient quality of the plant. The
 CC heterologous nucleic acid is contained within a bacterial artificial
 CC chromosome (BAC) or a yeast artificial chromosome (YAC). This
 CC polynucleotide sequence represents an oligo relating to the method for
 CC producing plant artificial chromosomes of the invention.
 XX
 SQ Sequence 25 BP; 5 A; 3 C; 6 G; 11 T; 0 other;
 Query Match 100.0%; Score 25; DB 25; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.25;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
 DB 1 GTTCAGCTTTTGTACAAAGTTGG 25
 RESULT 9
 AAS06179
 ID AAS06179 standard; DNA; 27 BP.
 AC AAS06179;
 XX 12-SEP-2001 (first entry)
 DT Phase-lambda recombination site attP1.
 DE Bacteriophage lambda; recombination; att site; PCR primer; lambda Int;
 KW lambda integrase; therapeutic; ss.
 XX Bacteriophage lambda.
 OS WO200142509-A1.
 PN 14-JUN-2001.
 XX 11-DEC-2000; 2000WO-US33546.
 PF
 XX

PR 10-DEC-1999; 99US-0169983.
 PR 09-MAR-2000; 2000US-0188020.
 XX (CHEO/) CHEO D.
 PA (BRAS/) BRASCH M A.
 PA (TEME/) TEMPLE G F.
 PA (HART/) HARTLEY J L.
 PA (BYRD/) BYRD D R N.
 XX
 PI Cheo D, Brasch MA, Temple GP, Hartley JL, Byrd DRN;
 XX WPI; 2001-356174/37.
 DR
 XX
 PT Producing hybrid nucleic acids, useful for expressing novel therapeutic
 PT polypeptides, by mixing the same or different nucleic acids having one
 PT or more recombination sites in the presence of recombination proteins,
 PT e.g. Cre -
 XX
 PS Disclosure; Fig 24A; 357pp; English.
 XX
 CC AAS06174-AAS06322 represent Bacteriophage lambda att recombination
 CC site nucleic acid sequences, and PCR primers of the invention. The
 CC att sequences are recognised by the recombination protein lambda
 CC integrase (Int). The invention is a new method of producing a population
 CC of hybrid nucleic acids comprising mixing at least a first population of
 CC nucleic acids comprising one or more recombination sites with at least
 CC one target nucleic acid comprising one or more recombination sites and
 CC causing some or all of the nucleic acids to recombine with all or some of
 CC the target nucleic acids. The method is useful for producing a population
 CC of hybrid nucleic acids which may be the same or different. The nucleic
 CC acids may be used to express therapeutic proteins or peptides and they
 CC may also be used to create novel fusion proteins by expressing different
 CC sequences linked to each other. The method allows simultaneous cloning of
 CC two or more different nucleic acids.
 XX
 SQ Sequence 27 BP; 6 A; 4 C; 6 G; 11 T; 0 other;
 Query Match 100.0%; Score 25; DB 22; Length 27;
 Best Local Similarity 100.0%; Pred. No. 0.25;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
 DB 1 GTTCAGCTTTTGTACAAAGTTGG 25
 RESULT 10
 ABZ58732
 ID ABZ58732 standard; DNA; 27 BP.
 XX
 AC ABZ58732;
 XX 01-MAY-2003 (first entry)
 DT Att site nucleotide sequence attP1.
 DE Nucleic acid insertion; recombination; nucleic acid selection;
 XX nucleic acid isolation; att; ds.
 KW Synthetic.
 OS WO200295055-A2.
 PN 28-NOV-2002.
 XX 21-MAY-2002; 2002WO-US15947.
 XX 21-MAY-2001; 2001US-291973P.
 PR (INVI-) INVITROGEN CORP.
 PA Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN;
 XX

PN WO200259294-A1.
XX
PD
XX
XX
PF 01-AUG-2002.
XX
XX
XX 24-JAN-2002; 2002WO-AU00073.
XX
XX 26-JAN-2001; 2001US-264067P.
FR 29-NOV-2001; 2001US-333743P.
XX
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
PA
XX Wesley S, Waterhouse P, Helliwell C;
PI
XX WPI; 2002-682669/73.
DR
XX
XX New vectors comprising operably linked DNA fragments having an origin
PT of replication, a selectable marker and a chimeric DNA construct,
PT useful for silencing target nucleic acids and for producing large
PT amounts of double-stranded RNA -
XX
XX
PS Claim 12; Page 15; 104pp; English.
XX
XX The present invention describes a vector (I) comprising operably linked
CC DNA fragments having: (a) origin of replication allowing replication in a
CC recipient cell, preferably in bacteria such as *Escherichia coli*;
CC (b) selectable marker region capable of being expressed in the recipient
CC cell; and (c) a chimeric DNA construct comprising: (i) promoter or
CC promoter region capable of being recognized by RNA polymerase of a
CC eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second,
CC third and fourth recombination sites; (iii) 3' transcription terminating
CC and polyadenylation region functional in the eukaryotic cell. The first
CC and fourth recombination sites, or the second and third recombination
CC sites are capable of reacting with a same recombination site, and
CC preferably are identical. The first and second recombination sites, or
CC the third and fourth recombination sites, do not recombine with each
CC other or with a same recombination site. The vector is useful for
CC producing large amounts of double-stranded RNA which can be used for
CC silencing target nucleic acid sequences. The vectors can also be used to
CC convert a DNA fragment into an inverted repeat structure. Plants
CC transformed with a vector from the present invention can be used in a
CC conventional breeding scheme to produce more plants with the same
CC characteristics or to introduce a chimeric gene for reduction of the
CC phenotypic expression of nucleic acids. The present sequence represents
CC the core sequence of recombination site attB1 which is given in the
CC exemplification of the present invention.
XX
SQ Sequence 25 BP; 5 A; 3 C; 6 G; 11 T; 0 other;
Query Match 100.0%; Score 25; DB 24; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.25; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25
RESULT 7
ACCA4664
ID ACCA4664 standard; DNA; 25 BP.
AC
AC ACCA4664;
XX
DT 29-MAY-2003 (first entry)
XX
DE Recombination site related oligonucleotide SEQ ID NO:55.
XX
KW Chromosome-based platform; artificial chromosome; eukaryotic chromosome;
KW att site; integrase; recombinase; ACes; gene therapy; transgenic animal;
KW Platform artificial chromosome expression system; PCR primer; ss.
XX
OS Synthetic.
XX

PN WO200297059-A2.
XX
PD
XX
XX 05-DEC-2002.
PF
XX 30-MAY-2002; 2002WO-US17452.
XX
XX 30-MAY-2001; 2001US-294758P.
PR 21-MAR-2002; 2002US-366891P.
XX
XX (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
PA
XX Perkins E, Perez C, Lindenbaum M, Greene A, Leung J, Fleming E;
PI Stewart S, Shellard J;
PI
XX WPI; 2003-140461/13.
DR
XX
XX Novel eukaryotic chromosome comprising one or many att sites which
PT permits site-directed integration in the presence of lambda-integrase,
PT useful for site-specific recombination-directed integration of DNA of
PT interest -
XX
XX
PS Claim 43; Page 143; 272pp; English.
XX
XX The present invention describes a eukaryotic chromosome (I) comprising
CC one or several att sites, where an att site is heterologous to the
CC chromosome, and permits site-directed integration in the presence of
CC lambda-integrase. Also described: (1) a platform artificial chromosome
CC expression system (ACes) (II) comprising several sites that participate
CC in recombinase catalysed recombination; and (2) a method (M1) for
CC introducing a heterologous nucleic acid into a platform artificial
CC chromosome. (I) can be used in gene therapy. (M1) is useful for
CC introducing a heterologous nucleic acid molecule into a platform
CC artificial chromosome, preferably an ACes. (II) is useful for producing a
CC transgenic animal (e.g. a fish, insect, reptile, amphibian, arachnid, or
CC mammal) by introducing (II) by cell fusion, lipid-mediated transfection
CC by a carrier system, microinjection, microcell fusion, electroporation,
CC microprojectile bombardment or direct DNA transfer into an embryonic
CC cell, preferably a stem cell or an embryo. (II) comprises a heterologous
CC nucleic acid that encodes a therapeutic product which is useful for
CC making a library of ACes comprising random portions of a genome. ACC44612
CC to ACC44732 and ABP96650 to ABP96657 represent sequences used in the
CC exemplification of the present invention.
XX
SQ Sequence 25 BP; 5 A; 3 C; 6 G; 11 T; 0 other;
Query Match 100.0%; Score 25; DB 25; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.25; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25
RESULT 8
ABT16634
ID ABT16634 standard; DNA; 25 BP.
XX
AC ABT16634;
XX
DT 03-APR-2003 (first entry)
XX
DE Artificial plant chromosome related oligo SEQ ID No 46.
XX
KW Plant artificial chromosome; PAC; transgenic plant; vaccine;
KW blood factor; herbicide; stress; agronomical; nutrient quality;
KW bacterial artificial chromosome; BAC; yeast artificial chromosome; YAC;
KW ds.
XX
OS Unidentified.
XX
PN WO200296923-A1.
XX

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 4
AAF55749
ID AAF55749 standard; DNA; 25 BP.

XX AC AAF55749;

DT 12-APR-2001 (first entry)

XX DE Recombination site attP1.

XX KW Recombination site; cloning; att; ss.

XX OS Unidentified.

XX PN US6171861-B1.

PD 09-JAN-2001.

XX PF 12-JAN-1998; 98US-0005476.

XX PR 07-JUN-1996; 96US-0663002.

XX PR 07-JUN-1995; 95US-0486139.

XX PA (LIFE-) LIFE TECHNOLOGIES INC.

XX PI Hartley JL, Brasch MA;

XX DR WPI; 2001-136877/14.

PT In vitro cloning of nucleic acid involves mixing vectors comprising recombination sites and/or nucleic acid, incubating mixture to produce chimeric molecule, contacting hosts with mixture and selecting host -

XX PS Claim 25; Column 46; 73pp; English.

XX CC The present invention relates to a method for in vitro cloning of a nucleic acid of interest. The method involves mixing in vitro two vectors each comprising at least one recombination site and the nucleic acid of interest; incubating the mixture in the presence of at least one recombination protein to result in recombination of the recombination sites, leading to production of a chimeric nucleic acid molecule comprising the nucleic acid of interest; contacting hosts with the mixture; and selecting for a host comprising the chimeric nucleic acid molecule, and selecting against a host comprising the vectors comprising the second vector, to clone the nucleic acid. The present sequence is a recombination site, which may be used in the method of the present invention.

XX SQ Sequence 25 BP; 5 A; 3 C; 6 G; 11 T; 0 other;

Query Match 100.0%; Score 25; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 5

XX ID AAC87880 standard; DNA; 25 BP.

XX AC AAC87880;

XX DT 02-MAR-2001 (first entry)

XX DE Escherichia coli core region recombinant site attP1 SEQ ID NO:15.

XX KW Core region; recombination site; cloning; chimeric DNA; characteristic; mutation; att site; lox site; ss.

XX OS Escherichia coli.

XX PN US6143557-A.

XX PD 07-NOV-2000.

XX PF 20-JAN-1999; 99US-0233493.

XX PR 07-JUN-1996; 96US-0663002.

XX PR 12-JAN-1998; 98US-0005476.

XX PR 07-JUN-1995; 95US-0486139.

XX PA (LIFE-) LIFE TECHNOLOGIES INC.

XX PI Brasch MA, Hartley JL;

XX DR WPI; 2001-049004/06.

XX PT Isolated nucleic acid molecules comprising a DNA segment having two engineered recombination sites, derived from att or lox, which flank a selectable marker and comprise a core region having an engineered mutation -

XX PS Claim 1; Column 18; 73pp; English.

XX CC The present invention describes an isolated nucleic acid molecule (I) comprising a first nucleic acid sequence having a defined sequence (AAC87866 to AAC87881), sequences complementary to AAC87866 to AAC87881, or an RNA sequence corresponding to AAC87866 to AAC87881. Also described are: (1) an isolated nucleic acid molecule (II) comprising a first mutated recombination site that removes one or more stop codons from the recombination site or avoids hairpin formation, the recombination site being an att or lox site; (2) an isolated nucleic acid molecule (III) comprising a first att recombination site comprising a mutation that enhances recombination specificity; (3) vectors (IV) comprising the above mentioned nucleic acids; and (4) cells comprising the above mentioned nucleic acids or (IV). The nucleic acids are used in engineering a core region of a given recombination site to provide mutative sites suitable for subcloning reactions. The use of nucleic acids for obtaining engineered recombination in vitro or in vivo makes the methods for DNA or RNA subcloning, highly specific, rapid, and less labour intensive.

XX SQ Sequence 25 BP; 5 A; 3 C; 6 G; 11 T; 0 other;

Query Match 100.0%; Score 25; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25

Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 6

XX ABQ82127

XX ID ABQ82127 standard; DNA; 25 BP.

XX AC ABQ82127;

XX DT 11-DEC-2002 (first entry)

XX DE Core sequence of recombination site attP1 SEQ ID NO:10.

XX KW Chimeric nucleic acid construct; recombinational cloning; silencing; recombination site; double stranded RNA; plant; ss.

XX OS Synthetic.

PT vitro or in vivo
 PS Claim 14; Page 56; 106pp; English.
 XX
 CC AAT48210-25 are att recombination site core region DNA sequences. The
 CC core region has at least one engineered mutation that enhances
 CC recombination in vitro in the formation of a Cointegrate or Product DNA.
 CC These core regions can be incorporated into novel vector donor DNA
 CC molecules. The nucleic acids, vectors and methods of the invention are
 CC used to obtain chimeric nucleic acid using recombination proteins and
 CC engineered recombination sites in vitro or in vivo. The improved
 CC specificity, speed and yields of the invention facilitates DNA or RNA
 CC subcloning, regulation or exchange useful for any related purpose, e.g.
 CC in vitro recombination of DNA segments, and in vitro or in vivo insertion
 CC or modification of transcribed, replicated, isolated or genomic DNA or
 CC RNA.
 XX
 SQ Sequence 25 BP; 5 A; 3 C; 6 G; 11 T; 0 other;
 Query Match 100.0%; Score 25; DB 18; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.25;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
 DB 1 GTTCAGCTTTTGTACAAAGTTGG 25
 RESULT 2
 AAX78949
 ID AAX78949 standard; DNA; 25 BP.
 XX
 AC AAX78949;
 DT 17-AUG-1999 (first entry)
 XX
 DE Oligonucleotide #15 for recombination and cloning method.
 XX
 KW Cloning; donor; recombination site; vector; chimeric; ss.
 XX
 OS Synthetic.
 XX
 PN WO921977-A1.
 XX
 PD 06-MAY-1999.
 XX
 PF 26-OCT-1998; 98WO-US22589.
 XX
 PR 23-OCT-1998; 98US-0177387.
 PR 24-OCT-1997; 97US-0065930.
 XX
 PA (LIFE-) LIFE TECHNOLOGIES INC.
 XX
 PI Brasch MA, Fox DK, Hartley JL, Temple GP;
 XX
 DR WPI; 1999-303011/25.
 XX
 PT New nucleic acid cloning methods
 PS Disclosure; Page 162; 185pp; English.
 XX
 CC The invention relates to novel methods for cloning or subcloning one or
 CC more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or
 CC in vivo: (1) at least one insert donor molecules (IDMs) comprising one
 CC or more desired nucleic acid segments flanked by at least 2
 CC recombination sites which do not recombine with each other; (2) one or
 CC more vector donor molecules (VDMs) comprising at least 2 recombination
 CC sites which do not recombine with each other; and (3) one or more
 CC site-specific recombination proteins; (b) incubating the combination to
 CC transfer one or more of the desired segments into one or more of the
 CC VDMs, thereby producing one or more desired product molecules (PMs). The
 CC methods can be used for the efficient and specific recombination of NAM
 CC segments. They can be used to generate chimeric DNA or RNA molecules that

CC have the desired characteristics and/or nucleic acid segments. The
 CC methods can also be used for changing vectors. The oligonucleotides
 CC AAX78935-X78994 are used in the method of the invention.
 XX
 SQ Sequence 25 BP; 5 A; 3 C; 6 G; 11 T; 0 other;
 Query Match 100.0%; Score 25; DB 20; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.25;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
 DB 1 GTTCAGCTTTTGTACAAAGTTGG 25
 RESULT 3
 AAD14443
 ID AAD14443 standard; DNA; 25 BP.
 XX
 AC AAD14443;
 DT 01-NOV-2001 (first entry)
 XX
 DE Recombination site attP1 DNA.
 XX
 KW Recombination site; copy number; replicon; recombinatorial cloning;
 XX attP1; ds.
 XX
 OS Unidentified.
 XX
 PN US6270969-B1.
 XX
 PD 07-AUG-2001.
 XX
 PF 20-JAN-1999; 99US-0233492.
 XX
 PR 07-JUN-1996; 96US-0663002.
 PR 07-JUN-1995; 95US-0486139.
 XX
 PA (INVI-) INVITROGEN CORP.
 XX
 PI Hartley JL, Brasch MA;
 XX
 DR WPI; 2001-488248/53.
 XX
 PT Methods for apposing nucleic acids comprising an expression signal and
 PT a gene/partial gene, using recombinatorial cloning by incubating the
 PT nucleic acids in the presence of a recombination protein under
 PT conditions for recombination -
 PS Claim 14; Column 18; 76pp; English.
 XX
 CC The invention relates to a method for apposing an expression signal and
 CC a gene or partial gene, using recombinatorial cloning. The method
 CC incubates nucleic acids comprising the expression signal and the gene/
 CC partial gene in the presence of a recombination protein under conditions
 CC sufficient to cause recombination and therefore appose the expression
 CC signal and the gene or partial gene. The methods are useful for apposing
 CC an expression signal and a gene or partial gene using recombinatorial
 CC cloning. The methods are also useful for changing vectors, constructing
 CC genes for fusion proteins, changing copy number, changing replicons,
 CC cloning into phages, and cloning e.g., PCR products (with an attB site
 CC at one end and a loxP site at the other end), genomic DNAs, and cDNAs.
 CC The methods are highly specific, rapid, and less labour intensive than
 CC prior art methods. The present sequence is a recombination site
 CC useful for recombination cloning.
 XX
 SQ Sequence 25 BP; 5 A; 3 C; 6 G; 11 T; 0 other;
 Query Match 100.0%; Score 25; DB 22; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.25;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OM nucleic - nucleic search, using sw model

Run on: November 6, 2003, 21:05:38 ; Search time 111.5 Seconds

(without alignments)

605.255 Million cell updates/sec

Title: US-10-055-001A-10

Perfect score: 25

Sequence: 1 gttcagctttttgtacaagtgtg 25

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	25	18 AAT48224	attP1 core region.
2	25	100.0	25	20 AAX78949	Oligonucleotide #1
3	25	100.0	25	22 AAD14443	Recombination site
4	25	100.0	25	22 AAF55749	Recombination site
5	25	100.0	25	22 AAC87880	Escherichia coli c
6	25	100.0	25	24 ABQ82127	Core sequence of r
7	25	100.0	25	25 ACC44664	Recombination site
8	25	100.0	25	25 ABT16634	Artificial plant c

9	25	100.0	27	22 AAS06179	Phage-lambda recom
10	25	100.0	27	25 ABZ58732	Att site nucleotid
11	25	100.0	233	21 AAC55382	Recombination site
12	25	100.0	4165	21 AAC55824	Donor plasmid pDON
13	25	100.0	4204	21 AAC55822	Donor plasmid pDON
14	25	100.0	4208	21 AAC55523	Donor plasmid pDON
15	25	100.0	4470	21 AAC55521	Donor plasmid pDON
16	25	100.0	4470	21 AAC55521	Destination plasm
17	25	100.0	4939	21 AAC55525	Donor plasmid pDON
18	25	100.0	5156	21 AAC55526	Donor plasmid pDON
19	25	100.0	5584	21 AAC55532	Donor plasmid pDON
20	25	100.0	5584	25 ABZ58766	Donor plasmid pDON
21	25	100.0	18691	24 ABQ82130	Acceptor vector pA
22	25	100.0	18691	24 ABQ82130	Oligonucleotide #4
23	23.8	95.2	25	20 AAX78977	attP2, P3 core regi
24	23.4	93.6	25	18 AAT48225	Oligonucleotide #1
25	23.4	93.6	25	20 AAX78950	Recombination site
26	23.4	93.6	25	22 AAD14439	Recombination site
27	23.4	93.6	25	22 AAD14444	Recombination site
28	23.4	93.6	25	22 AAF55745	Recombination site
29	23.4	93.6	25	22 AAF55750	Recombination site
30	23.4	93.6	25	22 AAC87876	Escherichia coli c
31	23.4	93.6	25	22 AAC87981	Escherichia coli c
32	23.4	93.6	25	23 AAS14786	Lambda phage int r
33	23.4	93.6	25	24 ABQ82123	Core sequence of r
34	23.4	93.6	25	24 ABQ82128	Core sequence of r
35	23.4	93.6	25	25 ACC44660	Recombination site
36	23.4	93.6	25	25 ACC44665	Recombination site
37	23.4	93.6	25	25 ABT16630	Artificial plant c
38	23.4	93.6	25	25 ABT16635	Artificial plant c
39	23.4	93.6	27	22 AAS06183	Phage-lambda recom
40	23.4	93.6	27	25 ABZ58736	Att site nucleotid
41	23.4	93.6	233	21 AAC55383	Recombination site
42	23.4	93.6	4165	21 AAC55524	Donor plasmid pDON
43	23.4	93.6	4204	21 AAC55522	Donor plasmid pDON
44	23.4	93.6	4208	21 AAC55523	Donor plasmid pDON
45	23.4	93.6	4428	25 ABZ58768	Destination plasm

ALIGNMENTS

RESULT 1
AAT48224
ID AAT48224 standard; DNA; 25 BP.

XX AC AAT48224;

XX DT 20-OCT-1997 (first entry)

XX DE attP1 core region.

XX DE att recombination site; core region; mutation; enhance; recombination;

XX KW vector; subcloning; regulation; exchange; ss.

XX OS Synthetic.

XX FN WO9640724-A1.

XX PD 19-DEC-1996.

XX PF 07-JUN-1996; 96WO-US10082.

XX PR 07-JUN-1995; 95US-0486139.

XX PA (LIFE-) LIFE TECHNOLOGIES INC.

XX PI Brasch MA, Hartley JL;

XX DR WPI; 1997-065168/06.

XX PT Nucleic acids, vectors and methods to obtain chimeric nucleic acid -
PT using recombinant proteins and engineered recombination sites in

PD 15-JAN-2002
PF 26-OCT-1998 JP 2000518069
PR 24-OCT-1997 US 60/065930, 23-OCT-1998 US 09/177387 PI
JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DONNA K FOX PC
C12N15/09, C12Q1/68, C12N15/00
CC Description of Unknown Organism: recombination products FH
Key Location/Qualifiers
FT source 1..25
FT /organism='Unknown'.
FEATURES
source Location/Qualifiers
1..25
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT 4 a 3 c 3 g 9 t 6 others
ORIGIN
Query Match 88.0%; Score 22; DB 6; Length 25;
Best Local Similarity 79.2%; Pred. No. 1.7e+02;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTTGTACAAAGTTG 24
|||||
Db 1 GTTCAGCTTTTTRTACWAASNG 24
|||||
RESULT 38
AR044609 201 bp DNA linear PAT 29-SEP-1999
LOCUS
DEFINITION Sequence 18 from patent US 5817506.
ACCESSION AR044609
VERSION AR044609.1 GI:5966074
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 201)
AUTHORS Okano, K. and Kambara, H.
TITLE Polynucleotide capturing support for capturing, eluting and collecting polynucleotides in a sample solution
JOURNAL Patent: US 5817506-A 18 06-OCT-1998;
FEATURES Location/Qualifiers
source 1..201
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Best Local Similarity 92.0%; Pred. No. 1.3e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTTGTACAAAGTTG 25
|||||
Db 40 GTTCAGCTTTTATATACTAAGTTG 64
|||||
RESULT 39
E05439 201 bp DNA linear PAT 29-SEP-1997
LOCUS
DEFINITION Oligonucleotide.
ACCESSION E05439
VERSION E05439.1 GI:2173628
KEYWORDS JP 1993236997-A/11.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 201)
AUTHORS Okano, K. and Kambara, H.
TITLE CHIP FOR CATCHING POLYNUCLEOTIDE
JOURNAL Patent: JP 1993236997-A 11 17-SEP-1993;
HITACHI LTD
COMMENT OS Artificial gene
OC Artificial sequence; Genes.

PN JP 1993236997-A/11
PD 17-SEP-1993
PF 28-FEB-1992 JP 1992042829
PI OKANO KAZUNOBU, KANBARA HIDEKI
PC C12Q1/68;
CC strandedness: single;
topology: linear.
FEATURES Location/Qualifiers
source 1..201
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
BASE COUNT 58 a 38 c 27 g 78 t
ORIGIN
Query Match 87.2%; Score 21.8; DB 6; Length 201;
Best Local Similarity 92.0%; Pred. No. 1.3e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTTGTACAAAGTTG 25
|||||
Db 40 GTTCAGCTTTTATATACTAAGTTG 64
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RESULT 40
I13139 201 bp DNA linear PAT 26-JUL-1995
LOCUS
DEFINITION Sequence 18 from patent US 5434049.
ACCESSION I13139
VERSION I13139.1 GI:910488
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 201)
AUTHORS Okano, K. and Kambara, H.
TITLE Separation of polynucleotides using supports having a plurality of electrode-containing cells
JOURNAL Patent: US 5434049-A 18 18-JUL-1995;
FEATURES Location/Qualifiers
source 1..201
/organism="unknown"
BASE COUNT 58 a 38 c 27 g 78 t
ORIGIN
Query Match 87.2%; Score 21.8; DB 6; Length 201;
Best Local Similarity 92.0%; Pred. No. 1.3e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTTGTACAAAGTTG 25
|||||
Db 40 GTTCAGCTTTTATATACTAAGTTG 64
|||||
Search completed: November 6, 2003, 23:06:42
Job time : 602 secs

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Replacement Plasmids
Unpublished
2 (bases 1 to 13990)
Haag,J.R., Lee,D.W. and Aramayo,R.
Direct Submission
Submitted (27-AUG-2002) Biology, Texas A&M University, BSBW #415,
College Station, TX 77843-3258, USA
FEATURES             Location/Qualifiers
     source            1..13990
                        /organism="his-3 integration vector pJHAM007"
                        /mol_type="genomic DNA"
                        /specific_host="Neurospora crassa"
                        /db_xref="taxon:211505"
     misc_feature      1..3173
                        /note="pGEM13Zf(+)"
     misc_feature      3174..8368
                        /note="his-3 left flank; his-3 target integration site"
     misc_feature      8430..8554
                        /note="attr1; Gateway; Bacteriophage Lambda recombination
                        site"
     CDS               8804..9463
                        /codon_start=1
                        /product="chloramphenicol acetyl transferase"
                        /protein_id="AA076304.1"
                        /db_xref="GI:25988998"
                        /translation="MEKKTIGYTVTDISQWHRKEHFEAFQSVAQCYNTQVQIDTAF
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                        SLSWSEYDDPFRQFLHIYSQDVACYGLENLAYFPKGIENMFVYSANPWYSFTSFQDLN
                        ANWDNEFAVPFTMGKYITQGDVKVLMPLAIQVHHAVCDGFHVHGMLNELQQYCDQWGGG
                        A"
     CDS               9805..10110
                        /note="ccdB"
                        /codon_start=1
                        /product="gyrase target toxin"
                        /protein_id="AA076305.1"
                        /db_xref="GI:25988999"
                        /translation="MOKVITYYKRSRYRIFVUVQSDIIDTPGRRMVIFLASARLLSD
                        KYSRELVPVYHIGDESWRMWTTDMASVPVSGIVEADVASHRENDIKNAINLMPWGI"
     misc_feature      10151..10275
                        /note="attR2; Gateway; Bacteriophage Lambda recombination
                        site"
     misc_feature      10419..13990
                        /note="his-3 right flank; his-3 target integration site"
BASE COUNT  3385 a  3549 c  3559 g  3497 t
ORIGIN
Query Match      89.6%; Score 22.4; DB 12; Length 13990;
Best Local Similarity 95.8%; Pred. No. 32;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  GTTCAGCTTTTGTACAAAGTTG  24
      |||
Db      8454 GTTCAGCTTTTGTACAACTTG  8431

RESULT 37
BD131368
LOCUS      BD131368.1 GI:23226313
DEFINITION      JP 202500861-A/42.
KEYWORDS      unidentifed
SOURCE      unclassified.
ORGANISM      unclassified.
REFERENCE      1 (bases 1 to 25)
AUTHORS      Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.
TITLE      Recombinational cloning using nucleic acids having recombination
JOURNAL      Patent: JP 2002500861-A 42 15-JAN-2002;
COMMENT      LIFE TECHNOLOGIES INC
              OS Unknown
              PN      JP 202500861-A/42

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polyA_signal 3072..3573
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gene         3574..7697
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            /complement(<7698..8147)
repeat_region 2952 a 2528 c 2491 g 3034 t
            /transposon="piggyBac transposable element"
BASE COUNT 2952 a 2528 c 2491 g 3034 t
ORIGIN
1 GTTCAGCTTTTGTACAAAGTTG 24
|||||
Db 1030 GTTCAGCTTTTGTACAAAGTTG 1007

Query Match      89.6%; Score 22.4; DB 12; Length 11005;
Best Local Similarity 95.8%; Pred. No. 34;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 32
AX196825
LOCUS      AX196825      12677 bp      DNA      circular SYN 26-FEB-2003
DEFINITION PiggyBac transformation vector pB-UGIR w+, complete sequence.
ACCESSION  AX196825
VERSION     AX196825.1 GI:28565731
KEYWORDS
SOURCE      piggyBac transformation vector pB-UGIR w+
ORGANISM    piggyBac transformation vector pB-UGIR w+
            artificial sequences; vectors.
REFERENCE   1 (bases 1 to 12677)
AUTHORS     Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE       A toolkit for transformation and mutagenesis in Drosophila using
            piggyBac
JOURNAL     Unpublished
AUTHORS      Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE       Direct Submission
JOURNAL     Submitted (13-DEC-2002) Invertebrate Targets, Syngenta
            Biotechnology, Inc., 3054 Cornwallis Rd, Research Triangle Park, NC
            27709, USA
FEATURES
            Location/Qualifiers
            source
            1..12677
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               /mol_type="genomic DNA"
               /db_xref="taxon:221642"
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            TATA_signal
            632..998
               /transposon="piggyBac transposable element"
            misc_feature
            1003..2713
               /note="5x UAS hsp70 TATA signal"
            intron
            2726..3040
               /note="RpS5"
               /number=3
            misc_feature
            complement(3076..4788)
               /note="Gateway recombination cassette A; attR1 Cmr ccdB
               attR2"
            polyA_signal
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               /note="SV40"
            gene
            5247..9369
               /gene="w"
            repeat_region
            complement(<9370..9819)
               /transposon="piggyBac transposable element"
            BASE COUNT 3423 a 2924 c 2833 g 3497 t
            ORIGIN
            1 GTTCAGCTTTTGTACAAAGTTG 24
            |||||
            Db 1030 GTTCAGCTTTTGTACAAAGTTG 1007

Query Match      89.6%; Score 22.4; DB 12; Length 12677;
Best Local Similarity 95.8%; Pred. No. 33;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 34
AX590202
LOCUS      AX590202      12789 bp      DNA      linear
DEFINITION Sequence 9 from Patent WO02083888.
ACCESSION  AX590202
VERSION     AX590202.1 GI:27901286
KEYWORDS
SOURCE      synthetic construct

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Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTG 24
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RESULT 33
AX196825/c
LOCUS      AX196825      12677 bp      DNA      circular SYN 26-FEB-2003
DEFINITION PiggyBac transformation vector pB-UGIR w+, complete sequence.
ACCESSION  AX196825
VERSION     AX196825.1 GI:28565731
KEYWORDS
SOURCE      piggyBac transformation vector pB-UGIR w+
ORGANISM    piggyBac transformation vector pB-UGIR w+
            artificial sequences; vectors.
REFERENCE   1 (bases 1 to 12677)
AUTHORS     Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE       A toolkit for transformation and mutagenesis in Drosophila using
            piggyBac
JOURNAL     Unpublished
AUTHORS      Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE       Direct Submission
JOURNAL     Submitted (13-DEC-2002) Invertebrate Targets, Syngenta
            Biotechnology, Inc., 3054 Cornwallis Rd, Research Triangle Park, NC
            27709, USA
FEATURES
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               /mol_type="genomic DNA"
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               /transposon="piggyBac transposable element"
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            intron
            2726..3040
               /note="RpS5"
               /number=3
            misc_feature
            complement(3076..4788)
               /note="Gateway recombination cassette B; attR1 Cmr ccdB
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            4789..5246
               /note="SV40"
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            5247..9369
               /gene="w"
            repeat_region
            complement(<9370..9819)
               /transposon="piggyBac transposable element"
            BASE COUNT 3423 a 2924 c 2833 g 3497 t
            ORIGIN
            1 GTTCAGCTTTTGTACAAAGTTG 24
            |||||
            Db 1030 GTTCAGCTTTTGTACAAAGTTG 1007

Query Match      89.6%; Score 22.4; DB 12; Length 12677;
Best Local Similarity 95.8%; Pred. No. 33;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTG 24
|||||
Db 1030 GTTCAGCTTTTGTACAAAGTTG 1007

RESULT 34
AX590202
LOCUS      AX590202      12789 bp      DNA      linear
DEFINITION Sequence 9 from Patent WO02083888.
ACCESSION  AX590202
VERSION     AX590202.1 GI:27901286
KEYWORDS
SOURCE      synthetic construct

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/codon_start=1
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/protein_id="AAM62301.1"
/db_xref="GI:21552738"
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KVSRELYPVVHIGDESRWMTTDMASVPVSVIGEEVADUSHRENDIKNAINLFWGI"
1610..1736
misc_feature
/notes="attr2 of Gateway conversion cassette frame A"
1762..2048
misc_feature
/notes="contains intron 1 of Arabidopsis thaliana WRKY
transcription factor 33"
complement(2073..3783)
repeat_region
/notes="antisense orientation of Gateway conversion
cassette frame A containing attr1-R2 repeats, Cmr gene and
ccdB gene"
misc_feature
complement(2073..2199)
/notes="attr2 of Gateway conversion cassette frame A"
gene
complement(2241..2546)
/genes="ccdB"
CDS
complement(2241..2546)
/notes="encodes a cytotoxic protein that is a potent poison
of DNA gyrase"
/codon_start=1
/product="CcDB"
/protein_id="AAM62303.1"
/db_xref="GI:21552740"
/translation="MFKVYTYKRSRYRLFVDVQSDIIDTPGRMVIPASARLLSD
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complement(2888..3547)
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complement(2888..3547)
CDS
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/protein_id="AAM62302.1"
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SSLWEKHDFRFLHYISQDVACYGELAYFPKGFIEHMFYSANPWVSFTSEDLNV
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complement(3657..3783)
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BASE COUNT 2337 a 2150 c 2185 g 2347 t
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Query Match 89.6%; Score 22.4; DB 12; Length 9019;
Best Local Similarity 95.8%; Pred. No. 35;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTG 24
|||||
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RESULT 30
AY196824 LOCUS 11005 bp DNA circular SYN 26-FEB-2003
DEFINITION PiggyBac transformation vector pB-UGateway w+
ACCESSION AY196824
VERSION AY196824.1 GI:28565716
KEYWORDS piggyBac transformation vector pB-UGateway w+
ORGANISM piggyBac transformation vector pB-UGateway w+
artificial sequences; vectors.
REFERENCE 1 (bases 1 to 11005)
AUTHORS Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE A toolkit for transformation and mutagenesis in Drosophila using
piggyBac
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 11005)
AUTHORS Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE Direct Submission
JOURNAL Submitted (13-DEC-2002) Invertebrate Targets, Syngenta
Biotechnology, Inc., 3054 Cornwallis Rd, Research Triangle Park, NC
27709, USA
FEATURES
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1..11005
/organism="piggyBac transformation vector pB-UGateway w+"
/mol_type="genomic DNA"
/db_xref="taxon:221641"
complement(11..2620)
repeat_region
cassette frame A containing attr1-R2 repeats, Cmr gene and
ccdB gene"
TATA_signal
1003..2713
misc_feature
/notes="5x UAS hsp70 TATA signal"
attR2"

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REFERENCE 2 (bases 1 to 11005)
AUTHORS Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE Direct Submission
JOURNAL Submitted (13-DEC-2002) Invertebrate Targets, Syngenta
Biotechnology, Inc., 3054 Cornwallis Rd, Research Triangle Park, NC
27709, USA
FEATURES
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:221641"
complement(11..2620)
repeat_region
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ccdB gene"
TATA_signal
643..999
misc_feature
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1003..2713
/notes="Gateway recombination cassette A; attr1 Cmr ccdB
attR2"
2726..3040
intron
/notes="RpS5"
/number=3
polyA_signal
3072..3573
/notes="SV40"
gene
3574..7697
/genes="w"
repeat_region
/notes="mini-white; derived from Drosophila"
complement(<7698..8147)
/transposon="piggyBac transposable element"
BASE COUNT 2952 a 2528 c 2491 g 3034 t
ORIGIN
Query Match 89.6%; Score 22.4; DB 12; Length 11005;
Best Local Similarity 95.8%; Pred. No. 34;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTG 24
|||||
Db 3089 GTTCAGCTTTTGTACAACTTG 3112

RESULT 31
AY196824/c LOCUS 11005 bp DNA circular SYN 26-FEB-2003
DEFINITION PiggyBac transformation vector pB-UGateway w+, complete sequence.
ACCESSION AY196824
VERSION AY196824.1 GI:28565716
KEYWORDS piggyBac transformation vector pB-UGateway w+
SOURCE piggyBac transformation vector pB-UGateway w+
ORGANISM piggyBac transformation vector pB-UGateway w+
artificial sequences; vectors.
REFERENCE 1 (bases 1 to 11005)
AUTHORS Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE A toolkit for transformation and mutagenesis in Drosophila using
piggyBac
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 11005)
AUTHORS Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE Direct Submission
JOURNAL Submitted (13-DEC-2002) Invertebrate Targets, Syngenta
Biotechnology, Inc., 3054 Cornwallis Rd, Research Triangle Park, NC
27709, USA
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/db_xref="taxon:221641"
complement(11..2620)
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ccdB gene"
TATA_signal
643..999
misc_feature
/notes="5x UAS hsp70 TATA signal"
1003..2713
/notes="Gateway recombination cassette A; attr1 Cmr ccdB
attR2"

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repeat_region
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/db_xref="taxon:176105"
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frame A containing attR1-R2 repeats, Cmr gene and ccdB
gene"
misc_feature
26..152
/notes="attR1 of Gateway conversion cassette frame A"
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262..921
/genes="Cmr"
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chloramphenicol"
/product="Cmr"
/protein_id="AAM62300.1"
/db_xref="GI:21552737"
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1263..1568
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1263..1568
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/notes="encodes a cytotoxic protein that is a potent poison
of DNA gyrase"
/codon_start=1
/product="CcdB"
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/db_xref="GI:21552738"
/translation="MQFKVYTYKRSRYELFVDVQSDIIDTPGRMWIPLASARLLSD
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1610..1736
/notes="attR2 of Gateway conversion cassette frame A"
1762..2048
/notes="contains intron 1 of Arabidopsis thaliana WRKY
transcription factor 33"
complement(2073..3783)
/notes="antisense orientation of Gateway conversion
cassette frame A containing attR1-R2 repeats, Cmr gene and
ccdB gene"
complement(2073..2199)
/notes="attR2 of Gateway conversion cassette frame A"
complement(2241..2546)
/genes="ccdB"
complement(2241..2546)
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/notes="encodes a cytotoxic protein that is a potent poison
of DNA gyrase"
/codon_start=1
/product="CcdB"
/protein_id="AAM62303.1"
/db_xref="GI:21552740"
/translation="MQFKVYTYKRSRYELFVDVQSDIIDTPGRMWIPLASARLLSD
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chloramphenicol"
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A"

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misc_feature complement(3657..3783)
/notes="attR1 of Gateway conversion cassette frame A"
BASE COUNT 2337 a 2150 c 2185 g 2347 t
ORIGIN
Query Match 89.6%; Score 22.4; DB 12; Length 9019;
Best Local Similarity 95.8%; Pred.No. 35;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTTGTACAAAGTTG 24
|||||
Db 3756 GTTCAGCTTTTGTACAAACTTG 3779
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RESULT 29
AF408413/c 9019 bp DNA circular SYN 25-JUN-2002
LOCUS AF408413
DEFINITION Binary vector pJawohl8-RNAi, complete sequence.
ACCESSION AF408413
VERSION AF408413.1 GI:21552736
KEYWORDS
SOURCE Binary vector pJawohl8-RNAi
ORGANISM Binary vector pJawohl8-RNAi
artificial sequences; vectors.
REFERENCE 1 (bases 1 to 9019)
AUTHORS Ulker,B., Lipka,V., Rademacher,T.R. and Somssich,I.E.
TITLE pJawohl8-RNAi a binary vector for gene silencing in plants
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 9019)
AUTHORS Ulker,B., Lipka,V., Rademacher,T.R. and Somssich,I.E.
TITLE Direct Submission
JOURNAL Submitted (08-AUG-2001) Biochemistry, Max-Planck-Institut
f. Zuechtungsforschung, Carl-von-Linne Weg 10, Koeln, NRW D-50829,
Germany
FEATURES
Location/Qualifiers
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/organism="Binary vector pJawohl8-RNAi"
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/db_xref="taxon:188084"
/focus
/notes="binary plant gene silencing vector for one-step
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3803..9019
/organism="Binary vector pJawohl8-RNAi"
/mol_type="genomic DNA"
/db_xref="taxon:176105"
26..1733
/notes="sense orientation of Gateway conversion cassette
frame A containing attR1-R2 repeats, Cmr gene and ccdB
gene"
misc_feature 26..152
/notes="attR1 of Gateway conversion cassette frame A"
gene 262..921
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262..921
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CDS
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chloramphenicol"
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SSLWSEYHDDRFQFLHIYSQDVACYGENLAVPPKGFIEFMFVSANPWVSTFDLNV
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A"
1263..1568
/genes="ccdB"
1263..1568
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/notes="encodes a cytotoxic protein that is a potent poison
of DNA gyrase"

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DEFINITION Transfection vector pBtdest.
ACCESSION AJ551314
VERSION AJ551314.1 GI:29335742
KEYWORDS amp gene; beta lactamase; cat gene; ccdB gene; chloramphenicol
          acetyl transferase; control of cell death B protein.
SOURCE Transfection vector pBtdest
ORGANISM Transfection vector pBtdest
          artificial sequences, vectors.
REFERENCE 1
AUTHORS Jakob, M.J., Heim, M.A. and Weisshaar, B.
TITLE Use of a gateway compatible vector for transient plant transfection
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 4462)
AUTHORS Jakob, M.J.
TITLE Direct Submission
JOURNAL Submitted (26-MAR-2003) Jakob M.J., Salamini, MPI for Plant
Breeding Research, Carl-von-Linne Weg 10, 50829 Koeln, GERMANY
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31..443
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421..424
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456..580
/note="attR1"
689..1348
/gene="cat"
689..1348
/gene="cat"
/codon_start=1
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/protein_id="CAD83080.1"
/db_xref="GI:29335743"
/translation="MEKKTGYTVDISQWHRKEHFEAFQSAQTYNTVQLDITAF
LTKVKNKHKFPFAPFHLARLNLNHAHPEFRMAKDGELVDSVHPCTVTFHEQETTF
SLWSYHDDRFQELHIYSQDVACYLEPFGKFIENMFVSNPWSFTSFDLNV
ANMNDFFAPVFMKYYTGQDKVLMPLAQVHHAVCBGFHVGRLNELQQYCDWQGG
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1690..1995
/gene="ccdB"
1690..1995
/gene="ccdB"
/codon_start=1
/product="control of cell death B protein"
/protein_id="CAD83081.1"
/db_xref="GI:29335744"
/translations="MQFKVYTYKRSRYRLFDVQSDIIDTPGRMVPIASARLLSD
KVSRELYPVVHIGDESWMMTDMASVPVSIVGEEVADLSHRENDIKNAINLFWGI"
2036..2160
/note="attR2"
2168..2463
/gene="nosT"
2168..2463
/gene="nosT"
2606..3466
/gene="amp"
2606..3466
/gene="amp"
/codon_start=1
/product="beta lactamase"
/protein_id="CAD83082.1"
/db_xref="GI:29335745"
/translation="MSIQHFRVALIPFAFCLVPFAHPETLVKVKDAEDQLGARVGY
IELDNSGKILDESFRPEERPMWTFKVLICGAVLSRIDAGQEQLGRRIHYSQNDLVE
YSPYVKHTIDGTMVRELCSAAITMSDNTAALLLTIGGPKELTAFHNGDHVTRL
DRWPELNEAIPNDERDTTPVAMATTLRKLLTGLLTLASRQQLIDWMEADKVGKPL
LRSLPAGWFTADSKGAGERSGRIIALGSDGPKPSRIIVITYTGSQTADWERNRQIA
EIGASLIKHW"
1223 a 995 c 1065 g 1179 t

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Query Match 89.6%; Score 22.4; DB 12; Length 4462;
Best Local Similarity 95.8%; Pred. No. 40;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTG 24
|||||
Db 480 GTTCAGCTTTTGTACAAACTTG 457

RESULT 27
AX306327/c LOCUS 5148 bp DNA linear PAT 11-DEC-2001
DEFINITION Sequence 10 from Patent WO0188121.
ACCESSION AX306327
VERSION AX306327.1 GI:17645566
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Plaetnick, G., Renard, J.P. and Bogaert, T.
TITLE Vector constructs
JOURNAL Patent: WO 0188121-A 10 22-NOV-2001;
Devgen NV (BE)
FEATURES
source
1..5148
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Plasmid pGN39"
BASE COUNT 1359 a 1199 c 1279 g 1311 t
ORIGIN

Query Match 89.6%; Score 22.4; DB 6; Length 5148;
Best Local Similarity 95.8%; Pred. No. 39;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTG 24
|||||
Db 171 GTTCAGCTTTTGTACAAACTTG 148

RESULT 28
AF408413 LOCUS 9019 bp DNA circular SYN 25-JUN-2002
DEFINITION Binary vector pJawohl8-RNAi, complete sequence.
ACCESSION AF408413
VERSION AF408413.1 GI:21552736
KEYWORDS Binary vector pJawohl8-RNAi
SOURCE Binary vector pJawohl8-RNAi
ORGANISM artificial sequences; vectors.
REFERENCE 1 (bases 1 to 9019)
AUTHORS Ulker, B., Lipka, V., Rademacher, T.R. and Somssich, I.E.
TITLE puawohl8-RNAi a binary vector for gene silencing in plants
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 9019)
AUTHORS Ulker, B., Lipka, V., Rademacher, T.R. and Somssich, I.E.
TITLE Direct Submission
JOURNAL Submitted (08-AUG-2001) Biochemistry, Max-Planck-Institut
f. Zuechtungsforschung, Carl-von-Linne Weg 10, Koeln, NRW D-50829,
Germany
FEATURES
source
1..9019
/organism="Binary vector pJawohl8-RNAi"
/mol_type="genomic DNA"
/db_xref="taxon:188084"
/focus
/note="binary plant gene silencing vector for one-step
cloning of inverted sequences"
3803..9019
/organism="Binary vector pJawohl8-RNAi"

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RESULT 22
AX498619          25 bp      DNA      linear      PAT 26-SEP-2002
LOCUS
DEFINITION
Sequence 9 from Patent EP1229113.
ACCESSION
AX498619
VERSION
AX498619.1 GI:23343416
KEYWORDS
SOURCE
unidentified
ORGANISM
unclassified.
REFERENCE
1
AUTHORS
Hartley,J.L. and Brasch,M.A.
TITLE
Recombinational cloning using engineered recombination sites
JOURNAL
Patent: EP 1229113-A 9 07-AUG-2002;
INVITROGEN CORPORATION (US)
FEATURES
source
1..25
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT      5 a      4 c      4 g      12 t
ORIGIN
Query Match      89.6%; Score 22.4; DB 6; Length 25;
Best Local Similarity 95.8%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTG 24
Db 1 GTTCAGCTTTTGTACAAAGTTG 24

RESULT 23
BD131335          25 bp      DNA      linear      PAT 18-SEP-2002
LOCUS
DEFINITION
Recombinational cloning using nucleic acids having recombination
sites.
ACCESSION
BD131335
VERSION
BD131335.1 GI:23226290
KEYWORDS
JP 2002500861-A/9.
SOURCE
unidentified
ORGANISM
unclassified.
REFERENCE
1 (bases 1 to 25)
AUTHORS
Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.
TITLE
Recombinational cloning using nucleic acids having recombination
sites.
JOURNAL
Patent: JP 2002500861-A 9 15-JAN-2002;
LIFE TECHNOLOGIES INC
COMMENT
OS Unknown
PN JP 2002500861-A/9
PD 15-JAN-2002
PF 26-OCT-1998 JP 2000518069
PR 24-OCT-1997 US 60/065930, 23-OCT-1998 US 09/177387 PI
JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DONNA K FOX PC
C12N15/09, C12Q1/68, C12N15/00
CC Description of Unknown Organism: recombination products FH
KEY source      1..25
FT      Location/Qualifiers
/organism="Unknown".
FEATURES
source
1..25
Location/Qualifiers
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT      5 a      4 c      4 g      12 t
ORIGIN
Query Match      89.6%; Score 22.4; DB 6; Length 25;
Best Local Similarity 95.8%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTG 24

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Db 1 GTTCAGCTTTTGTACAAAGTTG 24

RESULT 24
AX684690/c        35 bp      DNA      linear      PAT 29-MAR-2003
LOCUS
DEFINITION
Sequence 9 from Patent WO0224865.
ACCESSION
AX684690
VERSION
AX684690.1 GI:29371240
KEYWORDS
SOURCE
Escherichia coli
ORGANISM
Escherichia coli
REFERENCE
1
AUTHORS
Holtzman,D., Madden,K., Maxon,M. and Sherman,A.
TITLE
Modulation of secondary metabolite production by zinc binuclear
cluster proteins
JOURNAL
Patent: WO 0224865-A 9 28-MAR-2002;
Microbia, INC. (US)
FEATURES
source
1..35
Location/Qualifiers
/organism="Escherichia coli"
/mol_type="genomic DNA"
/db_xref="taxon:562"
BASE COUNT      14 a      7 c      7 g      7 t
ORIGIN
Query Match      89.6%; Score 22.4; DB 6; Length 35;
Best Local Similarity 95.8%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTG 24
Db 35 GTTCAGCTTTTGTACAAAGTTG 12

RESULT 25
AX703501/c        1846 bp     DNA      linear      PAT 03-APR-2003
LOCUS
DEFINITION
Sequence 63 from Patent WO0206653.
ACCESSION
AX703501
VERSION
AX703501.1 GI:29538461
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
artificial sequences.
REFERENCE
1
AUTHORS
Li,M. and Liu,Y.C.
TITLE
Prokaryotic libraries and uses
JOURNAL
Patent: WO 0206653-A 63 29-AUG-2002;
Xencor (US)
FEATURES
source
1..1846
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
BASE COUNT      527 a      381 c      434 g      504 t
ORIGIN
Query Match      89.6%; Score 22.4; DB 6; Length 1846;
Best Local Similarity 95.8%; Pred. No. 48;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTG 24
Db 25 GTTCAGCTTTTGTACAAAGTTG 2

RESULT 26
VFO551314/c       4462 bp     DNA      circular SYN 27-MAR-2003
LOCUS

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BASE COUNT      5 a      4 c      6 g      10 t
ORIGIN
Query Match      93.6%; Score 23.4; DB 6; Length 25;
Best Local Similarity 96.0%; Pred. No. 43;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTG 25
    |||||
Db 1 GTTCAGCTTTTGTACAAAGTTG 25

RESULT 18
BD131342      25 bp      DNA      linear      PAT 18-SEP-2002
LOCUS
DEFINITION
Recombinational cloning using nucleic acids having recombination
sites.
ACCESSION
BD131342
VERSION
BD131342.1 GI:23226287
KEYWORDS
JP 2002500861-A/16.
SOURCE
unidentified
ORGANISM
unclassified.
REFERENCE
1 (bases 1 to 25)
AUTHORS
Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.
TITLE
Recombinational cloning using nucleic acids having recombination
JOURNAL
Patent: JP 2002500861-A 16 15-JAN-2002;
LIFE TECHNOLOGIES INC
COMMENT
OS JP 2002500861-A/16
PD 15-JAN-2002
PF 26-OCT-1998 JP 2000518069
PR 24-OCT-1997 US 60/065930,23-OCT-1998 US 09/177387 PI
JAMES L HARTLEY,MICHAEL A BRASCH,GARY F TEMPLE,DONNA K FOX PC
C12N15/09,C12Q1/68,C12N15/00
CC Description of Unknown Organism: recombination products PH
Key source      1. .25
FT source      Location/Qualifiers
FT
FEATURES
source
Location/Qualifiers
1. .25
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT      5 a      4 c      6 g      10 t
ORIGIN
Query Match      93.6%; Score 23.4; DB 6; Length 25;
Best Local Similarity 96.0%; Pred. No. 43;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTG 25
    |||||
Db 1 GTTCAGCTTTTGTACAAAGTTG 25

RESULT 19
AR124529      25 bp      DNA      linear      PAT 16-MAY-2001
LOCUS
DEFINITION
Sequence 9 from patent US 6171861.
ACCESSION
AR124529
VERSION
AR124529.1 GI:14109890
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 25)
AUTHORS
Hartley,J.L. and Brasch,M.A.
TITLE
Recombinational cloning using engineered recombination sites
JOURNAL
Patent: US 6171861-A 9 09-JAN-2001;
LIFE TECHNOLOGIES INC
FEATURES
source
Location/Qualifiers
1. .25
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT      5 a      4 c      6 g      10 t
ORIGIN
Query Match      93.6%; Score 23.4; DB 6; Length 25;
Best Local Similarity 96.0%; Pred. No. 43;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTG 25
    |||||
Db 1 GTTCAGCTTTTGTACAAAGTTG 25

RESULT 20
AR163180      25 bp      DNA      linear      PAT 17-OCT-2001
LOCUS
DEFINITION
Sequence 9 from patent US 6270969.
ACCESSION
AR163180
VERSION
AR163180.1 GI:16233689
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 25)
AUTHORS
Hartley,J.L. and Brasch,M.A.
TITLE
Recombinational cloning using engineered recombination sites
JOURNAL
Patent: US 6270969-A 9 07-AUG-2001;
LIFE TECHNOLOGIES INC
FEATURES
source
Location/Qualifiers
1. .25
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT      5 a      4 c      6 g      10 t
ORIGIN
Query Match      93.6%; Score 22.4; DB 6; Length 25;
Best Local Similarity 95.8%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTG 24
    |||||
Db 1 GTTCAGCTTTTGTACAAAGTTG 24

RESULT 21
AX491648      25 bp      DNA      linear      PAT 16-AUG-2002
LOCUS
DEFINITION
Sequence 9 from Patent EP1227147.
ACCESSION
AX491648
VERSION
AX491648.1 GI:22324156
KEYWORDS
unidentified
SOURCE
unidentified
ORGANISM
unclassified.
REFERENCE
1
AUTHORS
Hartley,J.L. and Brasch,M.A.
TITLE
Recombinational cloning using engineered recombination sites
JOURNAL
Patent: EP 1227147-A 9 31-JUL-2002;
INVITROGEN CORPORATION (US)
FEATURES
source
Location/Qualifiers
1. .25
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT      5 a      4 c      6 g      10 t
ORIGIN
Query Match      89.6%; Score 22.4; DB 6; Length 25;
Best Local Similarity 95.8%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTG 24
    |||||
Db 1 GTTCAGCTTTTGTACAAAGTTG 24

RESULT 22
AX491648      25 bp      DNA      linear      PAT 16-AUG-2002
LOCUS
DEFINITION
Sequence 9 from Patent EP1227147.
ACCESSION
AX491648
VERSION
AX491648.1 GI:22324156
KEYWORDS
unidentified
SOURCE
unidentified
ORGANISM
unclassified.
REFERENCE
1
AUTHORS
Hartley,J.L. and Brasch,M.A.
TITLE
Recombinational cloning using engineered recombination sites
JOURNAL
Patent: EP 1227147-A 9 31-JUL-2002;
INVITROGEN CORPORATION (US)
FEATURES
source
Location/Qualifiers
1. .25
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT      5 a      4 c      6 g      10 t
ORIGIN
Query Match      89.6%; Score 22.4; DB 6; Length 25;
Best Local Similarity 95.8%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTG 24
    |||||
Db 1 GTTCAGCTTTTGTACAAAGTTG 24
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BASE COUNT      5 a      4 c      4 g      12 t
ORIGIN
Query Match      89.6%; Score 22.4; DB 6; Length 25;
Best Local Similarity 95.8%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTG 24
    |||||
Db 1 GTTCAGCTTTTGTACAAAGTTG 24

RESULT 20
AR163180      25 bp      DNA      linear      PAT 17-OCT-2001
LOCUS
DEFINITION
Sequence 9 from patent US 6270969.
ACCESSION
AR163180
VERSION
AR163180.1 GI:16233689
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 25)
AUTHORS
Hartley,J.L. and Brasch,M.A.
TITLE
Recombinational cloning using engineered recombination sites
JOURNAL
Patent: US 6270969-A 9 07-AUG-2001;
LIFE TECHNOLOGIES INC
FEATURES
source
Location/Qualifiers
1. .25
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT      5 a      4 c      4 g      12 t
ORIGIN
Query Match      89.6%; Score 22.4; DB 6; Length 25;
Best Local Similarity 95.8%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTG 24
    |||||
Db 1 GTTCAGCTTTTGTACAAAGTTG 24

RESULT 21
AX491648      25 bp      DNA      linear      PAT 16-AUG-2002
LOCUS
DEFINITION
Sequence 9 from Patent EP1227147.
ACCESSION
AX491648
VERSION
AX491648.1 GI:22324156
KEYWORDS
unidentified
SOURCE
unidentified
ORGANISM
unclassified.
REFERENCE
1
AUTHORS
Hartley,J.L. and Brasch,M.A.
TITLE
Recombinational cloning using engineered recombination sites
JOURNAL
Patent: EP 1227147-A 9 31-JUL-2002;
INVITROGEN CORPORATION (US)
FEATURES
source
Location/Qualifiers
1. .25
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT      5 a      4 c      4 g      12 t
ORIGIN
Query Match      89.6%; Score 22.4; DB 6; Length 25;
Best Local Similarity 95.8%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTG 24
    |||||
Db 1 GTTCAGCTTTTGTACAAAGTTG 24
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DEFINITION      Sequence 8 from Patent WO0174861.
ACCESSION       AX269137
VERSION         AX269137.1  GI:16542057
KEYWORDS        synthetic construct
SOURCE          synthetic construct
ORGANISM        artificial sequences.

REFERENCE       1
AUTHORS         Vile,R.G., Harrington,K., Murphy,S. and Bateman,A.
TITLE           Compositions and methods for tissue specific gene regulation
                therapy
JOURNAL         MAYO FOUNDATION FOR MEDICAL EDUCATION AND RESEARCH (US)
FEATURES        Location/Qualifiers
                source
                1..25
                /organism="synthetic construct"
                /mol_type="genomic DNA"
                /db_xref="taxon:32630"
                /note="Synthetically generated vector sequence"
BASE COUNT     5 a      4 c      6 g      10 t
ORIGIN
Query Match    93.6%; Score 23.4; DB 6; Length 25;
Best Local Similarity 96.0%; Pred. No. 43;
Matches        24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GTTCAGCTTTTGTGTACAAAGTTGG 25
        |||||
Db      1 GTTCAGCTTCTTGTACAAAGTTGG 25

RESULT 14
AX491650
LOCUS         AX491650                25 bp      DNA      linear      PAT 16-AUG-2002
DEFINITION   Sequence 11 from Patent EP1227147.
ACCESSION    AX491650
VERSION      AX491650.1  GI:22324158
KEYWORDS
SOURCE       unidentified
ORGANISM     unclassified.

REFERENCE     1
AUTHORS      Hartley,J.L. and Brasch,M.A.
TITLE        Recombinational cloning using engineered recombination sites
JOURNAL      INVITROGEN CORPORATION (US)
FEATURES     Location/Qualifiers
             source
             1..25
             /organism="unidentified"
             /mol_type="genomic DNA"
             /db_xref="taxon:32644"
BASE COUNT   5 a      4 c      6 g      10 t
ORIGIN
Query Match  93.6%; Score 23.4; DB 6; Length 25;
Best Local Similarity 96.0%; Pred. No. 43;
Matches      24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GTTCAGCTTTTGTGTACAAAGTTGG 25
        |||||
Db      1 GTTCAGCTTCTTGTACAAAGTTGG 25

RESULT 15
AX491655
LOCUS         AX491655                25 bp      DNA      linear      PAT 16-AUG-2002
DEFINITION   Sequence 16 from Patent EP1227147.
ACCESSION    AX491655
VERSION      AX491655.1  GI:22324163
KEYWORDS
SOURCE       unidentified
ORGANISM     unclassified.

REFERENCE     1
AUTHORS      Hartley,J.L. and Brasch,M.A.
TITLE        Recombinational cloning using engineered recombination sites
JOURNAL      INVITROGEN CORPORATION (US)
FEATURES     Location/Qualifiers
             source
             1..25
             /organism="unidentified"
             /mol_type="genomic DNA"
             /db_xref="taxon:32644"
BASE COUNT   5 a      4 c      6 g      10 t
ORIGIN
Query Match  93.6%; Score 23.4; DB 6; Length 25;
Best Local Similarity 96.0%; Pred. No. 43;
Matches      24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GTTCAGCTTTTGTGTACAAAGTTGG 25
        |||||
Db      1 GTTCAGCTTCTTGTACAAAGTTGG 25

RESULT 16
AX498621
LOCUS         AX498621                25 bp      DNA      linear      PAT 26-SEP-2002
DEFINITION   Sequence 11 from Patent EP1229113.
ACCESSION    AX498621
VERSION      AX498621.1  GI:23343418
KEYWORDS
SOURCE       unidentified
ORGANISM     unclassified.

REFERENCE     1
AUTHORS      Hartley,J.L. and Brasch,M.A.
TITLE        Recombinational cloning using engineered recombination sites
JOURNAL      INVITROGEN CORPORATION (US)
FEATURES     Location/Qualifiers
             source
             1..25
             /organism="unidentified"
             /mol_type="genomic DNA"
             /db_xref="taxon:32644"
BASE COUNT   5 a      4 c      6 g      10 t
ORIGIN
Query Match  93.6%; Score 23.4; DB 6; Length 25;
Best Local Similarity 96.0%; Pred. No. 43;
Matches      24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GTTCAGCTTTTGTGTACAAAGTTGG 25
        |||||
Db      1 GTTCAGCTTCTTGTACAAAGTTGG 25

RESULT 17
AX498626
LOCUS         AX498626                25 bp      DNA      linear      PAT 26-SEP-2002
DEFINITION   Sequence 16 from Patent EP1229113.
ACCESSION    AX498626
VERSION      AX498626.1  GI:23343423
KEYWORDS
SOURCE       unidentified
ORGANISM     unclassified.

REFERENCE     1
AUTHORS      Hartley,J.L. and Brasch,M.A.
TITLE        Recombinational cloning using engineered recombination sites
JOURNAL      INVITROGEN CORPORATION (US)
FEATURES     Location/Qualifiers
             source
             1..25
             /organism="unidentified"
             /mol_type="genomic DNA"
             /db_xref="taxon:32644"
BASE COUNT   5 a      4 c      6 g      10 t
ORIGIN
Query Match  93.6%; Score 23.4; DB 6; Length 25;
Best Local Similarity 96.0%; Pred. No. 43;
Matches      24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GTTCAGCTTTTGTGTACAAAGTTGG 25
        |||||
Db      1 GTTCAGCTTCTTGTACAAAGTTGG 25

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PN JP 2002500861-A/43
PD 15-JAN-2002 JP 2000518069
PF 26-OCT-1998 US 09/177387 PI
PR 24-OCT-1997 US 60/065930,23-OCT-1998 US 09/177387 PI
PJ JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DONNA K FOX PC
C12N15/09, C12Q1/68, C12N15/00
CC Description of Unknown Organism: recombination products FH
Key source Location/Qualifiers
FT source 1. .25 /organism='Unknown'.
FEATURES
    source
        Location/Qualifiers
            1. .25
            /organism='unidentified'
            /mol_type='genomic DNA'
            /db_xref='taxon:32644'
BASE COUNT 4 a 3 c 5 g 10 t 3 others
ORIGIN
    Query Match 95.2%; Score 23.8; DB 6; Length 25;
    Best Local Similarity 88.0%; Pred. No. 29;
    Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
    |||||
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25
    |||||
RESULT 9
AR124531 25 bp DNA linear PAT 16-MAY-2001
LOCUS
DEFINITION Sequence 11 from patent US 6171861.
ACCESSION AR124531
VERSION AR124531.1 GI:14109892
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley, J.L. and Brasch, M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6171861-A 11 09-JAN-2001;
FEATURES
    source
        Location/Qualifiers
            1. .25
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    Best Local Similarity 96.0%; Pred. No. 43;
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Db 1 GTTCAGCTTTTGTACAAAGTTGG 25
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RESULT 10
AR124536 25 bp DNA linear PAT 16-MAY-2001
LOCUS
DEFINITION Sequence 16 from patent US 6171861.
ACCESSION AR124536
VERSION AR124536.1 GI:14109897
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley, J.L. and Brasch, M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6171861-A 16 09-JAN-2001;
FEATURES
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    Best Local Similarity 96.0%; Pred. No. 43;
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RESULT 11
AR163182 25 bp DNA linear PAT 17-OCT-2001
LOCUS
DEFINITION Sequence 11 from patent US 6270969.
ACCESSION AR163182
VERSION AR163182.1 GI:16233692
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley, J.L. and Brasch, M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6270969-A 11 07-AUG-2001;
FEATURES
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            /organism='unknown'
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    Best Local Similarity 96.0%; Pred. No. 43;
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RESULT 12
AR163187 25 bp DNA linear PAT 17-OCT-2001
LOCUS
DEFINITION Sequence 16 from patent US 6270969.
ACCESSION AR163187
VERSION AR163187.1 GI:16233699
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley, J.L. and Brasch, M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6270969-A 16 07-AUG-2001;
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RESULT 13
AX269137 25 bp DNA linear PAT 29-OCT-2001
LOCUS
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Fri Nov 7 08:08:36 2003

kanamycin resistance protein; neomycin phosphotransferase II; nptII gene; promoter; speC gene; spectinomycin resistance protein; transposon Tn7.

SOURCE ORGANISM Cloning vector pHELLSGATE

REFERENCE AUTHORS Wesley, V.S., Helliwell, C., Smith, N.A., Wang, M.B., Rouse, D., Liu, O., Gooding, P.S., Singh, S.R., Abbott, D., Stoutjesdijk, A., Robinson, S.P., Gleave, A.P., Green, A.G., and Waterhouse, P.M.

TITLE Construct design for efficient, effective and high-throughput gene silencing in plants

JOURNAL Plant J. 27 (6), 581-590 (2001)

MEDLINE 21461301

PUBMED 11576441

REFERENCE 2 (bases 1 to 18691)

AUTHORS Waterhouse, P.M.

TITLE Direct Submission

JOURNAL Submitted (04-MAY-2001) Waterhouse P.M., Plant Industry, C.S.I.R.O., P.O. Box 1600, Canberra, ACT 2601, AUSTRALIA

FEATURES source

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/note="octopine esynthase (ocs) terminator"

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Best Local Similarity 100.0%; Pred. No. 2.4;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 13146 GTTCAGCTTTTGTGTAAGAATTGG 13122

RESULT 8

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LOCUS

DEFINITION BD131369 25 bp DNA linear PAT 18-SEP-2002

ACCSSION BD131369

VERSION BD131369.1 GI:23226314

KEYWORDS JP 2002500861-A/43.

SOURCE unidentified

ORGANISM unclassified.

REFERENCE 1 (bases 1 to 25)

AUTHORS Hartley, J.L., Brash, M.A., Temple, G.F. and Fox, D.K.

TITLE Recombinational cloning using nucleic acids having recombination

JOURNAL Patent: JP 2002500861-A 43 15-JAN-2002;

COMMENT LIFE TECHNOLOGIES INC

OS Unknown

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
 Db 1 GTTCAGCTTTTGTACAAAGTTGG 25
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 LOCUS Cloning vector pHELLSGATE.
 DEFINITION Cloning vector pHELLSGATE.
 ACCESSION AJ311874
 VERSION AJ311874.1 GI:15982218
 KEYWORDS kanamycin resistance protein; neomycin phosphotransferase II; nptII gene; promoter; spec gene; spectinomycin resistance protein; transposon Tn7.
 SOURCE Cloning vector pHELLSGATE
 ORGANISM Cloning vector pHELLSGATE
 artificial sequences; vectors.
 REFERENCE 1
 AUTHORS Wesley, V.S., Helliwell, C., Smith, N.A., Wang, M.B., Rouse, D., Liu, Q., Gooding, P.S., Singh, S.R., Abbott, D., Stoutjesdijk, A., Robinson, S.P., Gleave, A.P., Green, A.G. and Waterhouse, P.M.
 TITLE Construct design for efficient, effective and high-throughput gene silencing in plants
 JOURNAL Plant J. 27 (6), 581-590 (2001)
 MEDLINE 21461301
 PUBMED 11576441
 REFERENCE 2 (bases 1 to 18691)
 AUTHORS Waterhouse, P.M.
 TITLE Direct Submission
 JOURNAL Submitted (04-MAY-2001) Waterhouse P.M., Plant Industry, C.S.I.R.O., P.O. Box 1600, Canberra, ACT 2601, AUSTRALIA
 FEATURES
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 /organism="Escherichia coli K12"
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 265. 448
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 14660. 16258
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17922. 18691
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 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 LOCUS Cloning vector pHELLSGATE.
 DEFINITION Cloning vector pHELLSGATE.
 ACCESSION AJ311874
 VERSION AJ311874.1 GI:15982218

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RESULT 2
AX491654
LOCUS 25 bp DNA linear PAT 17-OCT-2001
DEFINITION
Sequence 15 from patent US 6270969.
ACCESSION AR163186
VERSION AR163186.1 GI:16233698
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 25)
Hartley,J.L. and Brasch,M.A.
AUTHORS
TITLE
Recombinational cloning using engineered recombination sites
JOURNAL
Patent: US 6270969-A 15 07-AUG-2001;
FEATURES
Location/Qualifiers
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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
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LOCUS 25 bp DNA linear PAT 16-AUG-2002
DEFINITION
Sequence 15 from Patent EP1227147.
ACCESSION AX491654
VERSION AX491654.1 GI:22324162
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
Hartley,J.L. and Brasch,M.A.
AUTHORS
TITLE
Recombinational cloning using engineered recombination sites
JOURNAL
Patent: EP 1227147-A 15 31-JUL-2002;
INVITROGEN CORPORATION (US)
FEATURES
Location/Qualifiers
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RESULT 4
AX498625
LOCUS 25 bp DNA linear PAT 26-SEP-2002
DEFINITION
Sequence 15 from Patent EP1229113.
ACCESSION AX498625
VERSION AX498625.1 GI:23343422
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
Hartley,J.L. and Brasch,M.A.
AUTHORS
TITLE
Recombinational cloning using engineered recombination sites
JOURNAL
Patent: EP 1229113-A 15 07-AUG-2002;
INVITROGEN CORPORATION (US)
FEATURES
Location/Qualifiers
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/db_xref="taxon:32644"
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RESULT 5
BD131341
LOCUS 25 bp DNA linear PAT 18-SEP-2002
DEFINITION
Recombinational cloning using nucleic acids having recombination
sites.
ACCESSION BD131341
VERSION BD131341.1 GI:23226286
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 25)
Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.
AUTHORS
TITLE
Recombinational cloning using nucleic acids having recombination
JOURNAL
Patent: JP 2002500861-A 15 15-JAN-2002;
LIFE TECHNOLOGIES INC
COMMENT
OS Unknown
PN JP 2002500861-A/15
PD 15-JAN-2002
PF 26-OCT-1998 JP 2000518069
PR 24-OCT-1997 US 60/065930,23-OCT-1998 US 09/177387 PI
C12N15/09,C12Q1/68,C12N15/00
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Location/Qualifiers
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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 6, 2003, 21:07:03 ; Search time 601 Seconds
(without alignments)
1701.732 Million cell updates/sec

Title: US-10-055-001A-10

Perfect score: 25

Sequence: 1 gttcagctttttgtacaaagtgg 25

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 288711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: gb_ba.*

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3: gb_in.*

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5: gb_cm.*

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14: gb_vi.*

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16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_cm.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

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26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

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37: em_htg_vrt.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	25	100.0	25	6	AR163186	Sequence
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4	25	100.0	25	6	AX498625	Sequence
5	25	100.0	25	6	BD131341	Sequence
6	25	100.0	18691	12	CVE311874	Recombina
7	25	100.0	18691	12	CVE311874	Cloning v
8	23.8	95.2	25	6	BD131369	Sequence
9	23.4	93.6	25	6	AR124531	Sequence
10	23.4	93.6	25	6	AR124536	Sequence
11	23.4	93.6	25	6	AR163182	Sequence
12	23.4	93.6	25	6	AR163187	Sequence
13	23.4	93.6	25	6	AX269137	Sequence
14	23.4	93.6	25	6	AX491650	Sequence
15	23.4	93.6	25	6	AX491655	Sequence
16	23.4	93.6	25	6	AX498621	Sequence
17	23.4	93.6	25	6	AX498626	Sequence
18	23.4	93.6	25	6	BD131342	Recombina
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20	22.4	89.6	25	6	AR163180	Sequence
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23	22.4	89.6	25	6	BD131335	Recombina
24	22.4	89.6	35	6	AX684690	Sequence
25	22.4	89.6	1846	6	AX703501	Sequence
26	22.4	89.6	4462	12	VFO551314	Transfect
27	22.4	89.6	5148	6	AX306327	Sequence
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40	21.8	87.2	201	6	I13139	Sequence 18
41	21.8	87.2	201	6	I36498	Sequence 18
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ALIGNMENTS

RESULT 1
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LOCUS AR124535
DEFINITION Sequence 15 from patent US 6171861.
ACCESSION AR124535
VERSION AR124535.1 GI:14109896
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6171861-A 15 09-JAN-2001;
FEATURES Location/Qualifiers

AR124535 25 bp DNA linear PAT 16-MAY-2001
Sequence 15 from patent US 6171861.
AR124535
AR124535.1 GI:14109896
Unknown.
Unclassified.
1 (bases 1 to 25)
Hartley,J.L. and Brasch,M.A.
Recombinational cloning using engineered recombination sites
Patent: US 6171861-A 15 09-JAN-2001;
Location/Qualifiers


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BASE COUNT      279 a 244 c 318 g 244 t 116 others
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Query Match      80.0%; Score 20; DB 9; Length 1201;
Best Local Similarity 90.9%; Pred. No. 6.5e+02;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db 33 CAGCTTTTCTTGTAACAACCTTGW 12

RESULT 37
BX363509/c
LOCUS
DEFINITION
BX363509 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
Homo sapiens cDNA clone CS0DL001YD08 5-PRIME, mRNA sequence.
ACCESSION
BX363509
VERSION
BX363509.1 GI:30376731
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2356.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DL001DB04QPI&cluster=2356.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DL001DB04QPI.

FEATURES
source
1. .1201
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DL001YD08"
/cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
/clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT
25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo (dtr)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT      335 a 140 c 217 g 340 t 169 others
ORIGIN
Query Match      80.0%; Score 20; DB 13; Length 1201;
Best Local Similarity 90.9%; Pred. No. 6.5e+02;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CAGCTTTCTTGTAACAACCTTGT 25
    ||||| ||||| ||||| ||||| |||||
Db 35 CWGCTTTTCTTGTAACAACCTTGT 14

RESULT 38
BX382731
LOCUS
DEFINITION
BX382731 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI085YB18 3-PRIME, mRNA sequence.
ACCESSION
BX382731

```

```

BX382731.1 GI:30443901
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9993.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI085DA09NP1&cluster=9993.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI085DA09NP1.

FEATURES
source
1. .1201
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI085YB18"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo (dtr)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT      219 a 297 c 379 g 218 t 98 others
ORIGIN
Query Match      80.0%; Score 20; DB 13; Length 1201;
Best Local Similarity 90.9%; Pred. No. 6.5e+02;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CAGCTTTCTTGTAACAACCTTGT 25
    ||||| ||||| ||||| ||||| |||||
Db 775 CTGCTTTTCTTGTAACAACCTTGT 796

RESULT 39
BX386369/c
LOCUS
DEFINITION
BX386369 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI071YA13 5-PRIME, mRNA sequence.
ACCESSION
BX386369
VERSION
BX386369.1 GI:30436794
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 95.r For more
information about this cluster, see http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS1AI018E07QPI&cluster=95.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS1AI018E07QPI.

```



```

SOURCE
ORGANISM      Homo sapiens (human)
REFERENCE     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE        1 (bases 1 to 1190)
JOURNAL      Full-length cDNA libraries and normalization
COMMENT      Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9817.f For
more information about this cluster, see
http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DC002AC03QP1&cluster=9817.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DC002AC03QP1.

FEATURES
source
1..1190
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DC002YE05"
/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoRV sites of the Not I and EcoRV
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT      248 a 332 c 362 g 209 t 39 others
ORIGIN
Query Match      80.0%; Score 20; DB 13; Length 1190;
Best Local Similarity 90.9%; Pred. No. 6.5e+02;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      4 CAGCTTCTTCTGTACAACTTGT 25
      :|||||
Db      38 CWGCTTTTGTGTACAACTTGT 17

RESULT 32
BX463747/c
LOCUS      BX463747      1198 bp      mRNA      linear      EST 22-MAY-2003
DEFINITION      CS0DF003YB02 5-PRIME, mRNA sequence.
ACCESSION      BX463747
VERSION      BX463747.1 GI:31031557
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1198)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3257.f,
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS1AF001ZF02QP1.

FEATURES
source
1..1198
/organism="Homo sapiens"
/mol_type="mRNA"

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/db_xref="taxon:9606"
/clone="CS0DF003YB02"
/tissue_type="FETAL BRAIN"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/notes="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
BASE COUNT      256 a 295 c 337 g 237 t 73 others
ORIGIN
Query Match      80.0%; Score 20; DB 13; Length 1198;
Best Local Similarity 90.9%; Pred. No. 6.5e+02;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      4 CAGCTTCTTCTGTACAACTTGT 25
      :|||||
Db      39 CWGCTTTTGTGTACAACTTGT 18

RESULT 33
AL513677/c
LOCUS      AL513677      1201 bp      mRNA      linear      EST 08-MAY-2003
DEFINITION      AL513677 Homo sapiens PLACENTA Homo sapiens cDNA clone CL0BA007ZB09
3-PRIME, mRNA sequence.
ACCESSION      AL513677
VERSION      AL513677.2 GI:30463562
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 13, 2001 this sequence version replaced gi:12777171.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CL0BA007ZB09FP1.

FEATURES
source
1..1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CL0BA007ZB09"
/tissue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/notes="vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and EcoRV sites
of the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
BASE COUNT      212 a 298 c 258 g 272 t 161 others
ORIGIN
Query Match      80.0%; Score 20; DB 9; Length 1201;
Best Local Similarity 90.9%; Pred. No. 6.5e+02;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      4 CAGCTTCTTCTGTACAACTTGT 25
      :|||||
Db      41 CAGCTTCTTCTGTACAAAGTKGT 20

RESULT 34

```

Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 3974.f For more information about this cluster, see <http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DB015ZG02FP1&cluster=3974.f>. Contact : Feng Liang Email : fliang@lifetech.com URL : <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0DB015ZG02FP1.

FEATURES

source

1. 959
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DB015ZG02"
/tissue_type="NEUROBLASTOMA"
/clone_lib="Homo sapiens NEUROBLASTOMA"
/note="Vector: PCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the PCMVSPORT 6 vector. Library was not normalized."
Library was not normalized."

BASE COUNT 210 a 203 c 232 g 227 t 87 others
ORIGIN

Query Match 80.0%; Score 20; DB 9; Length 959;
Best Local Similarity 90.9%; Pred. No. 6.2e+02;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCTTCTTGTTACAAACTTGT 25

Db 38 CAGCTTCTTGTTACAAAGTGT 17

RESULT 29

AL550767/c

LOCUS 1060 bp mRNA linear EST 31-MAY-2003
DEFINITION Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI056YC22 5-PRIME, mRNA sequence.

AL550767

AL550767.2 GI:31272584

EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1060)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished

On Feb 15, 2001 this sequence version replaced gi:12888058.

COMMENT

Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 629.f For more information about this cluster, see

<http://www.genoscope.cns.fr/>

<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0DI056BB11Q1P1.

FEATURES

source

1. 1060
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI056YC22"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoRV into the Not I and EcoRV

BASE COUNT

ORIGIN

243 a 276 c 226 g 257 t 58 others
sites of the PCMVSPORT 6 vector. Library was normalized."

Query Match

Best Local Similarity 80.0%; Score 20; DB 9; Length 1060;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCTTCTTGTTACAAACTTGT 25

Db 40 CAGCTTCTTGTTACAAACTTGT 19

RESULT 30

BX338865/c

LOCUS 1084 bp mRNA linear EST 02-MAY-2003
DEFINITION Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI064YH04 5-PRIME, mRNA sequence.

BX338865

BX338865.1 GI:30335745

EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1084)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5957.f For more information about this cluster, see

<http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DI064DD02Q1P1&cluster=5957.f>. Contact :

Feng Liang Email : fliang@lifetech.com URL :

<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600

Faraday Avenue Genoscope Sequence ID : CS0DI064DD02Q1P1.

FEATURES

source

1. 1084
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI064YH04"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoRV into the Not I and EcoRV sites of the PCMVSPORT 6 vector. Library was normalized."
sites of the PCMVSPORT 6 vector. Library was normalized."

BASE COUNT 207 a 276 c 314 g 250 t 37 others

ORIGIN

Query Match 80.0%; Score 20; DB 13; Length 1084;

Best Local Similarity 90.9%; Pred. No. 6.3e+02;

Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCTTCTTGTTACAAACTTGT 25

Db 33 CAGCTTCTTGTTACAAACTTGT 12

RESULT 31

BX374761/c

LOCUS 1190 bp mRNA linear EST 08-MAY-2003
DEFINITION Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
cDNA clone CS0DC002YE05 5-PRIME, mRNA sequence.

BX374761

BX374761.1 GI:30452336

EST.

KEYWORDS

```

source
1. .897
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSDDP027YH18"
/tissue_type="fetal"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo (dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
BASE COUNT 193 a 211 c 216 g 276 t 1 others
ORIGIN

Query Match 80.0%; Score 20; DB 9; Length 897;
Best Local Similarity 90.9%; Pred. No. 6.1e+02;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CAGCTTTCTTGTACAAACTTGT 25
|:|||||:|||||:|||||:|||||:
Db 30 CWGCTTTTGTACAAACTTGT 9

RESULT 26
BX395287 910 bp mRNA linear EST 13-MAY-2003
LOCUS
DEFINITION BX395287 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens
cDNA clone CSDD004YF19 5-PRIME, mRNA sequence.
ACCESSION BX395287
VERSION BX395287.1 GI:30624532
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1. (bases 1 to 910)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSDD004YF19.

FEATURES
source
Location/Qualifiers
1. .910
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSDD004YF19"
/tissue_type="NEUROBLASTOMA COT 50-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoRV
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 238 a 302 c 74 g 233 t 63 others
ORIGIN

Query Match 80.0%; Score 20; DB 13; Length 910;
Best Local Similarity 90.9%; Pred. No. 6.1e+02;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CAGCTTTCTTGTACAAACTTGT 25
|:|||||:|||||:|||||:|||||:
Db 825 CAGCTTTCTTGTACAAACTTGT 846

```

```

RESULT 27
BX334648/c
LOCUS
DEFINITION BX334648 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSODI005YI06 5-PRIME, mRNA sequence.
ACCESSION BX334648
VERSION BX334648.1 GI:30341342
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1. (bases 1 to 933)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 334.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODI005BE03QPI&cluster=334.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODI005BE03QPI.

FEATURES
source
Location/Qualifiers
1. .933
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI005YI06"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoRV
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 254 a 212 c 238 g 227 t 2 others
ORIGIN

Query Match 80.0%; Score 20; DB 13; Length 933;
Best Local Similarity 90.9%; Pred. No. 6.1e+02;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CAGCTTTCTTGTACAAACTTGT 25
|:|||||:|||||:|||||:|||||:
Db 38 CAGCTTTTGTACAAACTTGT 17

RESULT 28
AL514767/c
LOCUS
DEFINITION AL514767 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
CLOBB0152G02 3-PRIME, mRNA sequence.
ACCESSION AL514767
VERSION AL514767.2 GI:30464652
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1. (bases 1 to 959)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT On Feb 13, 2001 this sequence version replaced gi:12778260.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr

```

```

Query Match      80.8%; Score 20.2; DB 13; Length 991;
Best Local Similarity 88.0%; Pred. No. 5.1e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTGACAACTTGT 25
   ||| ||||| ||||| ||||| |||||
Db 50 GTCTCGCTTTGTGTGACAACTTGT 26

RESULT 23
BX428996/c
LOCUS
DEFINITION
  BX428996 Homo sapiens B CELLS (RAMOS CELL LINE) Homo sapiens cDNA
  clone CS0DG005YF18 5-PRIME, mRNA sequence.
ACCESSION
  BX428996
VERSION
  BX428996.1 GI:30780782
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  Full-length cDNA libraries and normalization
  Unpublished
  Contact: Genoscope
  Genoscope - Centre National de Sequencage
  BP 191 91006 EVRY cedex - France
  Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
  Library was constructed by Life Technologies, a division of
  Invitrogen. This sequence belongs to sequence cluster 7333.f For
  more information about this cluster, see
  http://www.genoscope.cns.fr/
  cgi-bin/cluster.cgi?seq=CS0AS009ZC07QP1&cluster=7333.f. Contact :
  Feng Liang Email : fliang@lifetech.com URL :
  http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
  Faraday Avenue Genoscope sequence ID : CS0AS009ZC07QP1.
  Location/Qualifiers
    1..1006
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="CS0DG005YF18"
    /tissue_type="B CELLS (RAMOS CELL LINE)"
    /cell_line="RAMOS CELL LINE"
    /clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE)"
    /notes="Vector: pCMVSPORT 6; 1st strand cDNA was primed
    with a NotI-oligo(GT) primer. Five prime end enriched,
    double-strand cDNA was digested with NotI and cloned into
    the NotI and EcoRV sites of the pCMVSPORT 6 vector.
    Library was not normalized."
  Library was not normalized."
BASE COUNT      268 a 231 c 306 g 190 t 11 others
ORIGIN
  1..1006
  /organism="Homo sapiens"
  /mol_type="mRNA"
  /db_xref="taxon:9606"
  /clone="CS0DG005YF18"
  /tissue_type="B CELLS (RAMOS CELL LINE)"
  /cell_line="RAMOS CELL LINE"
  /clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE)"
  /notes="Vector: pCMVSPORT 6; 1st strand cDNA was primed
  with a NotI-oligo(GT) primer. Five prime end enriched,
  double-strand cDNA was digested with NotI and cloned into
  the NotI and EcoRV sites of the pCMVSPORT 6 vector.
  Library was not normalized."
  Library was not normalized."
Query Match      80.8%; Score 20.2; DB 13; Length 1006;
Best Local Similarity 88.0%; Pred. No. 5.1e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTGACAACTTGT 25
   ||| ||||| ||||| ||||| |||||
Db 42 GTCTCGCTTTGTGTGACAACTTGT 18

RESULT 24
BX333971/c
LOCUS
DEFINITION
  BX333971 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens
  cDNA clone CS0DD004YN23 5-PRIME, mRNA sequence.
ACCESSION
  BX333971
VERSION
  BX333971.1 GI:30337270
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  Full-length cDNA libraries and normalization
  Unpublished
  Contact: Genoscope
  Genoscope - Centre National de Sequencage
  BP 191 91006 EVRY cedex - France
  Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
  Library was constructed by Life Technologies, a division of
  Invitrogen. This sequence belongs to sequence cluster 1734.r For
  more information about this cluster, see
  http://www.genoscope.cns.fr/
  cgi-bin/cluster.cgi?seq=CS0DF027DD09QPl&cluster=1734.r. Contact :
  Feng Liang Email : fliang@lifetech.com URL :
  http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
  Faraday Avenue Genoscope sequence ID : CS0DF027DD09QPl.
  Location/Qualifiers
    894 bp
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="CS0DD004YN23"
    /tissue_type="NEUROBLASTOMA COT 50-NORMALIZED"
    /clone_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"
    /note="1st strand cDNA was primed with a NotI-oligo(dT)
    primer. Five prime end enriched, double-strand cDNA was
    digested with NotI and cloned into the NotI and EcoRV
    sites of the pCMVSPORT 6 vector. Library was normalized."
  Library was normalized."
BASE COUNT      148 a 332 c 233 g 173 t 8 others
ORIGIN
  1..894
  /organism="Homo sapiens"
  /mol_type="mRNA"
  /db_xref="taxon:9606"
  /clone="CS0DD004YN23"
  /tissue_type="NEUROBLASTOMA COT 50-NORMALIZED"
  /clone_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"
  /note="1st strand cDNA was primed with a NotI-oligo(dT)
  primer. Five prime end enriched, double-strand cDNA was
  digested with NotI and cloned into the NotI and EcoRV
  sites of the pCMVSPORT 6 vector. Library was normalized."
  Library was normalized."
Query Match      80.0%; Score 20; DB 13; Length 894;
Best Local Similarity 90.9%; Pred. No. 6.1e+02;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCTTTCTGTGACAACTTGT 25
   ||| ||||| ||||| ||||| |||||
Db 37 CWGCTTTTGTGTGACAACTTGT 16

RESULT 25
AL538354/c
LOCUS
DEFINITION
  AL538354 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
  CS0DF027YH18 5-PRIME, mRNA sequence.
ACCESSION
  AL538354
VERSION
  AL538354.2 GI:31262948
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  Full-length cDNA libraries and normalization
  Unpublished
  Contact: Genoscope
  Genoscope - Centre National de Sequencage
  BP 191 91006 EVRY cedex - France
  Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
  Library was constructed by Life Technologies, a division of
  Invitrogen. This sequence belongs to sequence cluster 1734.r For
  more information about this cluster, see
  http://www.genoscope.cns.fr/
  cgi-bin/cluster.cgi?seq=CS0DF027DD09QPl&cluster=1734.r. Contact :
  Feng Liang Email : fliang@lifetech.com URL :
  http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
  Faraday Avenue Genoscope sequence ID : CS0DF027DD09QPl.
  Location/Qualifiers
    897 bp
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="CS0DF027YH18"
    /tissue_type="FETAL BRAIN"
    /clone_lib="Homo sapiens FETAL BRAIN"
    /note="5-PRIME, mRNA sequence."
  Library was not normalized."
BASE COUNT      148 a 332 c 233 g 173 t 8 others
ORIGIN
  1..897
  /organism="Homo sapiens"
  /mol_type="mRNA"
  /db_xref="taxon:9606"
  /clone="CS0DF027YH18"
  /tissue_type="FETAL BRAIN"
  /clone_lib="Homo sapiens FETAL BRAIN"
  /note="5-PRIME, mRNA sequence."
  Library was not normalized."
Query Match      80.0%; Score 20; DB 13; Length 894;
Best Local Similarity 90.9%; Pred. No. 6.1e+02;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCTTTCTGTGACAACTTGT 25
   ||| ||||| ||||| ||||| |||||
Db 37 CWGCTTTTGTGTGACAACTTGT 16

RESULT 26
AL538354/c
LOCUS
DEFINITION
  AL538354 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
  CS0DF027YH18 5-PRIME, mRNA sequence.
ACCESSION
  AL538354
VERSION
  AL538354.2 GI:31262948
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  Full-length cDNA libraries and normalization
  Unpublished
  Contact: Genoscope
  Genoscope - Centre National de Sequencage
  BP 191 91006 EVRY cedex - France
  Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
  Library was constructed by Life Technologies, a division of
  Invitrogen. This sequence belongs to sequence cluster 1734.r For
  more information about this cluster, see
  http://www.genoscope.cns.fr/
  cgi-bin/cluster.cgi?seq=CS0DF027DD09QPl&cluster=1734.r. Contact :
  Feng Liang Email : fliang@lifetech.com URL :
  http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
  Faraday Avenue Genoscope sequence ID : CS0DF027DD09QPl.
  Location/Qualifiers
    897 bp
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="CS0DF027YH18"
    /tissue_type="FETAL BRAIN"
    /clone_lib="Homo sapiens FETAL BRAIN"
    /note="5-PRIME, mRNA sequence."
  Library was not normalized."
BASE COUNT      148 a 332 c 233 g 173 t 8 others
ORIGIN
  1..897
  /organism="Homo sapiens"
  /mol_type="mRNA"
  /db_xref="taxon:9606"
  /clone="CS0DF027YH18"
  /tissue_type="FETAL BRAIN"
  /clone_lib="Homo sapiens FETAL BRAIN"
  /note="5-PRIME, mRNA sequence."
  Library was not normalized."

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ACCESSION      BX457051
VERSION        BX457051.1  GI:31034832
KEYWORDS
SOURCE
ORGANISM       Homo sapiens (human)
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS       Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE          1 (bases 1 to 956)
JOURNAL        Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
COMMENT        Full-length cDNA libraries and normalization
               Unpublished
               Contact: Genoscope
               Genoscope - Centre National de Sequencage
               BP 191 91006 EVRY cedex - France
               Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
               Library was constructed by Life Technologies, a division of
               Invitrogen. This sequence belongs to sequence cluster 6437.r For
               more information about this cluster, see
               http://www.genoscope.cns.fr/
               cgi-bin/cluster.cgi?seq=CS0CAP005DH01QP1&cluster=6437.r. Contact :
               Peng Liang Email : fliang@lifetech.com URL :
               http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
               Faraday Avenue Genoscope sequence ID : CS0CAP005DH01QP1.
FEATURES
source
1. .956
   /organism="Homo sapiens"
   /mol_type="mRNA"
   /db_xref="taxon:9606"
   /clone="CS0CAP005YP02"
   /tissue_type="THYMUS"
   /clone_lib="Homo sapiens THYMUS"
   /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
   with a NotI-oligo(dT) primer. Five prime end enriched,
   double-strand cDNA was digested with Not I and cloned into
   the Not I and EcoRV sites of the pCMVSPORT 6 vector.
   Library was not normalized."
BASE COUNT    209 a 286 c 234 g 220 t 7 others
ORIGIN
Query Match      80.8%; Score 20.2; DB 13; Length 956;
Best Local Similarity 88.0%; Pred. No. 5.1e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGACAACTTGT 25
Db 40 GCTCTGCTTTTGTACAACTTGT 16

RESULT 21
BX422399/c
LOCUS          BX422399 Homo sapiens FETAL LIVER Homo sapiens cDNA clone
DEFINITION    CS0DM004YD15 5-PRIME, mRNA sequence.
ACCESSION     BX422399
VERSION       BX422399.1  GI:30655319
KEYWORDS
SOURCE        Homo sapiens (human)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 973)
AUTHORS       Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE         Full-length cDNA libraries and normalization
JOURNAL       Unpublished
COMMENT       Contact: Genoscope
               Genoscope - Centre National de Sequencage
               BP 191 91006 EVRY cedex - France
               Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
               Library was constructed by Life Technologies, a division of
               Invitrogen. This sequence belongs to sequence cluster 7228.f For
               more information about this cluster, see
               http://www.genoscope.cns.fr/
               cgi-bin/cluster.cgi?seq=CS0DM004CE08QP1&cluster=7228.f. Contact :

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Peng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DM004CE08QP1.
FEATURES
source
1. .973
   /organism="Homo sapiens"
   /mol_type="mRNA"
   /db_xref="taxon:9606"
   /clone="CS0DM004YD15"
   /tissue_type="FETAL LIVER"
   /dev_stage="fetal"
   /clone_lib="Homo sapiens FETAL LIVER"
   /note="Organ: liver; Vector: pCMVSPORT 6; 1st strand cDNA
   was primed with a NotI-oligo(dT) primer. Five prime end
   enriched, double-strand cDNA was digested with Not I and
   cloned into the Not I and EcoRV sites of the pCMVSPORT 6
   vector. Library was not normalized."
BASE COUNT    287 a 205 c 218 g 260 t 3 others
ORIGIN
Query Match      80.8%; Score 20.2; DB 13; Length 973;
Best Local Similarity 88.0%; Pred. No. 5.1e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGACAACTTGT 25
Db 29 GCTCTGCTTTTGTACAACTTGT 5

RESULT 22
BX345037/c
LOCUS          BX345037 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
DEFINITION    Homo sapiens cDNA clone CS0DL007YB19 5-PRIME, mRNA sequence.
ACCESSION     BX345037
VERSION       BX345037.1  GI:30340331
KEYWORDS
SOURCE        Homo sapiens (human)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 991)
AUTHORS       Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE         Full-length cDNA libraries and normalization
JOURNAL       Unpublished
COMMENT       Contact: Genoscope
               Genoscope - Centre National de Sequencage
               BP 191 91006 EVRY cedex - France
               Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
               Library was constructed by Life Technologies, a division of
               Invitrogen. This sequence belongs to sequence cluster 6450.f For
               more information about this cluster, see
               http://www.genoscope.cns.fr/
               cgi-bin/cluster.cgi?seq=CS2BAX17ZG05_AX28ZC12_1&cluster=6450.f.
               Contact : Peng Liang Email : fliang@lifetech.com URL :
               http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
               Faraday Avenue Genoscope sequence ID : CS2BAX17ZG05_AX28ZC12_1.
FEATURES
source
1. .991
   /organism="Homo sapiens"
   /mol_type="mRNA"
   /db_xref="taxon:9606"
   /clone="CS0DL007YB19"
   /cell_type="B CELLS (RAMOS CELL LINE)"
   /cell_line="RAMOS CELL LINE"
   /clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT
   25-NORMALIZED"
   /note="1st strand cDNA was primed with a NotI-oligo(dT)
   primer. Five prime end enriched, double-strand cDNA was
   digested with Not I and cloned into the Not I and EcoRV
   sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT    170 a 274 c 100 g 441 t 6 others
ORIGIN

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5261647"
/tissue_type="hippocampus"
/lab_host="DH10B"
/clone_lib="NIH_MGC_95"
/notes="Organ: brain; Vector: pBluescriptPR (modified pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTNN-3', size-selected for average insert size 2.5 kb and normalized to R0T 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT 259 a 131 c 194 g 233 t
ORIGIN

Query Match 80.8%; Score 20.2; DB 12; Length 817;
Best Local Similarity 88.0%; Pred. No. 4.9e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTACAAACTTGT 25
Db 542 GTTCAAATTTCTGTACAAATTTGT 566

RESULT 18
BF669965 884 bp mRNA linear EST 21-DEC-2000
LOCUS 602118471F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4275664 5',
DEFINITION mRNA sequence.
ACCESSION BF669965
VERSION BF669965.1 GI:11943860
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 884)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1094 row: n column: 17
High quality sequence stop: 589.
Location/Qualifiers
1. .884
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4275664"
/tissue_type="primitive neuroectoderm"
/lab_host="DH10B (TI phage-resistant)"
/clone_lib="NIH_MGC_56"
/notes="Organ: brain; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggcgctcgcc); Site 2: SfiI (ggcgattatggc); SfiI (ggcgctcgcc); Site 2: SfiI (ggcgattatggc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence: 5'-ATTCAGAGCGGCGGCGGACATG-DT(30)BN-3' (where B = A, C, G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for

full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
BASE COUNT 240 a 155 c 247 g 242 t
ORIGIN

Query Match 80.8%; Score 20.2; DB 10; Length 884;
Best Local Similarity 88.0%; Pred. No. 5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTACAAACTTGT 25
Db 534 GTTAACTTTCTGTACAAATTTGT 558

RESULT 19
AL519260/c 914 bp mRNA linear EST 12-MAY-2003
LOCUS AL519260 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
DEFINITION CSODA012YH14 5-PRIME, mRNA sequence.
ACCESSION AL519260
VERSION AL519260.2 GI:30538367
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 914)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT On Feb 13, 2001 this sequence version replaced gi:12782753.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segre@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 3874.r For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODA012DD07QP1&cluster=3874.r. Contact:
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID: CSODA012DD07QP1.
Location/Qualifiers
1. .914
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODA012YH14"
/tissue_type="NEUROBLASTOMA"
/clone_lib="Homo sapiens NEUROBLASTOMA"
/notes="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector.. Library was not normalized."
BASE COUNT 186 a 310 c 254 g 156 t
ORIGIN

Query Match 80.8%; Score 20.2; DB 9; Length 914;
Best Local Similarity 88.0%; Pred. No. 5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTACAAACTTGT 25
Db 39 GCTCTGCTTTTGTACAAACTTGT 15

RESULT 20
BX457051/c 956 bp mRNA linear EST 22-MAY-2003
LOCUS BX457051 Homo sapiens THYMUS Homo sapiens cDNA clone CSOCAP005YP02
DEFINITION 5-PRIME, mRNA sequence.

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BG573114      706 bp      mRNA      linear      EST 10-APR-2001
LOCUS         602594115F1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4721474 5',
DEFINITION    mRNA sequence.
ACCESSION     BG573114
VERSION       BG573114.1 GI:13580767
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 706)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL       Unpublished
COMMENT       Contact: Robert Strausberg, Ph.D.
              Email: cgabs-r@mail.nih.gov
              Tissue Procurement: CLONTECH Laboratories, Inc.
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LCM1577 row: n column: 03
              High quality sequence stop: 639.
              Location/Qualifiers
                1..706
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:4721474"
                /lab_host="DH10B (T1 phage-resistant)"
                /note="Organ: placenta; Vector: pDNR-LIB (Clontech);
                Site 1: SfiI (ggcgctcgcc); Site 2: SfiI (ggcattatggcc
                ); 5' and 3' adaptors were used in cloning as follows: 5'
                adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor
                sequence: 5'-ATTCTAGAGCGCGCGCGCATG-dt(30)BN-3',
                (where B = A, C, or G and N = A, C, G, or T). Average
                insert size 1.3 kb (range 0.5-4.0 kb). 15/15 colonies
                contained inserts by PCR. This library was enriched for
                full-length clones and was constructed by Clontech
                Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
                Library."
              BASE COUNT      205 a      117 c      143 g      241 t
              ORIGIN
                Query Match      80.8%; Score 20.2; DB 10; Length 706;
                Best Local Similarity 88.0%; Pred. No. 4.7e+02;
                Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

              QY      1 GTTCAGCTTTCTTGTACAAACTTGT 25
                ||| ||||| ||||| ||||| |||||
              Db      186 GTTAAACTTTCTTGTACAAATTGT 210

              RESULT 16
              BF695849      812 bp      mRNA      linear      EST 22-DEC-2000
              LOCUS         601852207F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076328 5',
              DEFINITION    mRNA sequence.
              ACCESSION     BF695849
              VERSION       BF695849.1 GI:11981257
              KEYWORDS      EST.
              SOURCE        Homo sapiens (human)
              ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
              REFERENCE     1 (bases 1 to 812)
              AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
              TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
              JOURNAL       Unpublished

              BASE COUNT      205 a      117 c      143 g      241 t
              ORIGIN
                Query Match      80.8%; Score 20.2; DB 10; Length 706;
                Best Local Similarity 88.0%; Pred. No. 4.7e+02;
                Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

              QY      1 GTTCAGCTTTCTTGTACAAACTTGT 25
                ||| ||||| ||||| ||||| |||||
              Db      186 GTTAAACTTTCTTGTACAAATTGT 210

              RESULT 16
              BF695849      812 bp      mRNA      linear      EST 22-DEC-2000
              LOCUS         601852207F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076328 5',
              DEFINITION    mRNA sequence.
              ACCESSION     BF695849
              VERSION       BF695849.1 GI:11981257
              KEYWORDS      EST.
              SOURCE        Homo sapiens (human)
              ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
              REFERENCE     1 (bases 1 to 812)
              AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
              TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
              JOURNAL       Unpublished

```

```

COMMENT       Contact: Robert Strausberg, Ph.D.
              Email: cgabs-r@mail.nih.gov
              Tissue Procurement: ATCC
              cDNA Library Arrayed by: CLONTECH Laboratories, Inc.
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LCM929 row: m column: 01
              High quality sequence stop: 637.
              Location/Qualifiers
                1..812
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:4076328"
                /tissue_type="primitive neuroectoderm"
                /lab_host="DH10B (T1 phage-resistant)"
                /clone_lib="NIH_MGC 56"
                /note="Organ: brain; Vector: pDNR-LIB (Clontech); Site 1:
                SfiI (ggcgctcgcc); Site 2: SfiI (ggcattatggcc);
                Double-stranded cDNA was prepared from cell line RNA. 5'
                and 3' adaptors were used in cloning as follows: 5'
                adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor
                sequence: 5'-ATTCTAGAGCGCGCGCGCATG-dt(30)BN-3',
                (where B = A, C, or G and N = A, C, G, or T). Average
                insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies
                contained inserts by PCR. This library was enriched for
                full-length clones and was constructed by Clontech
                Laboratories (Palo Alto, CA)."
              BASE COUNT      259 a      113 c      221 g      219 t
              ORIGIN
                Query Match      80.8%; Score 20.2; DB 10; Length 812;
                Best Local Similarity 88.0%; Pred. No. 4.9e+02;
                Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

              QY      1 GTTCAGCTTTCTTGTACAAACTTGT 25
                ||| ||||| ||||| ||||| |||||
              Db      535 GTTAAACTTTCTTGTACAAATTGT 559

              RESULT 17
              BI547007      817 bp      mRNA      linear      EST 05-SEP-2001
              LOCUS         603190229F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5361647 5',
              DEFINITION    mRNA sequence.
              ACCESSION     BI547007
              VERSION       BI547007.1 GI:15434319
              KEYWORDS      EST.
              SOURCE        Homo sapiens (human)
              ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
              REFERENCE     1 (bases 1 to 817)
              AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
              TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
              JOURNAL       Unpublished
              COMMENT       Contact: Robert Strausberg, Ph.D.
              Email: cgabs-r@mail.nih.gov
              Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
              cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
              Toshiyuki and Piero Carninci (RIKEN)
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LLM11659 row: i column: 08
              High quality sequence stop: 795.
              Location/Qualifiers
                1..817

```

TITLE
JOURNAL
COMMENT

Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6911.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DC019BC08QP1&cluster=6911.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DC019BC08QP1.

FEATURES

source

Location/Qualifiers
1..1145
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DC019YE16"
/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 298 a 226 c 244 g 308 t 69 others

ORIGIN

Query Match 81.6%; Score 20.4; DB 13; Length 1145;
Best Local Similarity 95.5%; Pred. No. 4.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCTTTCTTGTAACAACCTTGT 25

Db 39 CAGCTTTCTTGTAACAACCTTGT 18

RESULT 13

BX361644/c

LOCUS 1201 bp mRNA linear EST 05-MAY-2003
DEFINITION BX361644 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
Homo sapiens cDNA clone CS0DJ001YF12 5-PRIME, mRNA sequence.

ACCESSION BX361644

VERSION BX361644.1 GI:30366552

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1201)

AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished

COMMENT

Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7763.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DJ001DC06QP1&cluster=7763.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DJ001DC06QP1.

FEATURES

source

Location/Qualifiers
1..1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DJ001YE12"
/cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"

/cell_line="JURKAT"
/clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT
10-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 278 a 308 c 341 g 205 t 69 others

ORIGIN

Query Match 81.6%; Score 20.4; DB 13; Length 1201;
Best Local Similarity 95.5%; Pred. No. 4.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCTTTCTTGTAACAACCTTGT 25

Db 35 CAGCTTTCTTGTAACAACCTTGT 14

RESULT 14

B1858895

LOCUS 645 bp mRNA linear EST 10-OCT-2001

DEFINITION 603389227F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:5398255 5',

RNA sequence.

ACCESSION B1858895

VERSION B1858895.1 GI:15999642

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 645)

AUTHORS NIH-MGC http://mgc.ncbi.nlm.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: DCTD/DP
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM12015 row: e column: 08

High quality sequence stop: 643.

FEATURES

Location/Qualifiers

1..645

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5398255"

/tissue_type="mammary adenocarcinoma, cell line"

/lab_host="PH108 (phage-resistant)"

/clone_lib="NIH_MGC_87"

/note="Organ: breast; Vector: pCMV-SPORT6; Site: 1: NotI;
Site: 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.383 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

BASE COUNT 217 a 97 c 159 g 173 t

ORIGIN

Query Match 80.8%; Score 20.2; DB 12; Length 645;
Best Local Similarity 88.0%; Pred. No. 4.6e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGTAACAACCTTGT 25

Db 524 GTTAAACTTTCTTGTAACAACCTTGT 548

RESULT 15

FEATURES
source

Location/Qualifiers
1. .934
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODF014YA08"
/tissue_type="FETAL BRAIN"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."
BASE COUNT 233 a 233 c 278 g 189 t 1 others
ORIGIN

Query Match 81.6%; Score 20.4; DB 13; Length 934;
Best Local Similarity 95.5%; Pred. No. 4.2e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CAGCTTCTTGTACAACTTGT 25
|||||
Db 35 CAGCTTTTGTACAACTTGT 14

RESULT 10
BX359829/c
LOCUS
DEFINITION BX359829 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSODI062YG23 5-PRIME, mRNA sequence.
ACCESSION BX359829
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1092)
Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6269.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODI062AD12QF1&cluster=6269.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODI062AD12QF1.

FEATURES
source

Location/Qualifiers
1. .1092
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI062YG23"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 237 a 268 c 322 g 207 t 58 others
ORIGIN

Query Match 81.6%; Score 20.4; DB 13; Length 1092;
Best Local Similarity 95.5%; Pred. No. 4.3e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CAGCTTCTTGTACAACTTGT 25
|||||
Db 36 CAGCTTTTGTACAACTTGT 15

RESULT 11
AL515449/c
LOCUS
DEFINITION AL515449 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
clone CLOBB018ZD09 3-PRIME, mRNA sequence.
ACCESSION AL515449
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1097)
Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 13, 2001 this sequence version replaced gi:12778942.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3923.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CLOBB018ZD09FP1&cluster=3923.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CLOBB018ZD09FP1.

FEATURES
source
Location/Qualifiers
1. .1097
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CLOBB018ZD09"
/tissue_type="NEUROBLASTOMA"
/clone_lib="Homo sapiens NEUROBLASTOMA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."
BASE COUNT 250 a 249 c 312 g 249 t 37 others
ORIGIN

Query Match 81.6%; Score 20.4; DB 9; Length 1097;
Best Local Similarity 95.5%; Pred. No. 4.3e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CAGCTTCTTGTACAACTTGT 25
|||||
Db 39 CAGCTTTTGTACAACTTGT 18

RESULT 12
BX394655/c
LOCUS
DEFINITION BX394655 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
cDNA clone CSODC019YE16 5-PRIME, mRNA sequence.
ACCESSION BX394655
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1145)
Li.W.B., Gruber,C., Jessee,J. and Polayes,D.

```

QY      4 CAGCTTCTTGACAACTTGT 25
Db      36 CTGCTTCTTGACAACTTGT 15

RESULT 7
BG775435      821 bp      mRNA      linear      EST 15-MAY-2001
DEFINITION    602649314T1 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:4760955 3',
              mRNA sequence.
ACCESSION     BG775435
VERSION       BG775435.1 GI:14045752
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens

REFERENCE     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS       Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE         NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL       National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT       Unpublished
              Contact: Robert Strausberg, Ph.D.
              Email: cgapbs@mail.nih.gov
              Tissue Procurement: DCTP/DTP
              cDNA Library Preparation: Ling Hong/Rubin Laboratory
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LLCM1612 row: k column: 04
              High quality sequence start: 2
              High quality sequence stop: 816.

FEATURES     Location/Qualifiers
              1..821
               /organism="Homo sapiens"
               /mol_type="mRNA"
               /db_xref="taxon:9606"
               /clone="IMAGE:4760955"
               /tissue_type="carcinoma, cell line"
               /lab_host="DH10B (phage-resistant)"
               /note="Organ: prostate; Vector: pOTB7; Site 1: XhoI;
               Site 2: EcoRI; cDNA made by oligo-dT priming.
               Directionally cloned into EcoRI/XhoI sites using the
               following 5' adaptor: GGCACGAG(G). Library constructed by
               Ling Hong in the laboratory of Gerald M. Rubin (University
               of California, Berkeley) using ZAP-cDNA synthesis kit
               (Stratagene) and Superscript II RT (Life Technologies).
               Note: this is a NIH MGC Library."
BASE COUNT    202 a 200 c 214 g 205 t
ORIGIN
Query Match    81.6%; Score 20.4; DB 12; Length 821;
Best Local Similarity 95.8%; Pred. No. 4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 CAGCTTCTTGACAACTTGT 25
Db      735 CTGCTTCTTGACAACTTGT 756

RESULT 8
AL536575/c     917 bp      mRNA      linear      EST 31-MAY-2003
LOCUS          AL536575
DEFINITION     CS0DF038YL18 5-PRIME, mRNA sequence.
ACCESSION     AL536575
VERSION       AL536575.2 GI:31261203
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens

Query Match    81.6%; Score 20.4; DB 12; Length 821;
Best Local Similarity 95.8%; Pred. No. 4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 917)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 13, 2001 this sequence version replaced gi:12800068.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2189.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DF038DF09QPl&cluster=2189.r. Contact :
Peng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DF038DF09QPl.

FEATURES
source

1..917
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DF038YL18"
/tissue_type="FETAL BRAIN"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
BASE COUNT 230 a 214 c 222 g 240 t 11 others
ORIGIN

Query Match 81.6%; Score 20.4; DB 9; Length 917;
Best Local Similarity 95.5%; Pred. No. 4.1e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCTTCTTGACAACTTGT 25
Db 32 CAGCTTCTTGACAACTTGT 11

RESULT 9
LOCUS

BX441089/c
BX441089 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
CS0DF014YA08 5-PRIME, mRNA sequence.
ACCESSION BX441089
VERSION BX441089.1 GI:30789927
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 934)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2850.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DF014BA04QPl&cluster=2850.r. Contact :
Peng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DF014BA04QPl.

TITLE A protein-protein interaction map of the Caenorhabditis elegans 26S

JOURNAL
MEDLINE
PUBMED

EMBO Rep. 2 (9), 821-828 (2001)
21443405

COMMENT

11559592
Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc.Vidal@dfci.harvard.edu
Trace dvpl6v51.x with Bait unknown
POLYA=No.

FEATURES

source

Location/Qualifiers

1. 598
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"

/note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

BASE COUNT 169 a 139 c 146 g 144 t

ORIGIN

Query Match 81.6%; Score 20.4; DB 14; Length 598;
Best Local Similarity 95.5%; Pred. No. 3.7e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CAGCTTTCTTGTACAAACTTGT 25

Db 106 CTGCTTTCTTGTACAAACTTGT 85

RESULT 5

CB104084/c

LOCUS ADP SQ015096 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA linear EST 28-JAN-2003
DEFINITION ADP SQ015096 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION CB104084
VERSION CB104084.1 GI:27929891

KEYWORDS

EST.

SOURCE

Caenorhabditis elegans
Caenorhabditis elegans

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea

; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 668)

Davy, A., Bello, P., Thierry-Mieg, N., Vaglio, P., Hitti, J.,

Doucette-Stamm, L., Thierry-Mieg, D., Reboul, J., Boulton, S., Walhout

, A.J., Coux, O. and Vidal, M.

A protein-protein interaction map of the Caenorhabditis elegans 26S

proteasome

EMBO Rep. 2 (9), 821-828 (2001)

JOURNAL

MEDLINE

PUBMED

21443405

Contact: Vidal M

Marc Vidal Laboratory

Dana Farber Cancer Institute

1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA

Tel: 617 632 5180

Fax: 617 632 5739

Email: Marc.Vidal@dfci.harvard.edu

Trace dvpl6v66.x with Bait unknown

POLYA=No.

FEATURES

source

Location/Qualifiers

1. 668
/organism="Caenorhabditis elegans"

/mol_type="mRNA"

/strain="N2"

/db_xref="taxon:6239"

/sex="Hermaphrodite and male"

/tissue_type="whole animal"

/dev_stage="mixed stage"

/clone_lib="AD-wrmcDNA"

/note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

BASE COUNT 188 a 159 c 181 g 140 t

ORIGIN

Query Match 81.6%; Score 20.4; DB 14; Length 668;
Best Local Similarity 95.5%; Pred. No. 3.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CAGCTTTCTTGTACAAACTTGT 25

Db 106 CTGCTTTCTTGTACAAACTTGT 85

RESULT 6

AL557510/c

LOCUS

AL557510 Homo sapiens T CELLS (JURKAT CELL LINE) Homo sapiens cDNA clone CS0DH006YE16 5-PRIME, mRNA sequence.

ACCESSION

AL557510

VERSION

AL557510.2

GI:31279310

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 801)

Li, W.B., Gruber, C., Jesse, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished

On Feb 15, 2001 this sequence version replaced gi:12901183.

COMMENT

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 Evry cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

was not normalized. Library was constructed by Life Technologies, a

division of Invitrogen. This sequence belongs to sequence cluster

5973.r For more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0DH006BC08QPI&cluster=5973.r. Contact :

Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/Invitrogen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0DH006BC08QPI.

Location/Qualifiers

1. 801

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clones="CS0DH006YE16"

/tissue_type="T CELLS (JURKAT CELL LINE)"

/cell_line="JURKAT CELL LINE"

/clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE)"

/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed

with a NotI-oligo(dT) primer. Five prime end enriched,

double-strand cDNA was digested with Not I and cloned into

the Not I and EcoRV sites of the pCMVSPORT 6 vector.

Library was not normalized."

BASE COUNT 268 a 158 c 249 g 119 t

ORIGIN

Query Match 81.6%; Score 20.4; DB 9; Length 801;

Best Local Similarity 95.5%; Pred. No. 4e+02;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Faraday Avenue Genoscope sequence ID : CS0DD006BC04QP1.

FEATURES

source

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DD006YB08"
/tissue_type="NEUROBLASTOMA COT 50-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 287 a 364 c 324 g 172 t 54 others
ORIGIN

Query Match 84.8%; Score 21.2; DB 13; Length 1201;
Best Local Similarity 95.5%; Pred. No. 2e+02;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTCTTGTACAACTTGT 25
|:|||||
DB 33 CDGCTTCTTGTACAACTTGT 12

RESULT 2
BX329816 996 bp mRNA linear EST 02-MAY-2003
LOCUS
DEFINITION
CDNA clone CS0DD005YCL5 3-PRIME, mRNA sequence.

ACCESSION
BX329816
VERSION
BX329816.1 GI:30342879
KEYWORDS
EST.

SOURCE
Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 996)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished

CONTACT: Genoscope
Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 4354.f For
more information about this cluster, see

http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0BAK021BF12NM1&cluster=4354.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0BAK021BF12NM1.

FEATURES

source

1. .996
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DD005YCL5"
/tissue_type="NEUROBLASTOMA COT 50-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 212 a 291 c 107 g 373 t 13 others
ORIGIN

Query Match 83.2%; Score 20.8; DB 13; Length 996;
Best Local Similarity 91.7%; Pred. No. 2.9e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTCAGCTTCTTGTACAACTTGT 25

DB 425 TTCTGCTTTTGTACAACTTGT 448

FEATURES

source

AL515389 559 bp mRNA linear EST 08-MAY-2003
LOCUS
DEFINITION
AL515389 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
CL0BB019ZB04 3-PRIME, mRNA sequence.

ACCESSION
AL515389
VERSION
AL515389.2 GI:30465271
KEYWORDS
EST.

SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 559)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization
Unpublished

On Feb 13, 2001 this sequence version replaced gi:12778862.

CONTACT: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1606.r For
more information about this cluster, see

http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CL0BB019ZB04FP1&cluster=1606.r. Contact :

Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

Faraday Avenue Genoscope sequence ID : CL0BB019ZB04FP1.

Location/Qualifiers

FEATURES

source

1. .559
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CL0BB019ZB04"
/tissue_type="NEUROBLASTOMA"
/clone_lib="Homo sapiens NEUROBLASTOMA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
BASE COUNT 190 a 78 c 68 g 163 t 60 others
ORIGIN

Query Match 81.6%; Score 20.4; DB 9; Length 559;

Best Local Similarity 95.5%; Pred. No. 3.7e+02;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCTTCTTGTACAACTTGT 25

DB 40 CAGCTTCTTGTACAACTTGT 19

FEATURES

source

CB104071 598 bp mRNA linear EST 28-JAN-2003
LOCUS
DEFINITION
ADP SQ0150E3 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.

ACCESSION
CB104071
VERSION
CB104071.1 GI:27929878
KEYWORDS
EST.

SOURCE
Caenorhabditis elegans

ORGANISM
Caenorhabditis elegans

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea

; Rhabditidae; Peloderinae; Caenorhabditis.

1. (bases 1 to 598)

Davy, A., Bello, P., Thierry-Mieg, N., Vaglio, P., Hitti, J.,

Doucette-Stamm, L., Thierry-Mieg, D., Reboul, J., Boulton, S., Walhout

, A.J., Coux, O. and Vidal, M.

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 6, 2003, 22:08:13 ; Search time 1093.75 Seconds
(without alignments)
555.531 Million cell updates/sec

Title: US-10-055-001A-5

Perfect score: 25

Sequence: 1 gttcagctttctgtacaactgt 25

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_htc:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_htc:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: em_gss_hum:*
- 18: em_gss_inv:*
- 19: em_gss_pln:*
- 20: em_gss_vit:*
- 21: em_gss_fun:*
- 22: em_gss_mam:*
- 23: em_gss_mus:*
- 24: em_gss_pro:*
- 25: em_gss_rod:*
- 26: em_gss_phg:*
- 27: em_gss_vrl:*
- 28: gb_gss1:*
- 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
c 1	21.2	84.8	1201	13 BX376823	BX376823 BX376823
c 2	20.8	83.2	996	13 BX329816	BX329816 BX329816
c 3	20.4	81.6	559	9 AL515389	AL515389 AL515389
c 4	20.4	81.6	598	14 CB104071	CB104071 ADP_SQ015

c 5	20.4	81.6	668	14 CB104084	CB104084 ADP_SQ015
c 6	20.4	81.6	801	9 AL557510	AL557510 AL557510
c 7	20.4	81.6	821	12 BG775435	BG775435 602649914
c 8	20.4	81.6	917	9 AL536575	AL536575 AL536575
c 9	20.4	81.6	934	13 BX441089	BX441089 BX441089
c 10	20.4	81.6	1092	13 BX359829	BX359829 BX359829
c 11	20.4	81.6	1097	9 AL515449	AL515449 AL515449
c 12	20.4	81.6	1145	13 BX394655	BX394655 BX394655
c 13	20.4	81.6	1201	13 BX316144	BX316144 BX316144
c 14	20.2	80.8	645	12 BI858895	BI858895 603389227
c 15	20.2	80.8	706	10 BG573114	BG573114 602594115
c 16	20.2	80.8	812	10 BF695849	BF695849 601852207
c 17	20.2	80.8	817	12 BF547007	BF547007 603190329
c 18	20.2	80.8	884	10 BF669965	BF669965 602118471
c 19	20.2	80.8	914	9 AL519260	AL519260 AL519260
c 20	20.2	80.8	956	13 BX457051	BX457051 BX457051
c 21	20.2	80.8	973	13 BX422399	BX422399 BX422399
c 22	20.2	80.8	991	13 BX345037	BX345037 BX345037
c 23	20.2	80.8	1006	13 BX428996	BX428996 BX428996
c 24	20.2	80.8	894	13 BX333971	BX333971 BX333971
c 25	20.2	80.8	897	9 AL538354	AL538354 AL538354
c 26	20.2	80.8	910	13 BX395287	BX395287 BX395287
c 27	20.2	80.8	933	13 BX334648	BX334648 BX334648
c 28	20.2	80.8	959	9 AL514767	AL514767 AL514767
c 29	20.2	80.8	1060	9 AL550767	AL550767 AL550767
c 30	20.2	80.8	1084	13 BX338865	BX338865 BX338865
c 31	20.2	80.8	1190	13 BX374761	BX374761 BX374761
c 32	20.2	80.8	1198	13 BX463747	BX463747 BX463747
c 33	20.2	80.8	1201	9 AL513677	AL513677 AL513677
c 34	20.2	80.8	1201	9 AL514171	AL514171 AL514171
c 35	20.2	80.8	1201	9 AL544923	AL544923 AL544923
c 36	20.2	80.8	1201	9 AL554071	AL554071 AL554071
c 37	20.2	80.8	1201	13 BX363509	BX363509 BX363509
c 38	20.2	80.8	1201	13 BX382731	BX382731 BX382731
c 39	20.2	80.8	1201	13 BX386369	BX386369 BX386369
c 40	20.2	80.8	1201	13 BX400983	BX400983 BX400983
c 41	20.2	80.8	1201	13 BX463202	BX463202 BX463202
c 42	19.8	79.2	402	12 BM953409	BM953409 952062A07
c 43	19.8	79.2	427	10 BG410582	BG410582 947050F08
c 44	19.8	79.2	436	13 BQ163507	BQ163507 952079D01
c 45	19.8	79.2	459	13 BQ163217	BQ163217 952079D01

ALIGNMENTS

RESULT 1	BX376823/c	BX376823	Homo sapiens	1201 bp	linear	EST 08-MAY-2003
LOCUS	BX376823	Homo sapiens	NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens			
DEFINITION	CDNA clone CS0DD006YE08 5-PRIME, mRNA sequence.					
ACCESSION	BX376823					
VERSION	BX376823.1	GI:30442822				
KEYWORDS	EST.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
AUTHORS	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.					
TITLE	Full-length cDNA libraries and normalization					
JOURNAL	Unpublished					
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 2992.f For more information about this cluster, see http://www.genoscope.cns.fr/ cgi-bin/cluster.cgi?seq=CS0DD006BC04QPI&cluster=2992.f. Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600					

RESULT 38
US-09-732-914-45/C
; Sequence 45, Application US/09732914
; Patent No. US20020007051A1
; GENERAL INFORMATION:
; APPLICANT: Cheo, David
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Hartley, James L.
; APPLICANT: Byrd, Devon R.N.
; TITLE OF INVENTION: Use of Multiple Recombination Sites with Unique Specificity in
; FILE OF INVENTION: Recombinational Cloning
; FILE REFERENCE: 0942.5010002
; CURRENT APPLICATION NUMBER: US/09/732,914
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/169,983
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 60/188,020
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45
; LENGTH: 43
; TYPE: DNA
; ORGANISM: attR2 PCR Primer
US-09-732-914-45

Query Match 93.6%; Score 23.4; DB 9; Length 43;
Best Local Similarity 96.0%; Pred. No. 1.6;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTTGTACAAACTTGT 25
DB 29 GTTCAGCTTTCGTACAAACTTGT 5

RESULT 39
US-09-855-797A-42
; Sequence 42, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855,797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-855-797A-42

Query Match 90.4%; Score 22.6; DB 9; Length 25;
Best Local Similarity 76.0%; Pred. No. 3.1;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTTGTACAAACTTGT 25
DB 1 GTTCAGCTTTCGTACAAACTTGT 25

RESULT 40
US-09-907-900-42
; Sequence 42, Application US/09907900
; Patent No. US20020172997A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,900
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-900-42

Query Match 90.4%; Score 22.6; DB 10; Length 25;
Best Local Similarity 76.0%; Pred. No. 3.1;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTTGTACAAACTTGT 25
DB 1 GTTCAGCTTTCGTACAAACTTGT 25

Search completed: November 7, 2003, 02:22:25
Job time : 103.25 secs

```

; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/058,292
; FILING DATE: 30-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/432,085
; FILING DATE: 1999-11-02
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-058-292-10

Query Match 93.6%; Score 23.4; DB 14; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.4;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 36
US-10-162-879-10
; Sequence 10, Application US/10162879
; Publication No. US20030068799A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; Brach, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/162,879
; FILING DATE: 06-Jun-2002

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; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,085
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-162-879-10

Query Match 93.6%; Score 23.4; DB 14; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.4;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 37
US-10-161-403-50
; Sequence 50, Application US/10161403
; Publication No. US20030119104A1
; GENERAL INFORMATION:
; APPLICANT: Perkins, Edward
; APPLICANT: Perez, Carl
; APPLICANT: Lindenbaum, Michael
; APPLICANT: Greene, Amy
; APPLICANT: Leung, Josephine
; APPLICANT: Fleming, Elena
; APPLICANT: Stewart, Sandra
; APPLICANT: Shellard, Joan
; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
; FILE REFERENCE: 24601-420
; CURRENT APPLICATION NUMBER: US/10/161,403
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/294,758
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 60/366,891
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: attr2
US-10-161-403-50

Query Match 93.6%; Score 23.4; DB 14; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.4;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

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; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-432-085-10

Query Match          93.6%; Score 23.4; DB 11; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.4;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAACTTGT 25
   |||||
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 32
US-09-985-448-10
; Sequence 10, Application US/09985448
; Publication No. US20030157716A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/985,448
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-985-448-10

Query Match          93.6%; Score 23.4; DB 12; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.4;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAACTTGT 25
   |||||
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 33
US-10-300-892-10
; Sequence 10, Application US/10300892
; Publication No. US20030175970A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
```

```
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/10/300,892
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/907,719
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-10-300-892-10

Query Match          93.6%; Score 23.4; DB 12; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.4;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAACTTGT 25
   |||||
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 34
US-10-055-001A-5
; Sequence 5, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: core sequence of recombination site attr2
US-10-055-001A-5

Query Match          93.6%; Score 23.4; DB 14; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.4;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAACTTGT 25
   |||||
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 35
US-10-058-292-10
; Sequence 10, Application US/10058292
; Publication No. US20030054552A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; RECOMBINATION SITES
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
```

RESULT 28
US-09-855-797A-10
; Sequence 10, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855,797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-855-797A-10

Query Match 93.6%; Score 23.4; DB 9; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.4;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
|||||
Db 1 GTTCAGCTTTCTGTACAAACTTGT 25

RESULT 29
US-09-907-900-10
; Sequence 10, Application US/09907900
; Patent No. US20020172997A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,900
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-900-10

Query Match 93.6%; Score 23.4; DB 10; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.4;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
|||||
Db 1 GTTCAGCTTTCTGTACAAACTTGT 25

RESULT 30
US-09-907-719-10
; Sequence 10, Application US/09907719
; Publication No. US20020192819A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,719
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-719-10

Query Match 93.6%; Score 23.4; DB 10; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.4;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
|||||
Db 1 GTTCAGCTTTCTGTACAAACTTGT 25

RESULT 31
US-09-432-085-10
; Sequence 10, Application US/09432085
; Publication No. US20030100110A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,085
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002

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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 17476
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: plasmid pHELLSGATE 8
US-10-385-546-7

Query Match      100.0%; Score 25; DB 12; Length 17476;
Best Local Similarity 100.0%; Pred. No. 0.95;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 13050 GTTCAGCTTTTGTACAAACTTGT 13026

RESULT 24
US-10-055-001A-24
; Sequence 24, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; FILE REFERENCE: HELIGA
; CURRENT FILING DATE: 2002-06-11
; CURRENT APPLICATION NUMBER: US/10/055,001A
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 17476
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE8
US-10-055-001A-24

Query Match      100.0%; Score 25; DB 14; Length 17476;
Best Local Similarity 100.0%; Pred. No. 0.95;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 16674 GTTCAGCTTTTGTACAAACTTGT 16698

RESULT 25
US-10-055-001A-24/c
; Sequence 24, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; FILE REFERENCE: HELIGA
; CURRENT FILING DATE: 2002-06-11
; CURRENT APPLICATION NUMBER: US/10/055,001A
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 17476
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE8
US-10-055-001A-24

Query Match      100.0%; Score 25; DB 12; Length 17476;
Best Local Similarity 100.0%; Pred. No. 0.95;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 13050 GTTCAGCTTTTGTACAAACTTGT 13026

RESULT 26
US-10-055-001A-26
; Sequence 26, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; FILE REFERENCE: HELIGA
; CURRENT FILING DATE: 2002-06-11
; CURRENT APPLICATION NUMBER: US/10/055,001A
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 17681
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE12
US-10-055-001A-26

Query Match      100.0%; Score 25; DB 14; Length 17681;
Best Local Similarity 100.0%; Pred. No. 0.95;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 16879 GTTCAGCTTTTGTACAAACTTGT 16903

RESULT 27
US-10-055-001A-26/c
; Sequence 26, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; FILE REFERENCE: HELIGA
; CURRENT FILING DATE: 2002-06-11
; CURRENT APPLICATION NUMBER: US/10/055,001A
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 17681
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE12
US-10-055-001A-26

Query Match      100.0%; Score 25; DB 14; Length 17681;
Best Local Similarity 100.0%; Pred. No. 0.95;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 13050 GTTCAGCTTTTGTACAAACTTGT 13026
```

; APPLICANT: Budworth, P.
; APPLICANT: Brown, D.
; APPLICANT: Chang, H.
; APPLICANT: Zhu, T.
; APPLICANT: Han, B.
; APPLICANT: Wang, X.
; APPLICANT: Cooper, Bret
; TITLE OF INVENTION: Promoters for regulation of plant expression
; FILE REFERENCE: 1360.001US1
; CURRENT APPLICATION NUMBER: US/09/887,576
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: US 60/213,848
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/214,087
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/258,692
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 875
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 581
; LENGTH: 11180
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-887-576-581

Query Match 100.0%; Score 25; DB 10; Length 11180;
Best Local Similarity 100.0%; Pred. No. 0.88;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
|||
DB 142 GTTCAGCTTTTGTACAAACTTGT 118

RESULT 20

US-10-055-001A-25
; Sequence 25, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 17458
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE11
US-10-055-001A-25

Query Match 100.0%; Score 25; DB 14; Length 17458;
Best Local Similarity 100.0%; Pred. No. 0.95;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
|||
DB 16656 GTTCAGCTTTTGTACAAACTTGT 16680

RESULT 21

US-10-055-001A-25/c
; Sequence 25, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter

; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 17458
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE11
US-10-055-001A-25

Query Match 100.0%; Score 25; DB 14; Length 17458;
Best Local Similarity 100.0%; Pred. No. 0.95;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
|||
DB 13050 GTTCAGCTTTTGTACAAACTTGT 13026

RESULT 22

US-10-385-546-7
; Sequence 7, Application US/10385546
; Publication No. US20030175783A1
; GENERAL INFORMATION:
; APPLICANT: Waterhouse, Peter
; APPLICANT: Wesley, Susan
; APPLICANT: Helliwell, Chris
; TITLE OF INVENTION: Methods and means for monitoring and modulating gene silencing
; FILE REFERENCE: COLINA-US2
; CURRENT APPLICATION NUMBER: US/10/385,546
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60363852
; PRIOR FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 17476
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: plasmid pHELLSGATE 8
US-10-385-546-7

Query Match 100.0%; Score 25; DB 12; Length 17476;
Best Local Similarity 100.0%; Pred. No. 0.95;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
|||
DB 16674 GTTCAGCTTTTGTACAAACTTGT 16698

RESULT 23

US-10-385-546-7/c
; Sequence 7, Application US/10385546
; Publication No. US20030175783A1
; GENERAL INFORMATION:
; APPLICANT: Waterhouse, Peter
; APPLICANT: Wesley, Susan
; APPLICANT: Helliwell, Chris
; TITLE OF INVENTION: Methods and means for monitoring and modulating gene silencing
; FILE REFERENCE: COLINA-US2
; CURRENT APPLICATION NUMBER: US/10/385,546
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60363852
; PRIOR FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 7

```
; FILE REFERENCE: A-70174-1/RPT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/10/023,208
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: US 60/256,163
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 1846
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-023-208-63

Query Match      100.0%; Score 25; DB 14; Length 1846;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTTCAGCTTTTGTGACAAACTTGT 25
Db      25 GTTCAGCTTTTGTGACAAACTTGT 1

RESULT 17
US-10-241-596-137/c
; Sequence 137, Application US/10241596
; Publication No. US20030166238A1
; GENERAL INFORMATION:
; APPLICANT: Microbiological Research Authority
; APPLICANT: The Speywood Laboratory Limited
; TITLE OF INVENTION: Recombinant Toxin Fragments
; FILE REFERENCE: 1581.0130003
; CURRENT APPLICATION NUMBER: US/10/241,596
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 09/255,829
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: US 09/242,689
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: PCT/GB97/02273
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 08/782,893
; PRIOR FILING DATE: 1996-12-27
; PRIOR APPLICATION NUMBER: GB 9625996.5
; PRIOR FILING DATE: 1996-12-13
; PRIOR APPLICATION NUMBER: GB 9617671.4
; PRIOR FILING DATE: 1996-08-23
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 137
; LENGTH: 5558
; TYPE: DNA
; ORGANISM: Clostridium botulinum
US-10-241-596-137

Query Match      100.0%; Score 25; DB 12; Length 5558;
Best Local Similarity 100.0%; Pred. No. 0.78;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTTCAGCTTTTGTGACAAACTTGT 25
Db      1666 GTTCAGCTTTTGTGACAAACTTGT 1642

RESULT 18
US-10-151-690-20/c
; Sequence 20, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
```

```
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MO
; FILE REFERENCE: 0942.5120001
; CURRENT APPLICATION NUMBER: US/10/151,690
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 6464
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: plasmid pDEST1
; NAME/KEY: gene
; LOCATION: (216)..(257)
; OTHER INFORMATION: Trc promoter
; NAME/KEY: gene
; LOCATION: (273)..(393)
; OTHER INFORMATION: attR1
; NAME/KEY: gene
; LOCATION: (1426)..(1510)
; OTHER INFORMATION: inactivated ccdA
; NAME/KEY: gene
; LOCATION: (1648)..(1953)
; OTHER INFORMATION: ccdB
; NAME/KEY: gene
; LOCATION: (1994)..(2118)
; OTHER INFORMATION: attR2
; NAME/KEY: gene
; LOCATION: (2598)..(3503)
; OTHER INFORMATION: ampR
; NAME/KEY: gene
; LOCATION: (4104)..(4264)
; OTHER INFORMATION: ori
; NAME/KEY: gene
; LOCATION: (4504)..(4941)
; OTHER INFORMATION: flori (fl intergenic region)
; NAME/KEY: gene
; LOCATION: (5340)..(6420)
; OTHER INFORMATION: lacIq
US-10-151-690-20

Query Match      100.0%; Score 25; DB 14; Length 6464;
Best Local Similarity 100.0%; Pred. No. 0.8;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTTCAGCTTTTGTGACAAACTTGT 25
Db      297 GTTCAGCTTTTGTGACAAACTTGT 273

RESULT 19
US-09-887-576-581/c
; Sequence 581, Application US/09887576
; Patent No. US20020144047A1
; GENERAL INFORMATION:
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; Sequence 32, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MO
; FILE REFERENCE: 0942.5120001
; CURRENT APPLICATION NUMBER: US/10/151,690
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 25
; TYPE: DNA
; ORGANISM: attR1
US-10-151-690-32

Query Match 100.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 13
US-09-974-760B-33/c
; Sequence 33, Application US/09974760B
; Publication No. US20030143705A1
; GENERAL INFORMATION:
; APPLICANT: Roberts, Shannon
; APPLICANT: Sherman, Amir
; APPLICANT: Trueheart, Joshua
; APPLICANT: Milne, G. Todd
; TITLE OF INVENTION: LOVE VARIANT REGULATOR MOLECULES
; FILE REFERENCE: 14184-009001
; CURRENT APPLICATION NUMBER: US/09/974,760B
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-974-760B-33

Query Match 100.0%; Score 25; DB 12; Length 35;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 35 GTTCAGCTTTTGTACAAACTTGT 11

RESULT 14
US-09-732-914-44/c
; Sequence 44, Application US/09732914
; Patent No. US20020007051A1
; GENERAL INFORMATION:
; APPLICANT: Cheo, David
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.

; APPLICANT: Hartley, James L.
; APPLICANT: Byrd, Devon R.N.
; TITLE OF INVENTION: Use of Multiple Recombination Sites with Unique Specificity in
; TITLE OF INVENTION: Recombinational Cloning
; FILE REFERENCE: 0942.5010002
; CURRENT APPLICATION NUMBER: US/09/732,914
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/169,983
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 60/188,020
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 44
; LENGTH: 43
; TYPE: DNA
; ORGANISM: attR1 PCR Primer
US-09-732-914-44

Query Match 100.0%; Score 25; DB 9; Length 43;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 29 GTTCAGCTTTTGTACAAACTTGT 5

RESULT 15
US-10-151-690-19/c
; Sequence 19, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MO
; FILE REFERENCE: 0942.5120001
; CURRENT APPLICATION NUMBER: US/10/151,690
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 120
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: plasmid pDEST1
US-10-151-690-19

Query Match 100.0%; Score 25; DB 14; Length 120;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 118 GTTCAGCTTTTGTACAAACTTGT 94

RESULT 16
US-10-023-208-63/c
; Sequence 63, Application US/10023208
; Publication No. US20030124537A1
; GENERAL INFORMATION:
; APPLICANT: Li, Min
; APPLICANT: Liu, Yuan-Ching
; TITLE OF INVENTION: PROCAROTIC LIBRARIES AND USES

/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20005-3934
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA: US/10/058,292
/ FILING DATE: 30-Jan-2002
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/432,085
/ FILING DATE: 1999-11-02
/ APPLICATION NUMBER: 09/233,493
/ FILING DATE: 20-JAN-1999
/ APPLICATION NUMBER: 09/005,476
/ FILING DATE: 12-JAN-1998
/ APPLICATION NUMBER: 08/663,002
/ FILING DATE: 07-JUN-1996
/ APPLICATION NUMBER: 08/486,139
/ FILING DATE: 07-JUN-1995
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-371-2600
/ TELEFAX: 202-371-2540
/ INFORMATION FOR SEQ ID NO: 9:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 25 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: both
/ TOPOLOGY: both
/ MOLECULE TYPE: cdna
/ SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-058-292-9

Query Match 100.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTGT 25
Db 1 GTTCAGCTTTTGTACAACTTGT 25

RESULT 10
US-10-162-879-9
/ Sequence 9, Application US/10162879
/ Publication No. US20030086799A1
/ GENERAL INFORMATION:
/ APPLICANT: Hartley, James L.
/ Braesch, Michael A.
/ TITLE OF INVENTION: Recombinational Cloning Using Engineered
/ RECOMBINATION SITES
/ NUMBER OF SEQUENCES: 35
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
/ STREET: 1100 New York Ave., N. W. Suite 600
/ CITY: Washington
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20005-3934
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/162,879
/ FILING DATE: 06-Jun-2002
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/432,085

/ FILING DATE: <Unknown>
/ APPLICATION NUMBER: 09/233,493
/ FILING DATE: 20-JAN-1999
/ APPLICATION NUMBER: 09/005,476
/ FILING DATE: 12-JAN-1998
/ APPLICATION NUMBER: 08/663,002
/ FILING DATE: 07-JUN-1996
/ APPLICATION NUMBER: 08/486,139
/ FILING DATE: 07-JUN-1995
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-371-2600
/ TELEFAX: 202-371-2540
/ INFORMATION FOR SEQ ID NO: 9:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 25 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: both
/ TOPOLOGY: both
/ MOLECULE TYPE: cdna
/ SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-162-879-9

Query Match 100.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTGT 25
Db 1 GTTCAGCTTTTGTACAACTTGT 25

RESULT 11
US-10-161-403-49
/ Sequence 49, Application US/10161403
/ Publication No. US20030119104A1
/ GENERAL INFORMATION:
/ APPLICANT: Perkins, Edward
/ APPLICANT: Perez, Carl
/ APPLICANT: Lindenbaum, Michael
/ APPLICANT: Greene, Amy
/ APPLICANT: Leung, Josephine
/ APPLICANT: Fleming, Elena
/ APPLICANT: Stewart, Sandra
/ APPLICANT: Shellard, Joan
/ TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
/ FILE REFERENCE: 24601-420
/ CURRENT APPLICATION NUMBER: US/10/161,403
/ CURRENT FILING DATE: 2002-05-30
/ PRIOR APPLICATION NUMBER: 60/294,758
/ PRIOR FILING DATE: 2001-05-30
/ PRIOR APPLICATION NUMBER: 60/366,891
/ PRIOR FILING DATE: 2002-03-21
/ NUMBER OF SEQ ID NOS: 129
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 49
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: attR1
US-10-161-403-49

Query Match 100.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTGT 25
Db 1 GTTCAGCTTTTGTACAACTTGT 25

RESULT 12
US-10-151-690-32

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; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-432-085-9

Query Match 100.0%; Score 25; DB 11; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 6
US-09-985-448-9
; Sequence 9, Application US/09985448
; Publication No. US20030157716A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/985,448
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
US-09-985-448-9

Query Match 100.0%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 7
US-10-300-892-9
; Sequence 9, Application US/10300892
; Publication No. US20030175970A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
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; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/10/300,892
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/907,719
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
US-10-300-892-9

Query Match 100.0%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 8
US-10-055-001A-4
; Sequence 4, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: core sequence of recombination site attr1
US-10-055-001A-4

Query Match 100.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 9
US-10-058-292-9
; Sequence 9, Application US/10058292
; Publication No. US20030054552A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
```

; Patent No. US2002009457AA1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855,797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-855-797A-9

Query Match 100.0%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.3; 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
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DB 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 3
US-09-907-900-9
; Sequence 9, Application US/09907900
; Patent No. US20020172997A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,900
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-900-9

Query Match 100.0%; Score 25; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
|||||
DB 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 4
US-09-907-719-9

; Sequence 9, Application US/09907719
; Publication No. US20020192819A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,719
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-719-9

Query Match 100.0%; Score 25; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
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DB 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 5
US-09-432-085-9
; Sequence 9, Application US/09432085
; Publication No. US20030100110A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,085
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

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OM nucleic - nucleic search, using sw model

Run on: November 6, 2003, 23:06:49 ; Search time 102.25 Seconds
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Title: US-10-055-001A-4

Perfect score: 25

Sequence: 1 gttcagctttttgtacaaactgt 25

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Total number of hits satisfying chosen parameters: 4282708

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	25	100.0	25	9	US-09-855-797A-9
3	25	100.0	25	10	US-09-907-900-9
4	25	100.0	25	10	US-09-907-719-9
5	25	100.0	25	11	US-09-432-085-9
6	25	100.0	25	12	US-09-985-448-9
7	25	100.0	25	12	US-10-300-892-9
8	25	100.0	25	14	US-10-055-001A-4
9	25	100.0	25	14	US-10-058-292-9
10	25	100.0	25	14	US-10-162-879-9
11	25	100.0	25	14	US-10-161-403-49
12	25	100.0	25	14	US-10-151-690-32
13	25	100.0	35	12	US-09-974-760B-33
14	25	100.0	43	9	US-09-732-914-44
15	25	100.0	120	14	US-10-151-690-19
16	25	100.0	1846	14	US-10-023-208-63

C 17	25	100.0	5558	12	US-10-241-596-137	Sequence 137, Appl
C 18	25	100.0	6464	14	US-10-151-690-20	Sequence 20, Appl
C 19	25	100.0	11180	10	US-09-887-576-591	Sequence 581, Appl
C 20	25	100.0	17458	14	US-10-055-001A-25	Sequence 25, Appl
C 21	25	100.0	17458	14	US-10-055-001A-25	Sequence 25, Appl
C 22	25	100.0	17476	12	US-10-385-546-7	Sequence 7, Appl
C 23	25	100.0	17476	12	US-10-385-546-7	Sequence 7, Appl
C 24	25	100.0	17476	14	US-10-055-001A-24	Sequence 24, Appl
C 25	25	100.0	17476	14	US-10-055-001A-24	Sequence 24, Appl
C 26	25	100.0	17681	14	US-10-055-001A-26	Sequence 26, Appl
C 27	25	100.0	17681	14	US-10-055-001A-26	Sequence 26, Appl
C 28	23.4	93.6	25	9	US-09-855-797A-10	Sequence 10, Appl
C 29	23.4	93.6	25	10	US-09-907-900-10	Sequence 10, Appl
C 30	23.4	93.6	25	10	US-09-907-719-10	Sequence 10, Appl
C 31	23.4	93.6	25	11	US-09-432-085-10	Sequence 10, Appl
C 32	23.4	93.6	25	12	US-09-985-448-10	Sequence 10, Appl
C 33	23.4	93.6	25	12	US-10-300-892-10	Sequence 10, Appl
C 34	23.4	93.6	25	14	US-10-058-292-10	Sequence 5, Appl
C 35	23.4	93.6	25	14	US-10-058-292-10	Sequence 10, Appl
C 36	23.4	93.6	25	14	US-10-162-879-10	Sequence 10, Appl
C 37	23.4	93.6	25	14	US-10-161-403-50	Sequence 50, Appl
C 38	23.4	93.6	43	9	US-09-732-914-45	Sequence 45, Appl
C 39	22.6	90.4	25	9	US-09-855-797A-42	Sequence 42, Appl
C 40	22.6	90.4	25	10	US-09-907-900-42	Sequence 42, Appl
C 41	22.6	90.4	25	10	US-09-907-719-42	Sequence 42, Appl
C 42	22.6	90.4	25	12	US-09-985-448-42	Sequence 42, Appl
C 43	22.6	90.4	25	12	US-10-300-892-42	Sequence 42, Appl
C 44	22.4	89.6	25	9	US-09-855-797A-15	Sequence 15, Appl
C 45	22.4	89.6	25	10	US-09-907-900-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1

US-09-732-914-8
; Sequence 8, Application US/09732914
; Patent No. US20020007051A1
; GENERAL INFORMATION:
; APPLICANT: Cheo, David
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Hartley, James D.
; APPLICANT: Byrd, Devon R.N.
; TITLE OF INVENTION: Use of Multiple Recombination Sites with Unique Specificity in Recombinational Cloning
; FILE REFERENCE: 0942.5010002
; CURRENT APPLICATION NUMBER: US/09/732,914
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/169,983
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 60/188,020
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 25
; TYPE: DNA
; ORGANISM: attr1
US-09-732-914-8

Query Match 100.0%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAACTTGT 25

Db 1 GTTCAGCTTTTGTACAACTTGT 25

RESULT 2

US-09-855-797A-9
; Sequence 9, Application US/09855797A

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25

Db 166 GTTCAGCTTTTGTACAAACTTGT 142

Search completed: November 6, 2003, 22:26:28
Job time : 112.5 secs

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTGT 25
 |||||
 Db 4022 GTTCAGCTTTTGTACAACTTGT 3998

RESULT 39
 AAC55464/C
 ID AAC55464 standard; DNA; 5957 BP.
 XX
 AC AAC55464;
 XX
 DT 11-JAN-2001 (first entry)
 XX
 DE Destination vector pDEST5 nucleotide sequence.
 XX
 KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
 KW mutant; recombinational cloning; entry vector; destination vector;
 KW gene product targeting; fusion tag cleavage; ds.
 XX
 OS Bacteriophage lambda.
 OS Synthetic.
 XX
 FN WO200052027-A1.
 XX
 PD 08-SEP-2000.
 XX
 PF 02-MAR-2000; 2000WO-US05432.
 XX
 PR 02-MAR-1999; 99US-0122389.
 PR 23-MAR-1999; 99US-0126049.
 PR 28-MAY-1999; 99US-0136744.
 XX
 PA (LIFE-) LIFE TECHNOLOGIES INC.
 XX
 PI Hartley JL, Brasch MA, Temple GF, Cheo D;
 XX
 DR WPI; 2000-543948/49.
 XX
 PT Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 PT recombinational cloning of polypeptides -
 XX
 PS Example 15; Fig 25; 459pp; English.
 XX
 CC The present invention describes isolated nucleic acid molecules (I)
 CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
 CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity
 CC of interaction between the recombination site and a second att
 CC recombination site; and (2) an isolated nucleic acid molecule (III)
 CC comprising one or more mutated att recombination sites comprising at
 CC least one mutation in its core region that enhances the efficiency of
 CC recombination between a first nucleic acid molecule comprising the
 CC mutated att recombination site and a second nucleic acid molecule
 CC comprising a second recombination site that interacts with the mutated
 CC att recombination site. (I), (II), (III), primers, vectors and methods
 CC from the present invention are used for the recombinational cloning of
 CC nucleic acid molecules. They can be used for changing vectors, targeting
 CC gene products to intracellular locations, cleaving fusion tags from
 CC desired proteins, operably linking nucleic acid molecules of interest to
 CC regulatory genetic sequences, constructing genes for fusion proteins,
 CC changing copy number, changing replicons, cloning into phages and
 CC cloning. (I), (II), (III), host cells and vectors can be used in the
 CC production of polypeptides and antibodies. The present sequence is
 CC used in the exemplification of the present invention.
 XX
 SQ Sequence 5957 BP; 1509 A; 1443 C; 1498 G; 1507 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 5957;
 Best Local Similarity 100.0%; Pred. No. 0.48;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTGT 25
 |||||
 Db 205 GTTCAGCTTTTGTACAACTTGT 181

RESULT 40
 AAC55467/C
 ID AAC55467 standard; DNA; 5957 BP.
 XX
 AC AAC55467;
 XX
 DT 11-JAN-2001 (first entry)
 XX
 DE Destination vector pDEST6 nucleotide sequence.
 XX
 KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
 KW mutant; recombinational cloning; entry vector; destination vector;
 KW gene product targeting; fusion tag cleavage; ds.
 XX
 OS Bacteriophage lambda.
 OS Synthetic.
 XX
 FN WO200052027-A1.
 XX
 PD 08-SEP-2000.
 XX
 PF 02-MAR-2000; 2000WO-US05432.
 XX
 PR 02-MAR-1999; 99US-0122389.
 PR 23-MAR-1999; 99US-0126049.
 PR 28-MAY-1999; 99US-0136744.
 XX
 PA (LIFE-) LIFE TECHNOLOGIES INC.
 XX
 PI Hartley JL, Brasch MA, Temple GF, Cheo D;
 XX
 DR WPI; 2000-543948/49.
 XX
 PT Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 PT recombinational cloning of polypeptides -
 XX
 PS Example 15; Fig 26; 459pp; English.
 XX
 CC The present invention describes isolated nucleic acid molecules (I)
 CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
 CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity
 CC of interaction between the recombination site and a second att
 CC recombination site; and (2) an isolated nucleic acid molecule (III)
 CC comprising one or more mutated att recombination sites comprising at
 CC least one mutation in its core region that enhances the efficiency of
 CC recombination between a first nucleic acid molecule comprising the
 CC mutated att recombination site and a second nucleic acid molecule
 CC comprising a second recombination site that interacts with the mutated
 CC att recombination site. (I), (II), (III), primers, vectors and methods
 CC from the present invention are used for the recombinational cloning of
 CC nucleic acid molecules. They can be used for changing vectors, targeting
 CC gene products to intracellular locations, cleaving fusion tags from
 CC desired proteins, operably linking nucleic acid molecules of interest to
 CC regulatory genetic sequences, constructing genes for fusion proteins,
 CC changing copy number, changing replicons, cloning into phages and
 CC cloning. (I), (II), (III), host cells and vectors can be used in the
 CC production of polypeptides and antibodies. The present sequence is
 CC used in the exemplification of the present invention.
 XX
 SQ Sequence 5957 BP; 1530 A; 1445 C; 1496 G; 1486 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 5957;
 Best Local Similarity 100.0%; Pred. No. 0.48;

comprising a second recombination site that interacts with the mutated att recombination site. (I), (II), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning (I), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.

XX SQ Sequence 4554 BP; 1194 A; 1070 C; 1113 G; 1177 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 4554;

Best Local Similarity 100.0%; Pred. No. 0.47; Indels 0; Gaps 0; Matches 25; Conservative 0; Mismatches 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
|||||
Db 310 GTTCAGCTTTTGTACAAACTTGT 286

RESULT 37

AAD27063/c

ID AAD27063 standard; DNA; 5148 BP.

AC AAD27063;

XX 09-APR-2002 (first entry)

DT Plasmid pGN39 DNA.

DE Vector construct; RNA inhibition; RNAi; gene expression control;

XX pGN39 plasmid; ds.

XX Unidentified.

XX WO200188121-A1.

XX 22-NOV-2001.

XX 18-MAY-2001; 2001WO-IB01068.

XX 19-MAY-2000; 2000GB-0012233.

XX (DEVG-) DEVGEN NV.

XX Plaetinck G, Renard J, Bogaert T;

XX WPI; 2002-121984/16.

XX A new DNA vector construct containing opposable promoter and terminator

XX sequences flanking a cloning site are useful for the expression of

XX PT double stranded RNA useful for inhibition of RNA in gene expression

XX PT control -

XX Claim 24; Fig 12; 75pp; English.

XX The present invention relates to improved vector constructs comprising

XX two promoters in opposite orientation to each other, an inter-promoter

XX region downstream of the 3' end of both promoters, a cloning site in

XX the inter-promoter region and a transcription terminator downstream

XX of the 3' end of the first promoter and the cloning site and operably

XX linked to the first promoter. The constructs of the invention and the

XX bacteria harbouring the constructs are used to produce double stranded

XX RNA for RNA inhibition (RNAi) and can be used as a tool for controlling

XX gene expression. The present sequence is pGN39 plasmid DNA.

XX SQ Sequence 5148 BP; 1359 A; 1199 C; 1279 G; 1311 T; 0 other;

Query Match 100.0%; Score 25; DB 24; Length 5148;

Best Local Similarity 100.0%; Pred. No. 0.47;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
|||||
Db 171 GTTCAGCTTTTGTACAAACTTGT 147

RESULT 38

AAC55481/c

ID AAC55481 standard; DNA; 5848 BP.

XX AAC55481;

XX 11-JAN-2001 (first entry)

XX Destination vector pDEST13 nucleotide sequence.

XX Bacteriophage lambda; att; recombination site; attB; attP; attL; attR; attL;

XX mutant; recombinational cloning; entry vector; destination vector;

XX gene product targeting; fusion tag cleavage; ds.

XX Bacteriophage lambda.

XX Synthetic.

XX WO200052027-A1.

XX 08-SEP-2000.

XX 02-MAR-2000; 2000WO-US05432.

XX 02-MAR-1999; 99US-0122389.

XX 23-MAR-1999; 99US-0126049.

XX 28-MAY-1999; 99US-0136744.

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Hartley JL, Brasch MA, Temple GF, Cheo D;

XX WPI; 2000-543948/49.

XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,

XX attL1, attL2, attR1, and attR2 nucleotide sequence useful for the

XX recombinational cloning of polypeptides -

XX Disclosure; Fig 33; 459pp; English.

XX The present invention describes isolated nucleic acid molecules (I)

XX encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2

XX nucleotide sequence. Also described are: (1) an isolated nucleic acid

XX molecule (II) comprising one or more att recombination sites comprising

XX at least one mutation in its core region that increases the specificity

XX of interaction between the recombination site and a second att

XX recombination site; and (2) an isolated nucleic acid molecule (III)

XX comprising one or more mutated att recombination sites comprising at

XX least one mutation in its core region that enhances the efficiency of

XX recombination between a first nucleic acid molecule comprising the

XX mutated att recombination site and a second nucleic acid molecule

XX comprising a second recombination site that interacts with the mutated

XX att recombination site. (I), (II), (III), primers, vectors and methods

XX from the present invention are used for the recombinational cloning of

XX nucleic acid molecules. They can be used for changing vectors, targeting

XX gene products to intracellular locations, cleaving fusion tags from

XX desired proteins, operably linking nucleic acid molecules of interest to

XX regulatory genetic sequences, constructing genes for fusion proteins,

XX changing copy number, changing replicons, cloning into phages and

XX cloning (I), (II), (III), host cells and vectors can be used in the

XX production of polypeptides and antibodies. The present sequence is

XX used in the exemplification of the present invention.

XX SQ Sequence 5848 BP; 1563 A; 1364 C; 1379 G; 1542 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 5848;

Best Local Similarity 100.0%; Pred. No. 0.48;

CC least one mutation in its core region that enhances the efficiency of
 CC recombination between a first nucleic acid molecule comprising the
 CC mutated att recombination site and a second nucleic acid molecule
 CC comprising a second recombination site that interacts with the mutated
 CC att recombination site. (i), (ii), (iii), primers, vectors and methods
 CC from the present invention are used for the recombinational cloning of
 CC nucleic acid molecules. They can be used for changing vectors, targeting
 CC gene products to intracellular locations, cleaving fusion tags from
 CC desired proteins, operably linking nucleic acid molecules of interest to
 CC regulatory genetic sequences, constructing genes for fusion proteins,
 CC changing copy number, changing replicons, cloning into phages and
 CC cloning. (i), (ii), (iii), host cells and vectors can be used in the
 CC production of polypeptides and antibodies. The present sequence is
 CC used in the exemplification of the present invention.

XX SQ Sequence 420 BP; 134 A; 77 C; 88 G; 121 T; 0 other;
 Query Match 100.0%; Score 25; DB 21; Length 420;
 Best Local Similarity 100.0%; Pred. No. 0.39;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTGT 25
 |||
 Db 402 GTTCAGCTTTTGTACAACTTGT 378

RESULT 35
 AAD44626/C
 ID AAD44626 standard; DNA; 1846 BP.

XX AC AAD44626;

XX DT 13-DEC-2002 (first entry)

XX DE Gateway transfer cassette DNA.

XX Prokaryotic library; candidate protein; nucleic acid modification; NAM;
 KW enzyme attachment sequence; EAS; clinical pharmacology; chemical sensor;
 KW enzymology; cosmetic research; toxic; environmental safety assessment;
 KW nutrient biology; gateway transfer cassette; gene; ds.

XX OS Unidentified.

XX PN WO200266653-A2.

XX PD 29-AUG-2002.

XX PF 14-DEC-2001; 2001WO-US49058.

XX PR 14-DEC-2000; 2000US-256163P.

XX PA (XENC-) XENCOR INC.

XX PI Li M, Liu Y;

XX PS WPI; 2002-667068/71.

XX New library of prokaryotic pET-24a expression vectors, host cells or
 PT nucleic acid/protein conjugates, useful for screening candidate
 PT proteins and their nucleic acids or modification enzymes for
 PT pharmacogenetic analysis -

XX Example 2; Fig 59B; 127pp; English.

XX The invention relates to methods and compositions for the construction
 CC of prokaryotic libraries expressing candidate proteins and the use of
 CC these libraries to identify candidate proteins and the nucleic acids
 CC encoding them. The invention provides a library of prokaryotic pET-24a
 CC vectors comprising a fusion nucleic acid consisting of a nucleic acid
 CC encoding a nucleic acid modification (NAM) enzyme or a candidate
 CC protein, or a nucleic acid having a T7 promoter operably linked to the
 CC NAM enzyme or the candidate protein, and an enzyme attachment sequence
 CC (EAS) recognised by the NAM enzyme. The library is used for identifying

CC candidate proteins and nucleic acids encoding these proteins, in
 CC screening for NAM enzymes with decreased toxicity for the host cells,
 CC or in identifying novel or improved EASs, which may be used for
 CC understanding cellular processes or any subsequent therapeutic or toxic
 CC activities. The nucleic acid/protein (NAP) conjugates are useful in
 CC diagnostic assays and in research including clinical pharmacology,
 CC functional genomics, pharmacogenomics, agricultural chemicals,
 CC environmental safety assessment, chemical sensor, nutrient biology,
 CC cosmetic research or enzymology. These may also be used in vitro
 CC screening techniques and in assays with target molecules. The present
 CC sequence is gateway transfer cassette DNA used in the invention.

XX SQ Sequence 1846 BP; 527 A; 381 C; 434 G; 504 T; 0 other;

Query Match 100.0%; Score 25; DB 24; Length 1846;
 Best Local Similarity 100.0%; Pred. No. 0.44;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTGT 25
 |||
 Db 25 GTTCAGCTTTTGTACAACTTGT 1

RESULT 36

RAC55541/C

ID AAC55541 standard; DNA; 4554 BP.

XX AC AAC55541;

XX XX 11-JAN-2001 (first entry)

XX attR reading frame C parent plasmid prfC Parent III nucleotide sequence.

XX Bacteriophage lambda; att; recombination site; attB; attP; attL; attR2;

KW mutant; recombinational cloning; entry vector; destination vector;

KW gene product targeting; fusion tag cleavage; ds.

XX Bacteriophage lambda.

OS Synthetic.

XX PN WO200052027-A1.

XX PD 08-SEP-2000.

XX PF 02-MAR-2000; 2000WO-US05432.

XX PR 02-MAR-1999; 99US-0122389.

XX PR 23-MAR-1999; 99US-0126049.

XX PR 28-MAY-1999; 99US-0136744.

XX PA (LIFE-) LIFE TECHNOLOGIES INC.

XX Hartley JL, Brasch MA, Temple GF, Cheo D;

XX WPI; 2000-543948/49.

XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 PT recombinational cloning of polypeptides -

XX Example 14; Fig 83; 459pp; English.

XX The present invention describes isolated nucleic acid molecules (I)
 CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
 CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity
 CC of interaction between the recombination site and a second att
 CC recombination site; and (2) an isolated nucleic acid molecule (III)
 CC comprising one or more mutated att recombination sites comprising at
 CC least one mutation in its core region that enhances the efficiency of
 CC recombination between a first nucleic acid molecule comprising the
 CC mutated att recombination site and a second nucleic acid molecule

CC least one mutation in its core region that enhances the efficiency of
 CC recombination between a first nucleic acid molecule comprising the
 CC mutated att recombination site and a second nucleic acid molecule
 CC comprising a second recombination site that interacts with the mutated
 CC att recombination site. (I), (II), (III), primers, vectors and methods
 CC from the present invention are used for the recombinational cloning of
 CC nucleic acid molecules. They can be used for changing vectors, targeting
 CC gene products to intracellular locations, cleaving fusion tags from
 CC desired proteins, operably linking nucleic acid molecules of interest to
 CC regulatory genetic sequences, constructing genes for fusion proteins,
 CC changing copy number, changing replicons, cloning into phages and
 CC cloning. (I), (II), (III), host cells and vectors can be used in the
 CC production of polypeptides and antibodies. The present sequence is
 CC used in the exemplification of the present invention.

XX SQ Sequence 306 BP; 87 A; 77 C; 80 G; 62 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 306;
 Best Local Similarity 100.0%; Pred. No. 0.38;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTGT 25
 |||
 Db 301 GTTCAGCTTTTGTACAACTTGT 277

RESULT 33
 AAC5514/c
 ID AAC5514 standard; DNA; 306 BP.
 AC AAC5514;
 XX
 DT 11-JAN-2001 (first entry)
 XX
 DE Destination vector pBEST26 fragment nucleotide sequence.
 XX
 KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
 KW mutant; recombinational cloning; entry vector; destination vector;
 KW gene product targeting; fusion tag cleavage; ds.
 XX
 OS Bacteriophage lambda.
 OS Synthetic.
 XX
 PN WO200052027-A1.
 XX
 PD 08-SEP-2000.
 XX
 PF 02-MAR-2000; 2000WO-US05432.
 XX
 PR 02-MAR-1999; 99US-0122389.
 PR 23-MAR-1999; 99US-0126049.
 PR 28-MAY-1999; 99US-0136744.
 XX
 PA (LIFE-) LIFE TECHNOLOGIES INC.
 XX
 PI Hartley JL, Brasch MA, Temple GF, Cheo D;
 XX
 DR WPI; 2000-543948/49.
 XX
 PT Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 PT recombinational cloning of polypeptides -
 XX
 PS Disclosure; Fig 46; 459pp; English.
 XX
 CC The present invention describes isolated nucleic acid molecules (I)
 CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
 CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity
 CC of interaction between the recombination site and a second att
 CC recombination site; and (2) an isolated nucleic acid molecule (III)
 CC comprising one or more mutated att recombination sites comprising at

CC least one mutation in its core region that enhances the efficiency of
 CC recombination between a first nucleic acid molecule comprising the
 CC mutated att recombination site and a second nucleic acid molecule
 CC comprising a second recombination site that interacts with the mutated
 CC att recombination site. (I), (II), (III), primers, vectors and methods
 CC from the present invention are used for the recombinational cloning of
 CC nucleic acid molecules. They can be used for changing vectors, targeting
 CC gene products to intracellular locations, cleaving fusion tags from
 CC desired proteins, operably linking nucleic acid molecules of interest to
 CC regulatory genetic sequences, constructing genes for fusion proteins,
 CC changing copy number, changing replicons, cloning into phages and
 CC cloning. (I), (II), (III), host cells and vectors can be used in the
 CC production of polypeptides and antibodies. The present sequence is
 CC used in the exemplification of the present invention.

XX SQ Sequence 306 BP; 84 A; 83 C; 74 G; 65 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 306;
 Best Local Similarity 100.0%; Pred. No. 0.38;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTGT 25
 |||
 Db 301 GTTCAGCTTTTGTACAACTTGT 277

RESULT 34
 AAC55492/c
 ID AAC55492 standard; DNA; 420 BP.
 AC AAC55492;
 XX
 DT 11-JAN-2001 (first entry)
 XX
 DE Destination vector pBEST18 fragment nucleotide sequence.
 XX
 KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
 KW mutant; recombinational cloning; entry vector; destination vector;
 KW gene product targeting; fusion tag cleavage; ds.
 XX
 OS Bacteriophage lambda.
 OS Synthetic.
 XX
 PN WO200052027-A1.
 XX
 PD 08-SEP-2000.
 XX
 PF 02-MAR-2000; 2000WO-US05432.
 XX
 PR 02-MAR-1999; 99US-0122389.
 PR 23-MAR-1999; 99US-0126049.
 PR 28-MAY-1999; 99US-0136744.
 XX
 PA (LIFE-) LIFE TECHNOLOGIES INC.
 XX
 PI Hartley JL, Brasch MA, Temple GF, Cheo D;
 XX
 DR WPI; 2000-543948/49.
 XX
 PT Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 PT recombinational cloning of polypeptides -
 XX
 PS Disclosure; Fig 38; 459pp; English.
 XX
 CC The present invention describes isolated nucleic acid molecules (I)
 CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
 CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity
 CC of interaction between the recombination site and a second att
 CC recombination site; and (2) an isolated nucleic acid molecule (III)
 CC comprising one or more mutated att recombination sites comprising at

CC least one mutation in its core region that enhances the efficiency of
 CC recombination between a first nucleic acid molecule comprising the
 CC mutated att recombination site and a second nucleic acid molecule
 CC comprising a second recombination site that interacts with the mutated
 CC att recombination site. (I), (II), (III), primers, vectors and methods
 CC from the present invention are used for the recombinational cloning of
 CC nucleic acid molecules. They can be used for changing vectors, targeting
 CC gene products to intracellular locations, cleaving fusion tags from
 CC desired proteins, operably linking nucleic acid molecules of interest to
 CC regulatory genetic sequences, constructing genes for fusion proteins,
 CC changing copy number, changing replicons, cloning into phages and
 CC cloning. (I), (II), (III), host cells and vectors can be used in the
 CC production of polypeptides and antibodies. The present sequence is
 CC used in the exemplification of the present invention.

XX
 XX Sequence 255 BP; 88 A; 57 C; 50 G; 60 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 255;
 Best Local Similarity 100.0%; Pred. No. 0.38;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
 |||||
 DB 253 GTTCAGCTTTTGTACAAACTTGT 229

RESULT 31
 AAC55478/c
 ID AAC55478 standard; DNA; 255 BP.
 XX AC AAC55478;
 XX DT 11-JAN-2001 (first entry)
 XX DE Destination vector pDEST12 fragment nucleotide sequence.
 XX KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
 XX mutant; recombinational cloning; entry vector; destination vector;
 XX gene product targeting; fusion tag cleavage; ds.
 XX OS Bacteriophage lambda.
 XX OS Synthetic.
 XX PN WO200052027-A1.
 XX PD 08-SEP-2000.
 XX PF 02-MAR-2000; 2000WO-US05432.
 XX PR 02-MAR-1999; 99US-0122389.
 XX PR 23-MAR-1999; 99US-0126049.
 XX PR 28-MAY-1999; 99US-0136744.
 XX PA (LIFE-) LIFE TECHNOLOGIES INC.
 XX PI Hartley JL, Brasch MA, Temple GF, Cheo D;
 XX WPI; 2000-543948/49.
 XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 XX attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 XX recombinational cloning of polypeptides -
 XX Example 15; Fig 32; 459pp; English.
 XX The present invention describes isolated nucleic acid molecules (I)
 XX encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
 XX nucleotide sequence. Also described are: (1) an isolated nucleic acid
 XX molecule (II) comprising one or more att recombination sites comprising
 XX at least one mutation in its core region that increases the specificity
 XX of interaction between the recombination site and a second att
 XX recombination site; and (2) an isolated nucleic acid molecule (III)
 XX comprising one or more mutated att recombination sites comprising at

CC least one mutation in its core region that enhances the efficiency of
 CC recombination between a first nucleic acid molecule comprising the
 CC mutated att recombination site and a second nucleic acid molecule
 CC comprising a second recombination site that interacts with the mutated
 CC att recombination site. (I), (II), (III), primers, vectors and methods
 CC from the present invention are used for the recombinational cloning of
 CC nucleic acid molecules. They can be used for changing vectors, targeting
 CC gene products to intracellular locations, cleaving fusion tags from
 CC desired proteins, operably linking nucleic acid molecules of interest to
 CC regulatory genetic sequences, constructing genes for fusion proteins,
 CC changing copy number, changing replicons, cloning into phages and
 CC cloning. (I), (II), (III), host cells and vectors can be used in the
 CC production of polypeptides and antibodies. The present sequence is
 CC used in the exemplification of the present invention.

XX
 XX Sequence 255 BP; 80 A; 67 C; 58 G; 50 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 255;
 Best Local Similarity 100.0%; Pred. No. 0.39;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
 |||||
 DB 235 GTTCAGCTTTTGTACAAACTTGT 211

RESULT 32
 AAC55468/c
 ID AAC55468 standard; DNA; 306 BP.
 XX AC AAC55468;
 XX DT 11-JAN-2001 (first entry)
 XX DE Destination vector pDEST7 fragment nucleotide sequence.
 XX KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
 XX mutant; recombinational cloning; entry vector; destination vector;
 XX gene product targeting; fusion tag cleavage; ds.
 XX OS Bacteriophage lambda.
 XX OS Synthetic.
 XX PN WO200052027-A1.
 XX PD 08-SEP-2000.
 XX PF 02-MAR-2000; 2000WO-US05432.
 XX PR 02-MAR-1999; 99US-0122389.
 XX PR 23-MAR-1999; 99US-0126049.
 XX PR 28-MAY-1999; 99US-0136744.
 XX PA (LIFE-) LIFE TECHNOLOGIES INC.
 XX PI Hartley JL, Brasch MA, Temple GF, Cheo D;
 XX WPI; 2000-543948/49.
 XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 XX attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 XX recombinational cloning of polypeptides -
 XX Example 15; Fig 27; 459pp; English.
 XX The present invention describes isolated nucleic acid molecules (I)
 XX encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
 XX nucleotide sequence. Also described are: (1) an isolated nucleic acid
 XX molecule (II) comprising one or more att recombination sites comprising
 XX at least one mutation in its core region that increases the specificity
 XX of interaction between the recombination site and a second att
 XX recombination site; and (2) an isolated nucleic acid molecule (III)
 XX comprising one or more mutated att recombination sites comprising at

CC least one mutation in its core region that enhances the efficiency of
 CC recombination between a first nucleic acid molecule comprising the
 CC mutated att recombination site and a second nucleic acid molecule
 CC comprising a second recombination site that interacts with the mutated
 CC att recombination site. (I), (II), (III), primers, vectors and methods
 CC from the present invention are used for the recombinational cloning of
 CC nucleic acid molecules. They can be used for changing vectors, targeting
 CC gene products to intracellular locations, cleaving fusion tags from
 CC desired proteins, operably linking nucleic acid molecules of interest to
 CC regulatory genetic sequences, constructing genes for fusion proteins,
 CC changing copy number, changing replicons, cloning into phages and
 CC cloning. (I), (II), (III), host cells and vectors can be used in the
 CC production of polypeptides and antibodies. The present sequence is
 CC used in the exemplification of the present invention.

XX
 SQ Sequence 204 BP; 80 A; 35 C; 31 G; 58 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 204;
 Best Local Similarity 100.0%; Pred. No. 0.37;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
 |||||
 Db 184 GTTCAGCTTTTGTACAAACTTGT 160

RESULT 29
 AAC55476/c
 ID AAC55476 standard; DNA; 204 BP.
 XX
 AC AAC5476;
 XX
 DT 11-JAN-2001 (first entry)
 XX
 DE Destination vector pDEST11 fragment nucleotide sequence.
 XX
 KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
 KW mutant; recombinational cloning; entry vector; destination vector;
 KW gene product targeting; fusion tag cleavage; ds.

OS Bacteriophage lambda.
 OS Synthetic.
 XX WO200052027-A1.
 XX
 XX 08-SEP-2000.
 XX
 XX 02-MAR-2000; 2000WO-US05432.
 XX
 XX 02-MAR-1999; 99US-0122389.
 XX 23-MAR-1999; 99US-0126049.
 XX 28-MAY-1999; 99US-0136744.
 XX
 XX (LIFE-) LIFE TECHNOLOGIES INC.
 XX
 XX Hartley JL, Brasch MA, Temple GF, Cheo D;
 XX WPI; 2000-543948/49.
 XX
 XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 XX attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 XX recombinational cloning of polypeptides -
 XX
 XX Example 13; Fig 31; 459pp; English.

XX The present invention describes isolated nucleic acid molecules (I)
 CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
 CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity
 CC of interaction between the recombination site and a second att
 CC recombination site; and (2) an isolated nucleic acid molecule (III)
 CC comprising one or more mutated att recombination sites comprising at

CC least one mutation in its core region that enhances the efficiency of
 CC recombination between a first nucleic acid molecule comprising the
 CC mutated att recombination site and a second nucleic acid molecule
 CC comprising a second recombination site that interacts with the mutated
 CC att recombination site. (I), (II), (III), primers, vectors and methods
 CC from the present invention are used for the recombinational cloning of
 CC nucleic acid molecules. They can be used for changing vectors, targeting
 CC gene products to intracellular locations, cleaving fusion tags from
 CC desired proteins, operably linking nucleic acid molecules of interest to
 CC regulatory genetic sequences, constructing genes for fusion proteins,
 CC changing copy number, changing replicons, cloning into phages and
 CC cloning. (I), (II), (III), host cells and vectors can be used in the
 CC production of polypeptides and antibodies. The present sequence is
 CC used in the exemplification of the present invention.

XX
 SQ Sequence 204 BP; 60 A; 53 C; 50 G; 41 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 204;
 Best Local Similarity 100.0%; Pred. No. 0.37;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
 |||||
 Db 181 GTTCAGCTTTTGTACAAACTTGT 157

RESULT 30
 AAC55460/c
 ID AAC55460 standard; DNA; 255 BP.
 XX
 AC AAC55460;
 XX
 DT 11-JAN-2001 (first entry)
 XX
 DE His6-Trx expression cassette for destination vector pDEST4.
 XX
 KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
 KW mutant; recombinational cloning; entry vector; destination vector;
 KW gene product targeting; fusion tag cleavage; ds.

OS Bacteriophage lambda.
 OS Escherichia coli.
 XX WO200052027-A1.
 XX
 XX 08-SEP-2000.
 XX
 XX 02-MAR-2000; 2000WO-US05432.
 XX
 XX 02-MAR-1999; 99US-0122389.
 XX 23-MAR-1999; 99US-0126049.
 XX 28-MAY-1999; 99US-0136744.
 XX
 XX (LIFE-) LIFE TECHNOLOGIES INC.
 XX
 XX Hartley JL, Brasch MA, Temple GF, Cheo D;
 XX WPI; 2000-543948/49.
 XX
 XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 XX attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 XX recombinational cloning of polypeptides -
 XX
 XX Disclosure; Fig 24; 459pp; English.

XX The present invention describes isolated nucleic acid molecules (I)
 CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
 CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity
 CC of interaction between the recombination site and a second att
 CC recombination site; and (2) an isolated nucleic acid molecule (III)
 CC comprising one or more mutated att recombination sites comprising at

CC least one mutation in its core region that enhances the efficiency of
 CC recombination between a first nucleic acid molecule comprising the
 CC mutated att recombination site and a second nucleic acid molecule
 CC comprising a second recombination site that interacts with the mutated
 CC att recombination site. (I), (II), (III), primers, vectors and methods
 CC from the present invention are used for the recombinational cloning of
 CC nucleic acid molecules. They can be used for changing vectors, targeting
 CC gene products to intracellular locations, cleaving fusion tags from
 CC desired proteins, operably linking nucleic acid molecules of interest to
 CC regulatory genetic sequences, constructing genes for fusion proteins,
 CC changing copy number, changing replicons, cloning into phages and
 CC cloning. (I), (II), (III), host cells and vectors can be used in the
 CC production of polypeptides and antibodies. The present sequence is
 CC used in the exemplification of the present invention.

XX Sequence 153 BP; 50 A; 28 C; 40 G; 35 T; 0 other;
 SQ

Query Match 100.0%; Score 25; DB 21; Length 153;
 Best Local Similarity 100.0%; Pred. No. 0.37;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTGT 25
 |||||
 DB 127 GTTCAGCTTTTGTACAACTTGT 103

RESULT 27
 AAC55465/c
 ID AAC55465 standard; DNA; 204 BP.
 XX
 AC AAC55465;
 XX
 DT 11-JAN-2001 (first entry)
 XX
 DE Destination vector pBEST6 fragment nucleotide sequence #1.
 XX
 KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
 KW mutant; recombinational cloning; entry vector; destination vector;
 KW gene product targeting; fusion tag cleavage; ds.
 XX
 OS Bacteriophage lambda.
 OS Synthetic.
 XX
 PN WO200052027-A1.
 XX
 PD 08-SEP-2000.
 XX
 PF 02-MAR-2000; 2000WO-US05432.
 XX
 PR 02-MAR-1999; 99US-0122389.
 PR 23-MAR-1999; 99US-0126049.
 PR 28-MAY-1999; 99US-0136744.
 XX
 PA (LIFE-) LIFE TECHNOLOGIES INC.
 XX
 PI Hartley JL, Brasch MA, Temple GF, Cheo D;
 XX
 DR WPI; 2000-543948/49.

XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 PT recombinational cloning of polypeptides -
 XX
 XX Example 15; Fig 26; 459pp; English.
 XX
 XX The present invention describes isolated nucleic acid molecules (I)
 CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
 CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity
 CC of interaction between the recombination site and a second att
 CC recombination site; and (2) an isolated nucleic acid molecule (III)
 CC comprising one or more mutated att recombination sites comprising at

CC least one mutation in its core region that enhances the efficiency of
 CC recombination between a first nucleic acid molecule comprising the
 CC mutated att recombination site and a second nucleic acid molecule
 CC comprising a second recombination site that interacts with the mutated
 CC att recombination site. (I), (II), (III), primers, vectors and methods
 CC from the present invention are used for the recombinational cloning of
 CC nucleic acid molecules. They can be used for changing vectors, targeting
 CC gene products to intracellular locations, cleaving fusion tags from
 CC desired proteins, operably linking nucleic acid molecules of interest to
 CC regulatory genetic sequences, constructing genes for fusion proteins,
 CC changing copy number, changing replicons, cloning into phages and
 CC cloning. (I), (II), (III), host cells and vectors can be used in the
 CC production of polypeptides and antibodies. The present sequence is
 CC used in the exemplification of the present invention.

XX Sequence 204 BP; 70 A; 40 C; 46 G; 48 T; 0 other;
 SQ

Query Match 100.0%; Score 25; DB 21; Length 204;
 Best Local Similarity 100.0%; Pred. No. 0.37;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTGT 25
 |||||
 DB 166 GTTCAGCTTTTGTACAACTTGT 142

RESULT 28
 AAC55470/c
 ID AAC55470 standard; DNA; 204 BP.
 XX
 AC AAC55470;
 XX
 DT 11-JAN-2001 (first entry)
 XX
 DE Destination vector pDEST8 fragment nucleotide sequence.
 XX
 KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
 KW mutant; recombinational cloning; entry vector; destination vector;
 KW gene product targeting; fusion tag cleavage; ds.
 XX
 OS Bacteriophage lambda.
 OS Synthetic.
 XX
 PN WO200052027-A1.
 XX
 PD 08-SEP-2000.
 XX
 PF 02-MAR-2000; 2000WO-US05432.
 XX
 PR 02-MAR-1999; 99US-0122389.
 PR 23-MAR-1999; 99US-0126049.
 PR 28-MAY-1999; 99US-0136744.
 XX
 PA (LIFE-) LIFE TECHNOLOGIES INC.
 XX
 PI Hartley JL, Brasch MA, Temple GF, Cheo D;
 XX
 DR WPI; 2000-543948/49.

XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 PT recombinational cloning of polypeptides -
 XX
 XX Example 15; Fig 28; 459pp; English.
 XX
 XX The present invention describes isolated nucleic acid molecules (I)
 CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
 CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity
 CC of interaction between the recombination site and a second att
 CC recombination site; and (2) an isolated nucleic acid molecule (III)
 CC comprising one or more mutated att recombination sites comprising at

CC least one mutation in its core region that enhances the efficiency of
 CC recombination between a first nucleic acid molecule comprising the
 CC mutated att recombination site and a second nucleic acid molecule
 CC comprising a second recombination site that interacts with the mutated
 CC att recombination site. (I), (II), (III), primers, vectors and methods
 CC from the present invention are used for the recombinational cloning of
 CC nucleic acid molecules. They can be used for changing vectors, targeting
 CC gene products to intracellular locations, cleaving fusion tags from
 CC desired proteins, operably linking nucleic acid molecules of interest to
 CC regulatory genetic sequences, constructing genes for fusion proteins,
 CC changing copy number, changing replicons, cloning into phages and
 CC cloning. (I), (II), (III), host cells and vectors can be used in the
 CC production of polypeptides and antibodies. The present sequence is
 CC used in the exemplification of the present invention.
 XX
 SQ Sequence 125 BP; 61 A; 18 C; 14 G; 32 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 125;
 Best Local Similarity 100.0%; Pred. No. 0.36;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTGT 25
 |||||
 DB 25 GTTCAGCTTTTGTACAACTTGT 1

RESULT 25
 AAC55485/c
 ID AAC55485 standard; DNA; 153 BP.
 XX
 AC AAC55485;
 XX
 DT 11-JAN-2001 (first entry)
 XX
 DE Destination vector pDEST15 fragment nucleotide sequence #2.
 XX
 KW Bacteriophage lambda; att; recombination site; attB; attP; attL; attR;
 KW mutant; recombinational cloning; entry vector; destination vector;
 KW gene product targeting; fusion tag cleavage; ds.
 XX
 OS Bacteriophage lambda.
 OS Synthetic.
 XX
 PN WO200052027-A1.
 XX
 PD 08-SEP-2000.
 XX
 PF 02-MAR-2000; 2000WO-US05432.
 XX
 PR 02-MAR-1999; 99US-0122389.
 PR 23-MAR-1999; 99US-0126049.
 PR 28-MAY-1999; 99US-0136744.
 XX
 PA (LIFE-) LIFE TECHNOLOGIES INC.
 XX
 PI Hartley JL, Brasch MA, Temple GF, Cheo D;
 XX
 DR WPI; 2000-543948/49.
 XX

Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 recombinational cloning of polypeptides -
 XX
 PS Disclosure; Fig 35; 459pp; English.

XX The present invention describes isolated nucleic acid molecules (I)
 CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
 CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity
 CC of interaction between the recombination site and a second att
 CC recombination site; and (2) an isolated nucleic acid molecule (III)
 CC comprising one or more mutated att recombination sites comprising att

CC least one mutation in its core region that enhances the efficiency of
 CC recombination between a first nucleic acid molecule comprising the
 CC mutated att recombination site and a second nucleic acid molecule
 CC comprising a second recombination site that interacts with the mutated
 CC att recombination site. (I), (II), (III), primers, vectors and methods
 CC from the present invention are used for the recombinational cloning of
 CC nucleic acid molecules. They can be used for changing vectors, targeting
 CC gene products to intracellular locations, cleaving fusion tags from
 CC desired proteins, operably linking nucleic acid molecules of interest to
 CC regulatory genetic sequences, constructing genes for fusion proteins,
 CC changing copy number, changing replicons, cloning into phages and
 CC cloning. (I), (II), (III), host cells and vectors can be used in the
 CC production of polypeptides and antibodies. The present sequence is
 CC used in the exemplification of the present invention.
 XX
 SQ Sequence 153 BP; 52 A; 29 C; 33 G; 39 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 153;
 Best Local Similarity 100.0%; Pred. No. 0.37;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTGT 25
 |||||
 DB 103 GTTCAGCTTTTGTACAACTTGT 79

RESULT 26
 AAC55488/c
 ID AAC55488 standard; DNA; 153 BP.
 XX
 AC AAC55488;
 XX
 DT 11-JAN-2001 (first entry)
 XX
 DE Destination vector pDEST16 fragment nucleotide sequence #2.
 XX
 KW Bacteriophage lambda; att; recombination site; attB; attP; attL;
 KW mutant; recombinational cloning; entry vector; destination vector;
 KW gene product targeting; fusion tag cleavage; ds.
 XX
 OS Bacteriophage lambda.
 OS Synthetic.
 XX
 PN WO200052027-A1.
 XX
 PD 08-SEP-2000.
 XX
 PF 02-MAR-2000; 2000WO-US05432.
 XX
 PR 02-MAR-1999; 99US-0122389.
 PR 23-MAR-1999; 99US-0126049.
 PR 28-MAY-1999; 99US-0136744.
 XX
 PA (LIFE-) LIFE TECHNOLOGIES INC.
 XX
 PI Hartley JL, Brasch MA, Temple GF, Cheo D;
 XX
 DR WPI; 2000-543948/49.
 XX

Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 recombinational cloning of polypeptides -
 XX
 PS Disclosure; Fig 36; 459pp; English.

XX The present invention describes isolated nucleic acid molecules (I)
 CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
 CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity
 CC of interaction between the recombination site and a second att
 CC recombination site; and (2) an isolated nucleic acid molecule (III)
 CC comprising one or more mutated att recombination sites comprising att

comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (I), (II), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (I), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.

Sequence 102 BP; 37 A; 24 C; 19 G; 21 T; 1 other;

Query Match 100.0%; Score 25; DB 21; Length 102;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTGACAAACTTGT 25
DB 92 GTTCAGCTTTTGTGACAAACTTGT 68

RESULT 23
AAC55453/c
ID AAC55453 standard; DNA; 120 BP.

XX AC AAC55453;

XX DT 11-JAN-2001 (first entry)

XX DE Trc expression cassette for destination vector pDEST1.

XX KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
XX KW mutant; recombinational cloning; entry vector; destination vector;
XX KW gene product targeting; fusion tag cleavage; ds.

XX OS Bacteriophage lambda.
XX OS Escherichia coli.

XX PN WO200052027-A1.

XX PD 08-SEP-2000.

XX PF 02-MAR-2000; 2000WO-US05432.

XX PR 02-MAR-1999; 99US-0122389.

XX PR 23-MAR-1999; 99US-0126049.

XX PR 28-MAY-1999; 99US-0136744.

XX PA (LIFE-) LIFE TECHNOLOGIES INC.

XX PI Hartley JL, Brasch MA, Temple GF, Cheo D;

XX DR WPI; 2000-543948/49.

XX PT Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
XX PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
XX PT recombinational cloning of polypeptides -
XX PS Disclosure; Fig 21; 459pp; English.

XX CC The present invention describes isolated nucleic acid molecules (I)
XX CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
XX CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
XX CC molecule (II) comprising one or more att recombination sites comprising
XX CC at least one mutation in its core region that increases the specificity
XX CC of interaction between the recombination site and a second att
XX CC recombination site; and (2) an isolated nucleic acid molecule (III)

comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (I), (II), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (I), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.

Sequence 120 BP; 44 A; 19 C; 28 G; 29 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 120;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTGACAAACTTGT 25
DB 118 GTTCAGCTTTTGTGACAAACTTGT 94

RESULT 24

AAC55384/c

ID AAC55384 standard; DNA; 125 BP.

XX AC AAC55384;

XX DT 11-JAN-2001 (first entry)

XX DE Recombination site nucleotide sequence attR1.

XX KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
XX KW mutant; recombinational cloning; entry vector; destination vector;
XX KW gene product targeting; fusion tag cleavage; ds.

XX OS Bacteriophage lambda.

XX PN WO200052027-A1.

XX PD 08-SEP-2000.

XX PF 02-MAR-2000; 2000WO-US05432.

XX PR 02-MAR-1999; 99US-0122389.

XX PR 23-MAR-1999; 99US-0126049.

XX PR 28-MAY-1999; 99US-0136744.

XX PA (LIFE-) LIFE TECHNOLOGIES INC.

XX PI Hartley JL, Brasch MA, Temple GF, Cheo D;

XX DR WPI; 2000-543948/49.

XX PT Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
XX PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
XX PT recombinational cloning of polypeptides -
XX PS Claim 1; Fig 9; 459pp; English.

XX CC The present invention describes isolated nucleic acid molecules (I)
XX CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
XX CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
XX CC molecule (II) comprising one or more att recombination sites comprising
XX CC at least one mutation in its core region that increases the specificity
XX CC of interaction between the recombination site and a second att
XX CC recombination site; and (2) an isolated nucleic acid molecule (III)
XX CC comprising one or more mutated att recombination sites comprising at

comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (I), (II), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing fusion tags, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (I), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.

XX Sequence 102 BP; 40 A; 22 C; 18 G; 22 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 102;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAACTTGT 25
Db 83 GTTCAGCTTTTGTACAACTTGT 59

RESULT 21
AAC55508/c
ID AAC55508 standard; DNA; 102 BP.
XX AAC55508;
XX
XX 11-JAN-2001 (first entry)
XX Destination vector pDEST24 fragment nucleotide sequence #1.
XX Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
KW mutant; recombinational cloning; entry vector; destination vector;
KW gene product targeting; fusion tag cleavage; ds.
XX Bacteriophage lambda.
OS Synthetic.
OS
XX WO200052027-A1.
XX
XX 08-SEP-2000.
XX
XX 02-MAR-2000; 2000WO-US05432.
XX
XX 02-MAR-1999; 99US-0122389.
XX 23-MAR-1999; 99US-0126049.
XX 28-MAY-1999; 99US-0136744.
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX
XX Hartley JL, Brasch MA, Temple GF, Cheo D;
XX WPI; 2000-543948/49.
XX
XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides -

Example 5; Fig 44; 459pp; English.
XX The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence. Also described are: (1) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att recombination site; and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (I), (II), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing fusion tags, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (I), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.

XX Sequence 102 BP; 40 A; 22 C; 18 G; 22 T; 0 other;

comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (I), (II), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing fusion tags, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (I), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.

XX Sequence 102 BP; 37 A; 25 C; 19 G; 21 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 102;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAACTTGT 25
Db 95 GTTCAGCTTTTGTACAACTTGT 71

RESULT 22
AAC55511/c
ID AAC55511 standard; DNA; 102 BP.
XX AAC55511;
XX
XX 11-JAN-2001 (first entry)
XX Destination vector pDEST25 fragment nucleotide sequence #1.
XX Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
KW mutant; recombinational cloning; entry vector; destination vector;
KW gene product targeting; fusion tag cleavage; ds.
XX Bacteriophage lambda.
OS Synthetic.
OS
XX WO200052027-A1.
XX
XX 08-SEP-2000.
XX
XX 02-MAR-2000; 2000WO-US05432.
XX
XX 02-MAR-1999; 99US-0122389.
XX 23-MAR-1999; 99US-0126049.
XX 28-MAY-1999; 99US-0136744.
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX
XX Hartley JL, Brasch MA, Temple GF, Cheo D;
XX WPI; 2000-543948/49.
XX
XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides -

Example 5; Fig 45; 459pp; English.
XX The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence. Also described are: (1) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att recombination site; and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (I), (II), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing fusion tags, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (I), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.

XX Sequence 102 BP; 37 A; 25 C; 19 G; 21 T; 0 other;

comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (I), (II), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (I), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.

XX Sequence 102 BP; 35 A; 19 C; 20 G; 28 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 102;
Best Local Similarity 100.0%; Pred. No. 0.35; 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY 1 GTTCAGCTTTTGTACAACTTGT 25
DB 70 GTTCAGCTTTTGTACAACTTGT 46

RESULT 19
AAC55500/c
ID AAC55500 standard; DNA; 102 BP.

XX AAC55500;

AC AAC55500;

DT 11-JAN-2001 (first entry)

DE Destination vector pBEST21 fragment nucleotide sequence #2.

XX Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;

KW mutant; recombinational cloning; entry vector; destination vector;

KW gene product targeting; fusion tag cleavage; ds.

XX Bacteriophage lambda.

OS Synthetic.

XX WO200052027-A1.

PN 08-SEP-2000.

PD 02-MAR-2000; 2000WO-US05432.

PF 02-MAR-1999; 99US-0122389.

PR 23-MAR-1999; 99US-0126049.

PR 28-MAY-1999; 99US-0136744.

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Hartley JL, Brasch MA, Temple GF, Cheo D;

XX WPI; 2000-543948/49.

XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides -
XX Disclosure; Fig 41; 459pp; English.
XX The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence. Also described are: (1) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att recombination site; and (2) an isolated nucleic acid molecule (III)

comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (I), (II), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (I), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.

XX Sequence 102 BP; 45 A; 13 C; 24 G; 20 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 102;
Best Local Similarity 100.0%; Pred. No. 0.35; 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY 1 GTTCAGCTTTTGTACAACTTGT 25
DB 82 GTTCAGCTTTTGTACAACTTGT 58

RESULT 20

AAC55505/c

ID AAC55505 standard; DNA; 102 BP.

XX AAC55505;

DT 11-JAN-2001 (first entry)

DE Destination vector pBEST23 fragment nucleotide sequence #1.

XX Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;

KW mutant; recombinational cloning; entry vector; destination vector;

KW gene product targeting; fusion tag cleavage; ds.

XX Bacteriophage lambda.

OS Synthetic.

XX WO200052027-A1.

PN 08-SEP-2000.

PD 02-MAR-2000; 2000WO-US05432.

PF 02-MAR-1999; 99US-0122389.

PR 23-MAR-1999; 99US-0126049.

PR 28-MAY-1999; 99US-0136744.

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Hartley JL, Brasch MA, Temple GF, Cheo D;

XX WPI; 2000-543948/49.

XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides -
XX Example 5; Fig 43; 459pp; English.
XX The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence. Also described are: (1) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att recombination site; and (2) an isolated nucleic acid molecule (III)

comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (I), (II), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (I), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.

XX Sequence 87 BP; 26 A; 19 C; 21 G; 21 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 87;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
|||||
Db 79 GTTCAGCTTTTGTACAAACTTGT 55

RESULT 17
AAC55497/c
ID AAC55497 standard; DNA; 95 BP.
XX
AC AAC55497;
XX
XX 11-JAN-2001 (first entry)
XX
DE Destination vector pDEST20 fragment nucleotide sequence #2.
XX
XX Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
KW mutant; recombinational cloning; entry vector; destination vector;
KW gene product targeting; fusion tag cleavage; ds.
XX
OS Bacteriophage lambda.
OS Synthetic.
XX
XX WO200052027-A1.
XX
XX 08-SEP-2000.
XX
XX 02-MAR-2000; 2000WO-US05432.
XX
XX 02-MAR-1999; 99US-0122389.
PR
XX 23-MAR-1999; 99US-0126049.
PR
XX 28-MAY-1999; 99US-0136744.
XX
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX
XX Hartley JL, Brasch MA, Temple GF, Cheo D;
XX
XX WPI; 2000-543948/49.
XX
XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
PT recombinational cloning of polypeptides -
XX
XX Example 23; Fig 40; 459pp; English.

XX The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence. Also described are: (1) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att recombination site; and (2) an isolated nucleic acid molecule (III)

comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (I), (II), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (I), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.

XX Sequence 95 BP; 41 A; 13 C; 15 G; 26 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 95;
Best Local Similarity 100.0%; Pred. No. 0.35; 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
|||||
Db 52 GTTCAGCTTTTGTACAAACTTGT 28

RESULT 18
AAC55458/c
ID AAC55458 standard; DNA; 102 BP.
XX
AC AAC55458;
XX
XX 11-JAN-2001 (first entry)
XX
DE GST expression cassette for destination vector pDEST3 #2.
XX
XX Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
KW mutant; recombinational cloning; entry vector; destination vector;
KW gene product targeting; fusion tag cleavage; ds.
XX
OS Bacteriophage lambda.
OS Escherichia coli.
XX
XX WO200052027-A1.
XX
XX 08-SEP-2000.
XX
XX 02-MAR-2000; 2000WO-US05432.
XX
XX 02-MAR-1999; 99US-0122389.
PR
XX 23-MAR-1999; 99US-0126049.
PR
XX 28-MAY-1999; 99US-0136744.
XX
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX
XX Hartley JL, Brasch MA, Temple GF, Cheo D;
XX
XX WPI; 2000-543948/49.
XX
XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
PT recombinational cloning of polypeptides -
XX
XX Example 15; Fig 23; 459pp; English.

XX The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence. Also described are: (1) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att recombination site; and (2) an isolated nucleic acid molecule (III)

XX AAS06174-AAS06322 represent Bacteriophage lambda att recombination
CC site nucleic acid sequences, and PCR primers of the invention. The
CC att sequences are recognised by the recombination protein lambda
CC integrase (Int). The invention is a new method of producing a population
CC of hybrid nucleic acids comprising mixing at least a first population of
CC nucleic acids comprising one or more recombination sites with at least
CC one target nucleic acid comprising one or more recombination sites and
CC causing some or all of the nucleic acids to recombine with all or some of
CC the target nucleic acids. The method is useful for producing a population
CC of hybrid nucleic acids which may be the same or different. The nucleic
CC acids may be used to express therapeutic proteins or peptides and they
CC may also be used to create novel fusion proteins by expressing different
CC sequences linked to each other. The method allows simultaneous cloning of
CC two or more different nucleic acids.

XX SQ Sequence 43 BP; 20 A; 5 C; 11 G; 7 T; 0 other;

Query Match 100.0%; Score 25; DB 22; Length 43;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTTCAGCTTTTGTACAACTTGT 25
DB 29 GTTCAGCTTTTGTACAACTTGT 5

RESULT 15
AAC5503/c
ID AAC5503 standard; DNA; 82 BP.

XX AAC5503;
AC AAC5503;
XX 11-JAN-2001 (first entry)

DE Destination vector pEST22 fragment nucleotide sequence #2.

XX Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
KW mutant; recombinational cloning; entry vector; destination vector;
KW gene product targeting; fusion tag cleavage; ds.

XX Bacteriophage lambda.
OS Synthetic.

XX WO200052027-A1.

XX 08-SEP-2000.

XX 02-MAR-2000; 2000WO-US05432.

XX 02-MAR-1999; 99US-0122389.

XX 23-MAR-1999; 99US-0126049.

XX 28-MAY-1999; 99US-0136744.

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Hartley JL, Brasch MA, Temple GF, Cheo D;

XX WPI; 2000-543948/49.

XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
PT recombinational cloning of polypeptides -

XX Disclosure; Fig 42; 459pp; English.

XX The present invention describes isolated nucleic acid molecules (I)
CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
CC molecule (II) comprising one or more att recombination sites comprising
CC at least one mutation in its core region that increases the specificity
CC of interaction between the recombination site and a second att
CC recombination site; and (2) an isolated nucleic acid molecule (III)

CC comprising one or more mutated att recombination sites comprising at
CC least one mutation in its core region that enhances the efficiency of
CC recombination between a first nucleic acid molecule comprising the
CC mutated att recombination site and a second nucleic acid molecule
CC comprising a second recombination site that interacts with the mutated
CC att recombination site. (I), (II), (III), primers, vectors and methods
CC from the present invention are used for the recombinational cloning of
CC nucleic acid molecules. They can be used for changing vectors, targeting
CC gene products to intracellular locations, cleaving fusion tags from
CC desired proteins, operably linking nucleic acid molecules of interest to
CC regulatory genetic sequences, constructing genes for fusion proteins,
CC changing copy number, changing replicons, cloning into phages and
CC cloning. (II), (III), (IIV), host cells and vectors can be used in the
CC production of polypeptides and antibodies. The present sequence is
CC used in the exemplification of the present invention.

XX SQ Sequence 82 BP; 39 A; 16 C; 17 G; 10 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 82;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTTCAGCTTTTGTACAACTTGT 25
DB 70 GTTCAGCTTTTGTACAACTTGT 46

RESULT 16

AAC5517/c

ID AAC5517 standard; DNA; 87 BP.

XX AAC5517;

XX 11-JAN-2001 (first entry)

DE Destination vector pEST27 fragment nucleotide sequence #2.

XX Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
KW mutant; recombinational cloning; entry vector; destination vector;
KW gene product targeting; fusion tag cleavage; ds.

XX Bacteriophage lambda.
OS Synthetic.

XX WO200052027-A1.

XX 08-SEP-2000.

XX 02-MAR-2000; 2000WO-US05432.

XX 02-MAR-1999; 99US-0122389.

XX 23-MAR-1999; 99US-0126049.

XX 28-MAY-1999; 99US-0136744.

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Hartley JL, Brasch MA, Temple GF, Cheo D;

XX WPI; 2000-543948/49.

XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
PT recombinational cloning of polypeptides -

XX Disclosure; Fig 47; 459pp; English.

XX The present invention describes isolated nucleic acid molecules (I)
CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
CC molecule (II) comprising one or more att recombination sites comprising
CC at least one mutation in its core region that increases the specificity
CC of interaction between the recombination site and a second att
CC recombination site; and (2) an isolated nucleic acid molecule (III)

CC metabolite by a fungus. This involves modulating the expression of at
 CC least one ZBC (zinc binuclear cluster protein) gene in a manner to
 CC improve the yield of the secondary metabolite. Methods of the invention
 CC may be used for improving the production of the secondary metabolite e.g.
 CC antibacterial (such as beta-lactam), an anti-hypercholesterolaemic (such
 CC as lovastatin or mevastatin), an immunosuppressant (such as cyclosporin A),
 CC an ergot alkaloid (such as ergotamine), an angiogenesis inhibitor (such
 CC as ovalicin), a glucan synthase inhibitor, gliotoxin family of compounds,
 CC a fungal toxin, a modulator of cell surface receptor signalling, a plant
 CC growth regulator, a pigment, an insecticide, or an antineoplastic
 CC compound. The method results in a decrease in fermentor run-time, a
 CC decrease in the size of the fermentor required for the production of
 CC equivalent amounts of the secondary metabolite, or a decrease in the
 CC biomass required for the production, which translates into decreased
 CC waste that must be handled in downstream processing. The sequences given
 CC in records ABL58587-ABL58598 represent primers that are used in
 CC construction of vectors containing the ZBC genes of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 35 BP; 14 A; 7 C; 7 G; 7 T; 0 other;

Query Match 100.0%; Score 25; DB 24; Length 35;
 Best Local Similarity 100.0%; Pred. No. 0.33;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
 Db 35 GTTCAGCTTTTGTACAAACTTGT 11

RESULT 13

AAC55545/c
 ID AAC55545 standard; DNA; 43 BP.

AC AAC55545;

DT 11-JAN-2001 (first entry)

DE att site PCR primer attR1.

XX Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
 KW mutant; recombinational cloning; entry vector; destination vector;
 KW gene product targeting; fusion tag cleavage; PCR primer; ss.

XX Bacteriophage lambda.

OS Synthetic.

XX WO200052027-A1.

XX 08-SEP-2000.

XX 02-MAR-2000; 2000WO-US05432.

XX 02-MAR-1999; 99US-0122389.

XX 23-MAR-1999; 99US-0126049.

XX 28-MAY-1999; 99US-0136744.

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Hartley JL, Brasch MA, Temple GF, Cheo D;

XX WPI; 2000-543948/49.

XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 PT recombinational cloning of polypeptides -

XX Example 19; Page 142; 459pp; English.

XX The present invention describes isolated nucleic acid molecules (I)
 CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2

CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity
 CC of interaction between the recombination site and a second att
 CC recombination site; and (2) an isolated nucleic acid molecule (III)
 CC comprising one or more mutated att recombination sites comprising at
 CC least one mutation in its core region that enhances the efficiency of
 CC recombination between a first nucleic acid molecule comprising the
 CC mutated att recombination site and a second nucleic acid molecule
 CC comprising a second recombination site that interacts with the mutated
 CC att recombination site. (I), (II), (III) primers, vectors and methods
 CC from the present invention are used for the recombinational cloning of
 CC nucleic acid molecules. They can be used for changing fusion tags, targeting
 CC gene products to intracellular locations, cleaving fusion tags, forming
 CC desired proteins, operably linking nucleic acid molecules of interest to
 CC regulatory genetic sequences, constructing genes for fusion proteins,
 CC changing copy number, changing replicons, cloning into phages and
 CC cloning. (I), (II), (III), host cells and vectors can be used in the
 CC production of polypeptides and antibodies. The present sequence is
 CC used in the exemplification of the present invention.

XX Sequence 43 BP; 20 A; 5 C; 11 G; 7 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 43;
 Best Local Similarity 100.0%; Pred. No. 0.33;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
 Db 29 GTTCAGCTTTTGTACAAACTTGT 5

RESULT 14

AAS06217/c

ID AAS06217 standard; DNA; 43 BP.

AC AAS06217;

DT 12-SEP-2001 (first entry)

DE PCR primer attR1 used to produce a population of hybrid DNA molecules.

XX Bacteriophage lambda; recombination; att site; PCR primer; lambda Int;
 KW lambda integrase; therapeutic; ss.

XX Bacteriophage lambda.

OS Synthetic.

XX WO200142509-A1.

XX 14-JUN-2001.

XX 11-DEC-2000; 2000WO-US33546.

XX 10-DEC-1999; 99US-0169983.

XX 09-MAR-2000; 2000US-0188020.

XX (CHEO/) CHEO D.

XX (BRAS/) BRASCH M A.

XX (TEMP/) TEMPLE G F.

XX (HART/) HARTLEY J L.

XX (BYRD/) BYRD D R N.

XX Cheo D, Brasch MA, Temple GF, Hartley JL, Byrd DRN;

XX WPI; 2001-356174/37.

XX Producing hybrid nucleic acids, useful for expressing novel therapeutic
 PT polypeptides, by mixing the same or different nucleic acids having one
 PT or more recombination sites in the presence of recombination proteins,
 PT e.g. Cre -

XX Example 7; Page 209; 357pp; English.

PS Disclosure; Page 262; 269pp; English.

XX The invention relates to a novel method for producing plant artificial
 CC chromosomes. The invention also relates to methods for targeting
 CC insertion of heterologous DNA into plant artificial chromosomes, methods
 CC for delivery of plant chromosomes to selected cells and tissues. The
 CC isolated plant artificial chromosome (PAC) is useful for producing a
 CC transgenic plant, which involves introducing the PAC into a plant cell.
 CC The PAC comprises a heterologous nucleic acid encoding a gene product
 CC such as enzymes, antisense RNA, rDNA, structural proteins, marker
 CC proteins, ligands, receptors, ribozymes, therapeutic proteins, and
 CC biopharmaceutical proteins, vaccines, blood factors, antigens, hormones,
 CC cytokines, growth factors, antibodies, or a product that provides for
 CC resistance to diseases, insects, herbicides, or stress in a plant. The
 CC heterologous nucleic acid optionally encodes a product that provides an
 CC agronomically important trait in the plant, e.g. a product that alters
 CC nutrient use and/or improves the nutrient quality of the plant. The
 CC heterologous nucleic acid is contained within a bacterial artificial
 CC chromosome (BAC) or a yeast artificial chromosome (YAC). This
 CC polynucleotide sequence represents an oligo relating to the method for
 CC producing plant artificial chromosomes of the invention.

XX SQ Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 other;

Query Match 100.0%; Score 25; DB 25; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.32;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTACGCTTTTGTACAACTTGT 25
 |||||
 DB 1 GTTACGCTTTTGTACAACTTGT 25

RESULT 11

AAH19591/c
 ID AAH19591 standard; DNA; 35 BP.

XX AAH19591;

XX 30-JUL-2001 (first entry)

XX Plasmid pE2C7201 ccdB cassette PCR oligo MO511.

XX Secondary metabolite production; gene expression modulation;
 KW generically modified fungus; antibacterial; antihypercholesterolaemic;
 KW immunosuppressant; cell surface receptor signalling; pigment;
 KW plant growth regulator; insecticide; anti-neoplastic; ccdB; death gene;
 KW pE2C7201; PCR primer; ss.

XX Unidentified.

XX WO200129073-A1.

XX 26-APR-2001.

XX 18-OCT-2000; 2000WO-US28903.

XX 20-OCT-1999; 99US-0160587.

XX 19-JAN-2000; 2000US-0487358.

XX (MICR-) MICROBIA INC.

XX Busby R, Doten R, Cali B, Hecht P, Holtzman D, Madden K, Maxon M;
 PI Milne T, Norman T, Royer J, Salama S, Sherman A, Silva J;
 PI Summers E, Zhang L, Mayorga M, Feibelman T;

XX WPI; 2001-374304/39.

XX Improving production of secondary metabolite by fungus, for producing
 PT proteins of interest, involves modulating the expression of gene
 PT involved in regulation of secondary metabolite production

XX Example 1; Page 67; 139pp; English.

XX The present sequence is a primer which was used in an example
 CC illustrating an invention relating to a method for improving production
 CC of a secondary metabolite by a fungus. The method involves modulating
 CC the expression of a gene involved in the regulation of secondary
 CC metabolite production. The gene may be modulated in a manner that
 CC increases the yield or productivity of metabolite, increases
 CC efflux or excretion of the metabolite, decreases production of side
 CC effects or competing metabolites, alters the characteristics of the
 CC fungus in a manner that is beneficial to the production of the
 CC metabolite, causes conditional lysis of the fungus, or increases the
 CC resistance of the fungus to deleterious effects of exposure to the
 CC secondary metabolite. The method is useful for producing
 CC genetically modified fungi, which are useful for producing
 CC secondary metabolites such as antibacterial compounds,
 CC antihypercholesterolaemic compounds, immunosuppressants, modulators
 CC of cell surface receptor signalling, plant growth regulators, pigments,
 CC insecticides or anti-neoplastic compounds. The present sequence was
 CC used in the preparation of clones to regulate secondary metabolite
 CC production.

XX SQ Sequence 35 BP; 14 A; 7 C; 7 G; 7 T; 0 other;

Query Match 100.0%; Score 25; DB 22; Length 35;
 Best Local Similarity 100.0%; Pred. No. 0.33;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTACGCTTTTGTACAACTTGT 25
 |||||
 DB 35 GTTACGCTTTTGTACAACTTGT 11

RESULT 12

ABL58593/c

ID ABL58593 standard; DNA; 35 BP.

XX ABL58593;

XX 24-JUL-2002 (first entry)

XX Oligonucleotide MO511.

XX Secondary metabolite; fungus; ZBC gene; zinc binuclear cluster protein;
 KW antibacterial; beta-lactam; anti-hypercholesterolaemic; lovastatin;
 KW mevastatin; immunosuppressant; cyclosporin A; ergot alkaloid; ergotamine;
 KW angio genesis inhibitor; ovalicin; glucan synthase inhibitor; gliotoxin;
 KW fungal toxin; cell surface receptor; plant growth regulator; pigment;
 KW insecticide; antineoplastic; PCR; primer; ss.

XX Unidentified.

XX WO200224865-A2.

XX 28-MAR-2002.

XX 19-SEP-2001; 2001WO-US29288.

XX 19-SEP-2000; 2000US-233564P.

XX (MICR-) MICROBIA INC.

XX Holtzman D, Madden K, Maxon M, Sherman A;

XX WPI; 2002-352005/38.

XX New method for improving the production of a secondary metabolite e.g.
 PT antineoplastic agent, ergot alkaloid from a fungus involves modulation
 PT of the expression of at least one zinc binuclear cluster protein gene

XX Example 1; SEQ ID 7; 49pp + sequence listing; English.

XX The invention relates to improving the production of a secondary

PN US6143557-A.
XX PD 07-NOV-2000.
XX PF 20-JAN-1999; 99US-0233493.
XX PR 07-JUN-1996; 96US-0663002.
XX PR 12-JAN-1998; 98US-0005476.
XX PR 07-JUN-1995; 95US-0486139.
XX PA (LIFE-) LIFE TECHNOLOGIES INC.
XX PI Brasch MA, Hartley JL;
XX DR WPI; 2001-049004/06.
XX PT Isolated nucleic acid molecules comprising a DNA segment having two
PT engineered recombination sites, derived from att or lox, which flank a
PT selectable marker and comprise a core region having an engineered
PT mutation -
XX PT
XX PS Claim 1; Column 18; 73pp; English.
XX CC The present invention describes an isolated nucleic acid molecule (I)
CC comprising a first nucleic acid sequence having a defined sequence
CC (AAC87866 to AAC87881), sequences complementary to AAC87866 to AAC87881,
CC or an RNA sequence corresponding to AAC87866 to AAC87881. Also described
CC are: (1) an isolated nucleic acid molecule (II) comprising a first
CC mutated recombination site that removes one or more stop codons from the
CC recombination site or avoids hairpin formation, the recombination site
CC being an att or lox site; (2) an isolated nucleic acid molecule (III)
CC comprising a first att recombination site comprising a mutation that
CC enhances recombination specificity; (3) vectors (IV) comprising the
CC above mentioned nucleic acids; and (4) cells comprising the above
CC mentioned nucleic acids or (IV). The nucleic acids are used in
CC engineering a core region of a given recombination site to provide
CC mutative sites suitable for subcloning reactions. The use of nucleic
CC acids for obtaining engineered recombination in vitro or in vivo makes
CC the methods for DNA or RNA subcloning, highly specific, rapid, and
CC less labour intensive.
XX SQ Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 other;
SQ Query Match 100.0%; Score 25; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTTGTACAAACTTGT 25
DB 1 GTTCAGCTTTTGTACAAACTTGT 25
RESULT 7
AB082121
ID AB082121 standard; DNA; 25 BP.
XX AC AB082121;
XX DT 11-DEC-2002 (first entry)
XX DE Core sequence of recombination site attR1 SEQ ID NO:4.
XX KW Chimeric nucleic acid construct; recombinational cloning; silencing;
XX recombination site; double stranded RNA; plant; ss.
XX OS Synthetic.
XX PN WO200259294-A1.
XX PD 01-AUG-2002.
XX PF 24-JAN-2002; 2002WO-AU00073.
XX

PR 26-JAN-2001; 2001US-264067P.
PR 29-NOV-2001; 2001US-333743P.
XX PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX PI Wesley S, Waterhouse P, Helliwell C;
XX DR WPI; 2002-682669/73.
XX PT New vectors comprising operably linked DNA fragments having an origin
PT of replication, a selectable marker and a chimeric DNA construct,
PT useful for silencing target nucleic acids and for producing large
PT amounts of double-stranded RNA -
XX PT
XX PS Disclosure; Page 14; 104pp; English.
XX CC The present invention describes a vector (I) comprising operably linked
CC DNA fragments having: (a) origin of replication allowing replication in a
CC recipient cell, preferably in bacteria such as Escherichia coli;
CC (b) selectable marker region capable of being expressed in the recipient
CC cell; and (c) a chimeric DNA construct comprising: (i) promoter or
CC promoter region capable of being recognized by RNA polymerases of a
CC eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second,
CC third and fourth recombination sites; (iii) 3' transcription terminating
CC and polyadenylation region functional in the eukaryotic cell. The first
CC and fourth recombination sites, or the second and third recombination
CC sites are capable of reacting with a same recombination site, and
CC preferably are identical. The first and second recombination sites, or
CC the third and fourth recombination sites, do not recombine with each
CC other or with a same recombination site. The vector is useful for
CC producing large amounts of double-stranded RNA which can be used for
CC silencing target nucleic acid sequences. The vectors can also be used to
CC convert a DNA fragment into an inverted repeat structure. Plants
CC transformed with a vector from the present invention can be used in a
CC conventional breeding scheme to produce more plants with the same
CC characteristics or to introduce a chimeric gene for reduction of the
CC phenotypic expression of nucleic acids. The present sequence represents
CC the core sequence of recombination site attB1 which is given in the
CC exemplification of the present invention.
XX SQ Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 other;
SQ Query Match 100.0%; Score 25; DB 24; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTTGTACAAACTTGT 25
DB 1 GTTCAGCTTTTGTACAAACTTGT 25
RESULT 8
ACC44658
ID ACC44658 standard; DNA; 25 BP.
XX AC ACC44658;
XX DT 29-MAY-2003 (first entry)
XX DE Recombination site related oligonucleotide SEQ ID NO:49.
XX KW Chromosome-based platform; artificial chromosome; eukaryotic chromosome;
XX att site; integrase; recombinase; ACes; gene therapy; transgenic animal;
XX platform artificial chromosome expression system; PCR primer; ss.
XX OS Synthetic.
XX PN WO200297059-A2.
XX PD 05-DEC-2002.
XX PF 30-MAY-2002; 2002WO-US17452.
XX

RESULT 5

OS Escherichia c

PT vitro or in vivo
PS Claim 14; Page 55; 106pp; English.
XX
CC AAT48210-25 are att recombination site core region DNA sequences. The
CC core region has at least one engineered mutation that enhances
CC recombination in vitro in the formation of a Cointegrate or Product DNA.
CC These core regions can be incorporated into novel vector donor DNA
CC molecules. The nucleic acids, vectors and methods of the invention are
CC used to obtain chimeric nucleic acid using recombination proteins and
CC engineered recombination sites in vitro or in vivo. The improved
CC specificity, speed and yields of the invention facilitates DNA or RNA
CC subcloning, regulation or exchange useful for any related purpose, e.g.
CC in vitro recombination of DNA segments, and in vitro or in vivo insertion
CC or modification of transcribed, replicated, isolated or genomic DNA or
CC RNA.
XX
SQ Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 other;
Query Match 100.0%; Score 25; DB 18; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
DB 1 GTTCAGCTTTTGTACAAACTTGT 25
1 GTTCAGCTTTTGTACAAACTTGT 25
XX
RESULT 3
RAD14437
ID AAD14437 standard; DNA; 25 BP.
XX
AC AAD14437;
XX
DT 01-NOV-2001 (first entry)
XX
DE Recombination site attB3 DNA.
XX
KW Recombination site; copy number; replicon; recombinatorial cloning;
XX attB3; ds.
XX
OS Unidentified.
XX
PN US6270969-B1.
XX
PD 07-AUG-2001.
XX
PF 20-JAN-1999; 99US-0233492.
XX
PR 07-JUN-1996; 96US-0663002.
PR 07-JUN-1995; 95US-0486139.
XX
PA (INVI-) INVITROGEN CORP.
XX
PI Hartley JL, Brasch MA;
XX WPI; 2001-488248/53.
XX
PT Methods for apposing nucleic acids comprising an expression signal and
PT a gene/partial gene, using recombinatorial cloning by incubating the
PT nucleic acids in the presence of a recombination protein under
PT conditions for recombination -
XX
PS Claim 14; Column 18; 76pp; English.
XX
CC The invention relates to a method for apposing an expression signal and
CC a gene or partial gene, using recombinatorial cloning. The method
CC incubates nucleic acids comprising the expression signal and the gene/
CC partial gene in the presence of a recombination protein under conditions
CC sufficient to cause recombination and therefore appose the expression
CC signal and the gene or partial gene. The methods are useful for apposing
CC an expression signal and a gene or partial gene using recombinatorial
CC cloning. The methods are also useful for changing vectors, constructing
CC genes for fusion proteins, changing copy number, changing replicons,
CC cloning into phages, and cloning e.g., PCR products (with an attB site
CC at one end and a loxP site at the other end), genomic DNAs, and cDNAs.
CC The methods are highly specific, rapid, and less labour intensive than
CC prior art methods. The present sequence is a recombination site
CC useful for recombination cloning.
XX
SQ Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 other;
Query Match 100.0%; Score 25; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
PT vitro or in vivo
PS Claim 14; Page 55; 106pp; English.
XX
CC AAT48210-25 are att recombination site core region DNA sequences. The
CC core region has at least one engineered mutation that enhances
CC recombination in vitro in the formation of a Cointegrate or Product DNA.
CC These core regions can be incorporated into novel vector donor DNA
CC molecules. The nucleic acids, vectors and methods of the invention are
CC used to obtain chimeric nucleic acid using recombination proteins and
CC engineered recombination sites in vitro or in vivo. The improved
CC specificity, speed and yields of the invention facilitates DNA or RNA
CC subcloning, regulation or exchange useful for any related purpose, e.g.
CC in vitro recombination of DNA segments, and in vitro or in vivo insertion
CC or modification of transcribed, replicated, isolated or genomic DNA or
CC RNA.
XX
SQ Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 other;
Query Match 100.0%; Score 25; DB 18; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
DB 1 GTTCAGCTTTTGTACAAACTTGT 25
1 GTTCAGCTTTTGTACAAACTTGT 25
XX
RESULT 3
RAD14437
ID AAX78943 standard; DNA; 25 BP.
XX
AC AAX78943;
XX
DT 17-AUG-1999 (first entry)
XX
DE Oligonucleotide #9 for recombination and cloning method.
XX
KW Cloning; donor; recombination site; vector; chimeric; ss.
XX
OS Synthetic.
XX
PN WO9921977-A1.
XX
PD 06-MAY-1999.
XX
PF 26-OCT-1998; 98WO-US22589.
XX
PR 23-OCT-1998; 98US-0177387.
PR 24-OCT-1997; 97US-0065930.
XX
PA (LIFE-) LIFE TECHNOLOGIES INC.
XX
PI Brasch MA, Fox DK, Hartley JL, Temple GF;
XX WPI; 1999-303011/25.
XX
PT New nucleic acid cloning methods
XX
PS Disclosure; Page 161; 185pp; English.
XX
CC The invention relates to novel methods for cloning or subcloning one or
CC more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or
CC in vivo: (1) at least one insert donor molecules (IDMs) comprising one
CC or more desired nucleic acid segments flanked by at least 2
CC recombination sites which do not recombine with each other; (2) one or
CC more vector donor molecules (VDMs) comprising at least 2 recombination
CC sites which do not recombine with each other; and (3) one or more
CC site-specific recombination proteins; (b) incubating the combination to
CC transfer one or more of the desired segments into one or more of the
CC VDMs, thereby producing one or more desired product molecules (PMs). The
CC methods can be used for the efficient and specific recombination of NAM
CC segments. They can be used to generate chimeric DNA or RNA molecules that

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OM nucleic - nucleic search, using sw model

Run on: November 6, 2003, 21:05:38 ; Search time 111.5 Seconds
(without alignments)

605.255 Million cell updates/sec

Title: US-10-055-001A-4

Perfect score: 25

Sequence: 1 gttcagctttttgtacaaactgt 25

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 25: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	25	18	attR1 core region.
2	25	100.0	25	20	Oligonucleotide #9
3	25	100.0	25	22	Recombination site
4	25	100.0	25	22	Phage-lambda recom
5	25	100.0	25	22	Recombination site
6	25	100.0	25	22	Escherichia coli c
7	25	100.0	25	24	Core sequence of r
8	25	100.0	25	25	Recombination site

9	25	100.0	25	25	ABZ58734	Att site nucleotid
10	25	100.0	25	25	ABT16628	Artificial plant c
C 11	25	100.0	35	22	AAL19591	Plasmid pBZC7201 c
C 12	25	100.0	35	24	ABL58593	Oligonucleotide MO
C 13	25	100.0	43	21	AAC55545	att site PCR prime
C 14	25	100.0	43	22	AAS06217	PCR primer attR1 u
C 15	25	100.0	82	21	AAC55503	Destination vector
C 16	25	100.0	87	21	AAC55517	Destination vector
C 17	25	100.0	95	21	AAC55497	Destination vector
C 18	25	100.0	102	21	AAC55458	GST expression cas
C 19	25	100.0	102	21	AAC55500	Destination vector
C 20	25	100.0	102	21	AAC55505	Destination vector
C 21	25	100.0	102	21	AAC55508	Destination vector
C 22	25	100.0	102	21	AAC55511	Destination vector
C 23	25	100.0	120	21	AAC55453	Trc expression cas
C 24	25	100.0	125	21	AAC55384	Recombination site
C 25	25	100.0	153	21	AAC55485	Destination vector
C 26	25	100.0	153	21	AAC55488	Destination vector
C 27	25	100.0	204	21	AAC55465	Destination vector
C 28	25	100.0	204	21	AAC55470	Destination vector
C 29	25	100.0	204	21	AAC55476	Destination vector
C 30	25	100.0	255	21	AAC55460	His6-Trx expressio
C 31	25	100.0	255	21	AAC55478	Destination vector
C 32	25	100.0	306	21	AAC55468	Destination vector
C 33	25	100.0	306	21	AAC55514	Destination vector
C 34	25	100.0	420	21	AAC55492	Destination vector
C 35	25	100.0	1846	24	AAD44626	Gateway transfer c
C 36	25	100.0	4554	21	AAC55541	attR reading frame
C 37	25	100.0	5148	24	AAD27063	Plasmid pGN39 DNA.
C 38	25	100.0	5848	21	AAC55481	Destination vector
C 39	25	100.0	5957	21	AAC55464	Destination vector
C 40	25	100.0	5957	21	AAC55467	Destination vector
C 41	25	100.0	6025	21	AAC55469	Destination vector
C 42	25	100.0	6264	21	AAC55507	Destination vector
C 43	25	100.0	6354	21	AAC55491	Destination vector
C 44	25	100.0	6422	21	AAC55483	Destination vector
C 45	25	100.0	6464	21	AAC55454	Destination vector

ALIGNMENTS

RESULT 1
AAT48218
ID AAT48218 standard; DNA; 25 BP.
XX
XX
AC AAT48218;
XX
DT 20-OCT-1997 (first entry)
XX
DE attR1 core region.
XX
KW att recombination site; core region; mutation; enhance; recombination;
KW vector; subcloning; regulation; exchange; ss.
XX
OS Synthetic.
XX
PN WO9640724-A1.
XX
PD 19-DEC-1996.
XX
PF 07-JUN-1996; 96WO-US10082.
XX
PR 07-JUN-1995; 95US-0486139.
XX
PA (LIFE-) LIFE TECHNOLOGIES INC.
XX
PI Brasch MA, Hartley JL;
XX
DR WPI; 1997-065168/06.
XX
PT Nucleic acids, vectors and methods to obtain chimeric nucleic acid -
PT using recombinant proteins and engineered recombination sites in

TITLE Recombinational cloning using engineered recombination sites
 JOURNAL Patent: US 6171861-A 16 09-JAN-2001;
 FEATURES Location/Qualifiers
 source 1..25
 BASE COUNT 5 a 4 c 6 g 10 t
 ORIGIN
 Query Match 83.2%; Score 20.8; DB 6; Length 25;
 Best Local Similarity 91.7%; Pred.No. 4.3e+02;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GTTCAGCTTTTGTACAAACTTG 24
 |||||
 Db 1 GTTCAGCTTCTTGTACAAAGTTG 24
 |||||

Search completed: November 6, 2003, 23:06:41
 Job time : 603 secs

ORGANISM Danio rerio
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Danio.
 1 (bases 1 to 145569)
 Direct Submission
 Submitted (12-DEC-2002) Wellcome Trust Sanger Institute, Hinxton,
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zface@sanger.ac.uk
 Clone requests: clonerequest@sanger.ac.uk
 On Dec 16, 2002 this sequence version replaced gi:24940082.
 ----- Genome Center
 Center: Wellcome Trust Sanger Institute
 Center code: SC
 Web site: <http://www.sanger.ac.uk>
 Contact: zface@sanger.ac.uk

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
 This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
 Em.: EMBL; Sw.: SWISSPROT; Tr.: TREMBL; Wp.: WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/projects/C_elegans/wormpep Repeat names beginning 'dr' were identified by the Recon repeat discovery system (Zhong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see http://www/Projects/D_rerio/fishmask.shtml
 CH211-237E12 is from a CHORI-211 BAC library
 VECTOR: pTARBAC21.1.

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 /db_xref="taxon:7955"
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 /clone_lib="CHORI-211"

BASE COUNT 48166 a 26034 c 25755 g 45614 t
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Query Match 87.2%; Score 21.8; DB 5; Length 145569;
 Best Local Similarity 92.0%; Pred. No. 32;
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTGACAAACTTGT 25
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 Db 43543 GTTCGCTTTTGTGACAAACTTAT 43567

RESULT 38
 BD131369
 LOCUS 25 bp DNA linear PAT 18-SEP-2002
 DEFINITION Recombinational cloning using nucleic acids having recombination sites.
 ACCESSION BD131369
 VERSION BD131369.1 GI:23226314
 KEYWORDS JP 2002500861-A/43.
 SOURCE unidentified
 ORGANISM unclassified
 REFERENCE 1 (bases 1 to 25)
 AUTHORS

AUTHORS
 TITLE
 JOURNAL
 COMMENT

Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.
 Recombinational cloning using nucleic acids having recombination
 Patent: JP 2002500861-A 43 15-JAN-2002;
 LIFE TECHNOLOGIES INC
 OS Unknown
 PN JP 2002500861-A/43
 PD 15-JAN-2002
 PF 26-OCT-1998 JP 2000518069
 PR 24-OCT-1997 US 60/065930, 23-OCT-1998 US 09/177387 PT
 JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DONNA K FOX PC
 C12N15/09, C12Q1/68, C12N15/00
 CC Description of Unknown Organism: recombination products PH
 Key Location/Qualifiers
 FT source 1..25
 /organism="Unknown".

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BASE COUNT 4 a 3 c 5 g 10 t 3 others
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Query Match 84.8%; Score 21.2; DB 6; Length 25;
 Best Local Similarity 83.3%; Pred. No. 2.9e+02;
 Matches 20; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTGACAAACTTG 24
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RESULT 39
 AR124531
 LOCUS 25 bp DNA linear PAT 16-MAY-2001
 DEFINITION Sequence 11 from patent US 6171861.
 ACCESSION AR124531
 VERSION AR124531.1 GI:14109892
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 25)
 AUTHORS Hartley,J.L. and Brasch,M.A.
 TITLE Recombinational cloning using engineered recombination sites
 JOURNAL Patent: US 6171861-A 11 09-JAN-2001;
 FEATURES Location/Qualifiers
 source 1..25
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BASE COUNT 5 a 4 c 6 g 10 t
 ORIGIN

Query Match 83.2%; Score 20.8; DB 6; Length 25;
 Best Local Similarity 91.7%; Pred. No. 4.3e+02;
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QY 1 GTTCAGCTTTTGTGACAAACTTG 24
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 Db 1 GTTCAGCTTTTGTGACAAACTTG 24

RESULT 40
 AR124536
 LOCUS 25 bp DNA linear PAT 16-MAY-2001
 DEFINITION Sequence 16 from patent US 6171861.
 ACCESSION AR124536
 VERSION AR124536.1 GI:14109897
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 25)
 AUTHORS Hartley,J.L. and Brasch,M.A.

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 1 GTTCAGCTTCTTGTACAAACTTGT 25

RESULT 33
AX525413/c
LOCUS AX525413 51 bp DNA linear PAT 21-NOV-2002
DEFINITION Sequence 11 from Patent WO02066622.
ACCESSION AX525413
VERSION AX525413.1 GI:25170299
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Tautumi,N., Vind,J. and Patkar,S.A.
TITLE Lipolytic enzyme genes
JOURNAL Patent: WO 02066622-A 11 29-AUG-2002;
Novozymes A/S (DK)

FEATURES
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BASE COUNT 15 a 10 c 17 g 9 t
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Query Match 87.2%; Score 21.8; DB 6; Length 51;
Best Local Similarity 92.0%; Pred. No. 1.4e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 29 GTCTGCTTTTGTACAAACTTGT 5

RESULT 34
AX525421/c
LOCUS AX525421 51 bp DNA linear PAT 21-NOV-2002
DEFINITION Sequence 19 from Patent WO02066622.
ACCESSION AX525421
VERSION AX525421.1 GI:25170307
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Tautumi,N., Vind,J. and Patkar,S.A.
TITLE Lipolytic enzyme genes
JOURNAL Patent: WO 02066622-A 19 29-AUG-2002;
Novozymes A/S (DK)

FEATURES
Location/Qualifiers
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BASE COUNT 16 a 10 c 15 g 10 t
ORIGIN

Query Match 87.2%; Score 21.8; DB 6; Length 51;
Best Local Similarity 92.0%; Pred. No. 1.4e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 29 GTCTGCTTTTGTACAAACTTGT 5

RESULT 35

AX525429/c
LOCUS AX525429 51 bp DNA linear PAT 21-NOV-2002
DEFINITION Sequence 27 from Patent WO02066622.
ACCESSION AX525429
VERSION AX525429.1 GI:25170315
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Tautumi,N., Vind,J. and Patkar,S.A.
TITLE Lipolytic enzyme genes
JOURNAL Patent: WO 02066622-A 27 29-AUG-2002;
Novozymes A/S (DK)

FEATURES
Location/Qualifiers
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/db_xref="taxon:32630"
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BASE COUNT 14 a 12 c 16 g 9 t
ORIGIN

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Best Local Similarity 92.0%; Pred. No. 1.4e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 29 GTCTGCTTTTGTACAAACTTGT 5

RESULT 36
AX525456/c
LOCUS AX525456 51 bp DNA linear PAT 21-NOV-2002
DEFINITION Sequence 54 from Patent WO02066622.
ACCESSION AX525456
VERSION AX525456.1 GI:25170342
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Tautumi,N., Vind,J. and Patkar,S.A.
TITLE Lipolytic enzyme genes
JOURNAL Patent: WO 02066622-A 54 29-AUG-2002;
Novozymes A/S (DK)

FEATURES
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BASE COUNT 18 a 10 c 13 g 10 t
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Best Local Similarity 92.0%; Pred. No. 1.4e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 29 GTCTGCTTTTGTACAAACTTGT 5

RESULT 37
AL935194
LOCUS AL935194 145569 bp DNA linear VRT 13-DEC-2002
DEFINITION Zebrafish DNA sequence from clone CH211-237E12, complete sequence.
ACCESSION AL935194
VERSION AL935194.4 GI:26985414
KEYWORDS HTG.
SOURCE Danio rerio (zebrafish)

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JOURNAL      silencing in plants
MEDLINE      Plant J. 27 (6), 581-590 (2001)
PUBMED       21461301
REFERENCE    11576441
TITLES       2 (bases 1 to 18691)
AUTHORS      Waterhouse, P.M.
JOURNAL      Submitted (04-MAY-2001) Waterhouse P.M., Plant Industry,
              C.S.I.R.O., P.O. Box 1600, Canberra, ACT 2601, AUSTRALIA
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KEYWORDS kanomycin resistance protein; neomycin phosphotransferase II; nptII gene; promoter; spec gene; spectinomycin resistance protein; transposon Tn7.

SOURCE Cloning vector pHELLSGATE

ORGANISM artificial sequences; vectors.

REFERENCE 1

AUTHORS Wesley, V.S., Helliwell, C., Smith, N.A., Wang, M.B., Rouse, D., Liu, Q., Gooding, P.S., Singh, S.R., Abbott, D., Stoutjesdijk, A., Robinson, S.P., Gleave, A.P., Green, A.G. and Waterhouse, P.M.

TITLE Construct design for efficient, effective and high-throughput gene silencing in plants

JOURNAL Plant J. 27 (6), 581-590 (2001)

MEDLINE 21461301

PMID 11576441

REFERENCE 2 (bases 1 to 18691)

AUTHORS Waterhouse, P.M.

TITLE Direct Submission

JOURNAL Submitted (04-MAY-2001) Waterhouse P.M., Plant Industry, C.S.I.R.O., P.O. Box 1600, Canberra, ACT 2601, AUSTRALIA

FEATURES Location/Qualifiers

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promoter

/function="35S promoter"

14660..16258

gene

/gene="pdk"

14660..16258

intron

/gene="pdk"

/note="pyruvate orthophosphate dikinase (pdk)"

/number=2

17922..18697

terminator

/note="octopine esynthese (ocs) terminator"

BASE COUNT 4837 a 4621 c 4607 g 4626 t

ORIGIN

Query Match 89.6%; Score 22.4; DB 12; Length 18691;

Best Local Similarity 95.8%; Pred. No. 26;

Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTG 24

|||||

Db 17792 GTTCAGCTTTTGTACAACTTG 17815

RESULT 31

CVE311874/c

LOCUS 18691 bp DNA circular SYN 09-JUL-2002

DEFINITION Cloning vector pHELLSGATE.

ACCESSION AJ311874

VERSION AJ311874.1 GI:15982218

KEYWORDS kanomycin resistance protein; neomycin phosphotransferase II; nptII gene; promoter; spec gene; spectinomycin resistance protein; transposon Tn7.

SOURCE Cloning vector pHELLSGATE

ORGANISM Cloning vector pHELLSGATE

REFERENCE 1

Wesley, V.S., Helliwell, C., Smith, N.A., Wang, M.B., Rouse, D., Liu, Q., Gooding, P.S., Singh, S.R., Abbott, D., Stoutjesdijk, A., Robinson, S.P., Gleave, A.P., Green, A.G. and Waterhouse, P.M.

Construct design for efficient and high-throughput gene

TITLE

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Db      1 GTTCAGCTTTTGTACAAAGTTG 24

RESULT 26
LOCUS   AR163186                      25 bp    DNA
DEFINITION
Sequence 15 from patent US 6270969.
ACCESSION AR163186
VERSION   AR163186.1 GI:16233698
KEYWORDS
SOURCE   Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 25)
Hartley,J.L. and Brasch,M.A.
Recombinational cloning using engineered recombination sites
TITLE
Patent: US 6270969-A 15 07-AUG-2001;
JOURNAL
INVITROGEN CORPORATION (US)
FEATURES
location/Qualifiers
source
1..25
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT 5 a 3 c 6 g 11 t
ORIGIN

Query Match 89.6%; Score 22.4; DB 6; Length 25;
Best Local Similarity 95.8%; Pred. No. 90;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GTTCAGCTTTTGTACAAAGTTG 24
|||||
Db      1 GTTCAGCTTTTGTACAAAGTTG 24

RESULT 27
LOCUS   AX491654                      25 bp    DNA
DEFINITION
Sequence 15 from Patent EP1227147.
ACCESSION AX491654
VERSION   AX491654.1 GI:22324162
KEYWORDS
SOURCE   unidentified
ORGANISM
unclassified.
REFERENCE
1
Hartley,J.L. and Brasch,M.A.
Recombinational cloning using engineered recombination sites
TITLE
Patent: EP 1227147-A 15 31-JUL-2002;
JOURNAL
INVITROGEN CORPORATION (US)
FEATURES
location/Qualifiers
source
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT 5 a 3 c 6 g 11 t
ORIGIN

Query Match 89.6%; Score 22.4; DB 6; Length 25;
Best Local Similarity 95.8%; Pred. No. 90;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GTTCAGCTTTTGTACAAAGTTG 24
|||||
Db      1 GTTCAGCTTTTGTACAAAGTTG 24

RESULT 28
LOCUS   AX498625                      25 bp    DNA
DEFINITION
Sequence 15 from Patent EP1229113.
ACCESSION AX498625
VERSION   AX498625.1 GI:23343422
KEYWORDS
SOURCE   unidentified
ORGANISM
unclassified.
REFERENCE
1
Hartley,J.L. and Brasch,M.A.
Recombinational cloning using engineered recombination sites
TITLE
Patent: EP 1229113-A 15 07-AUG-2002;
JOURNAL
INVITROGEN CORPORATION (US)
FEATURES
location/Qualifiers
source
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT 5 a 3 c 6 g 11 t
ORIGIN

Query Match 89.6%; Score 22.4; DB 6; Length 25;
Best Local Similarity 95.8%; Pred. No. 90;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GTTCAGCTTTTGTACAAAGTTG 24
|||||
Db      1 GTTCAGCTTTTGTACAAAGTTG 24

RESULT 29
LOCUS   BD131341                      25 bp    DNA
DEFINITION
Recombinational cloning using nucleic acids having recombination
sites.
ACCESSION BD131341
VERSION   BD131341.1 GI:23226286
KEYWORDS
SOURCE   unidentified
ORGANISM
unclassified.
REFERENCE
1 (bases 1 to 25)
Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.
Recombinational cloning using nucleic acids having recombination
TITLE
Patent: JP 2002500861-A 15 15-JAN-2002;
JOURNAL
LIFE TECHNOLOGIES INC
COMMENT
OS Unknown
PN JP 2002500861-A/15
PD 15-JAN-2002
PF 26-OCT-1998 JP 2000518069
PR 24-OCT-1997 US 60/065930,23-OCT-1998 US 09/177387 PI
JAMES L HARTLEY,MICHAEL A BRASCH,GARY F TEMPLE,DONNA K FOX PC
C12N15/09,C12Q1/68,C12N15/00
CC Description of Unknown Organism: recombination products FH
Key Location/Qualifiers
FT source
1..25
/organism='Unknown'
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT 5 a 3 c 6 g 11 t
ORIGIN

Query Match 89.6%; Score 22.4; DB 6; Length 25;
Best Local Similarity 95.8%; Pred. No. 90;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GTTCAGCTTTTGTACAAAGTTG 24
|||||
Db      1 GTTCAGCTTTTGTACAAAGTTG 24

RESULT 30
LOCUS   CVE311874                      18691 bp   DNA
DEFINITION
Cloning vector pHELLSGATE.
ACCESSION AJ311874
VERSION   AJ311874.1 GI:15982218

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unclassified.

REFERENCE

1
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: EP 1229113-A 15 07-AUG-2002;
INVITROGEN CORPORATION (US)

FEATURES

source
1..25
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

BASE COUNT

5 a 3 c 6 g 11 t

ORIGIN

Query Match 89.6%; Score 22.4; DB 6; Length 25;

Best Local Similarity 95.8%; Pred. No. 90;

Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY

1 GTTCAGCTTTTGTACAAAGTTG 24

Db

1 GTTCAGCTTTTGTACAAAGTTG 24

RESULT 29

BD131341

LOCUS

BD131341 25 bp DNA linear PAT 18-SEP-2002
DEFINITION
Recombinational cloning using nucleic acids having recombination
sites.

ACCESSION

BD131341

VERSION

BD131341.1 GI:23226286

KEYWORDS

JP 2002500861-A/15.

SOURCE

unidentified

ORGANISM

unclassified.

REFERENCE

1 (bases 1 to 25)

AUTHORS

Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.

TITLE

Recombinational cloning using nucleic acids having recombination

JOURNAL

Patent: JP 2002500861-A 15 15-JAN-2002;

COMMENT

LIFE TECHNOLOGIES INC

OS

Unknown

PN

JP 2002500861-A/15

PD

15-JAN-2002

PF

26-OCT-1998 JP 2000518069

PR

24-OCT-1997 US 60/065930,23-OCT-1998 US 09/177387 PI

JAMES L HARTLEY,MICHAEL A BRASCH,GARY F TEMPLE,DONNA K FOX PC

C12N15/09,C12Q1/68,C12N15/00

CC

Description of Unknown Organism: recombination products FH

Key

Location/Qualifiers

FT

source 1..25 /organism='Unknown'

FEATURES

source 1..25 /organism="unidentified"

BASE COUNT

5 a 3 c 6 g 11 t

ORIGIN

Query Match 89.6%; Score 22.4; DB 6; Length 25;

Best Local Similarity 95.8%; Pred. No. 90;

Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY

1 GTTCAGCTTTTGTACAAAGTTG 24

Db

1 GTTCAGCTTTTGTACAAAGTTG 24

RESULT 30

CVE311874

LOCUS

CVE311874 18691 bp DNA circular SYN 09-JUL-2002
DEFINITION
Cloning vector pHELLSGATE.
ACCESSION AJ311874
VERSION AJ311874.1 GI:15982218

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RESULT 22
LOCUS AX498620 25 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 10 from Patent EP1229113.
ACCESSION AX498620
VERSION AX498620.1 GI:23343417
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE
1 Hartley,J.L. and Brasch,M.A.
AUTHORS
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: EP 1229113-A 10 07-AUG-2002;
INVITROGEN CORPORATION (US)
FEATURES
source 1. .25
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT 5 a 5 c 4 g 11 t
ORIGIN
Query Match 93.6%; Score 23.4; DB 6; Length 25;
Best Local Similarity 96.0%; Pred. No. 34;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAACTTGT 25
|||||
Db 1 GTTCAGCTTTTGTACAACTTGT 25

RESULT 23
LOCUS BD131336 25 bp DNA linear PAT 18-SEP-2002
DEFINITION Recombinational cloning using nucleic acids having recombination
sites.
ACCESSION BD131336
KEYWORDS JP 2002500861-A/10.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE
1 (bases 1 to 25)
AUTHORS Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.
TITLE Recombinational cloning using nucleic acids having recombination
JOURNAL Patent: JP 2002500861-A 10 15-JAN-2002;
LIFE TECHNOLOGIES INC
COMMENT
OS Unknown
PN JP 2002500861-A/10
PD 15-JAN-2002
PF 26-OCT-1998 JP 2000518069
PR 24-OCT-1997 US 60/065930, 23-OCT-1998 US 09/177387 PI
JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DONNA K FOX PC
C12N15/09, C12Q1/68, C12N15/00
CC Description of Unknown Organism: recombination products FH
KEY Location/Qualifiers
FT source 1. .25
/organism="Unknown".
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source 1. .25
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT 5 a 5 c 4 g 11 t
ORIGIN
Query Match 93.6%; Score 23.4; DB 6; Length 25;
Best Local Similarity 96.0%; Pred. No. 34;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAACTTGT 25
|||||
Db 1 GTTCAGCTTTTGTACAACTTGT 25

RESULT 24
LOCUS BD131336 25 bp DNA linear PAT 18-SEP-2002
DEFINITION Recombinational cloning using nucleic acids having recombination
sites.
ACCESSION BD131336
KEYWORDS JP 2002500861-A/42.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE
1 (bases 1 to 25)
AUTHORS Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.
TITLE Recombinational cloning using nucleic acids having recombination
JOURNAL Patent: JP 2002500861-A 42 15-JAN-2002;
LIFE TECHNOLOGIES INC
COMMENT
OS Unknown
PN JP 2002500861-A/42
PD 15-JAN-2002
PF 26-OCT-1998 JP 2000518069
PR 24-OCT-1997 US 60/065930, 23-OCT-1998 US 09/177387 PI
JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DONNA K FOX PC
C12N15/09, C12Q1/68, C12N15/00
CC Description of Unknown Organism: recombination products FH
KEY Location/Qualifiers
FT source 1. .25
/organism="Unknown".
FEATURES
source 1. .25
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT 4 a 3 c 3 g 9 t 6 others
ORIGIN
Query Match 90.4%; Score 22.6; DB 6; Length 25;
Best Local Similarity 76.0%; Pred. No. 74;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAACTTGT 25
|||||
Db 1 GTTCAGCTTTTGTACAACTTGT 25

RESULT 25
LOCUS AR124535 25 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 15 from patent US 6171861.
ACCESSION AR124535
VERSION AR124535.1 GI:14109896
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
1 (bases 1 to 25)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6171861-A 15 09-JAN-2001;
FEATURES
source 1. .25
/organism="unknown"
BASE COUNT 5 a 3 c 6 g 11 t
ORIGIN
Query Match 89.6%; Score 22.4; DB 6; Length 25;
Best Local Similarity 95.8%; Pred. No. 90;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAACTTGT 24
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Db 1 GTTCAGCTTTTGTACAACTTGT 25

RESULT 24
LOCUS BD131368 25 bp DNA linear PAT 18-SEP-2002
DEFINITION Recombinational cloning using nucleic acids having recombination
sites.
ACCESSION BD131368
KEYWORDS JP 2002500861-A/42.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE
1 (bases 1 to 25)
AUTHORS Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.
TITLE Recombinational cloning using nucleic acids having recombination
JOURNAL Patent: JP 2002500861-A 42 15-JAN-2002;
LIFE TECHNOLOGIES INC
COMMENT
OS Unknown
PN JP 2002500861-A/42
PD 15-JAN-2002
PF 26-OCT-1998 JP 2000518069
PR 24-OCT-1997 US 60/065930, 23-OCT-1998 US 09/177387 PI
JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DONNA K FOX PC
C12N15/09, C12Q1/68, C12N15/00
CC Description of Unknown Organism: recombination products FH
KEY Location/Qualifiers
FT source 1. .25
/organism="Unknown".
FEATURES
source 1. .25
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT 4 a 3 c 3 g 9 t 6 others
ORIGIN
Query Match 90.4%; Score 22.6; DB 6; Length 25;
Best Local Similarity 76.0%; Pred. No. 74;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAACTTGT 25
|||||
Db 1 GTTCAGCTTTTGTACAACTTGT 25

RESULT 25
LOCUS AR124535 25 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 15 from patent US 6171861.
ACCESSION AR124535
VERSION AR124535.1 GI:14109896
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
1 (bases 1 to 25)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6171861-A 15 09-JAN-2001;
FEATURES
source 1. .25
/organism="unknown"
BASE COUNT 5 a 3 c 6 g 11 t
ORIGIN
Query Match 89.6%; Score 22.4; DB 6; Length 25;
Best Local Similarity 95.8%; Pred. No. 90;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAACTTGT 24
|||||

```



```

Construction of Neurospora crassa Histidine-3 (his-3) -Gene
Replacement Plasmids
JOURNAL
REFERENCE 2 (bases 1 to 13990)
AUTHORS Haag, J.R., Lee, D.W. and Aramayo, R.
TITLE Direct Substitution
JOURNAL Submitted (27-AUG-2002) Biology, Texas A&M University, BSW #415,
College Station, TX 77843-3258, USA
FEATURES
source
1..13990
Location/Qualifiers
/organism="his-3 integration vector pUHAM007"
/mol_type="genomic DNA"
/specific_host="Neurospora crassa"
/db_xref="taxon:211505"
1..3173
/note="pCEM132f(+)"
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3174..8368
/note="his-3 left flank; his-3 target integration site"
misc_feature
8430..8554
/note="attR1; Gateway; Bacteriophage Lambda recombination
site"
CDS
8804..9463
/codon_start=1
/product="chloramphenicol acetyl transferase"
/protein_id="AA076304.1"
/db_xref="GI:25988998"
/translation="MEKKTGYTVDISQWHRKEHFEAFQSVAACTYNCTVOLDITAF
LKTVMKHKFPATPHILARLNNAHPERMAKDELVLWDSVHPCVTPHEQETEF
SSLSEYHDDPFLHIYSQDVACYNLAYFPKGFENWFFVSANPVVFTSFLNV
ANMDFAPFVFTMGKYYTGQDKVLMPLAIQVHHAVCDFGHVGRMLNELQQYCDWQGG
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CDS
9805..10110
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/protein_id="AA076305.1"
/db_xref="GI:25988999"
/translation="MOPKVYTYKRESRYRLFVDVSDIIDTPGRRMVPIPLASARLLSD
KVSRELYPVVHIGDSWRMTTDMASVPVSGEEVADLSHRENDIKNAINLMFWGI"
misc_feature
10151..10275
/note="attR2; Gateway; Bacteriophage Lambda recombination
site"
misc_feature
10419..13990
/note="his-3 right flank; his-3 target integration site"
BASE COUNT 3385 a 3549 c 3559 g 3497 t
ORIGIN
Query Match 100.0%; Score 25; DB 12; Length 13990;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTGACAAACTTGT 25
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Db 8454 GTTCAGCTTTTGTGACAAACTTGT 8430

RESULT 19
LOCUS AR124530 25 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 10 from patent US 6171861.
ACCESSION AR124530
VERSION AR124530.1 GI:14109891
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley, J.L. and Brasch, M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6171861-A 10 09-JAN-2001;
FEATURES
source
1..25
Location/Qualifiers
/organism="unknown"

QY 1 GTTCAGCTTTTGTGACAAACTTGT 25
|||||
Db 1 GTTCAGCTTTTGTGACAAACTTGT 25

BASE COUNT 5 a 5 c 4 g 11 t
ORIGIN
Query Match 93.6%; Score 23.4; DB 6; Length 25;
Best Local Similarity 96.0%; Pred. No. 34;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTGACAAACTTGT 25
|||||
Db 1 GTTCAGCTTTTGTGACAAACTTGT 25

RESULT 20
LOCUS AR163181 25 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 10 from patent US 6270969.
ACCESSION AR163181
VERSION AR163181.1 GI:16233690
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley, J.L. and Brasch, M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6270969-A 10 07-AUG-2001;
FEATURES
source
1..25
Location/Qualifiers
/organism="unknown"

BASE COUNT 5 a 5 c 4 g 11 t
ORIGIN
Query Match 93.6%; Score 23.4; DB 6; Length 25;
Best Local Similarity 96.0%; Pred. No. 34;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTGACAAACTTGT 25
|||||
Db 1 GTTCAGCTTTTGTGACAAACTTGT 25

RESULT 21
LOCUS AX491649 25 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 10 from Patent EP1227147.
ACCESSION AX491649
VERSION AX491649.1 GI:22324157
KEYWORDS
SOURCE unidentified
ORGANISM unidentified.
REFERENCE 1
AUTHORS Hartley, J.L. and Brasch, M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: EP 1227147-A 10 31-JUL-2002;
FEATURES
source
1..25
Location/Qualifiers
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

BASE COUNT 5 a 5 c 4 g 11 t
ORIGIN
Query Match 93.6%; Score 23.4; DB 6; Length 25;
Best Local Similarity 96.0%; Pred. No. 34;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTGACAAACTTGT 25
|||||
Db 1 GTTCAGCTTTTGTGACAAACTTGT 25

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Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 4760 GTTCAGCTTTTGTACAAACTTGT 4784

RESULT 15
AX196825/c
LOCUS AX196825 12677 bp DNA circular SYN 26-FEB-2003
DEFINITION PiggyBac transformation vector pB-UGIR w+, complete sequence.
ACCESSION AX196825
VERSION AX196825.1 GI:28565731
KEYWORDS piggyBac transformation vector pB-UGIR w+
SOURCE piggyBac transformation vector pB-UGIR w+
ORGANISM piggyBac transformation vector pB-UGIR w+
artificial sequences; vectors.
REFERENCE 1 (bases 1 to 12677)
AUTHORS Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE A toolkit for transformation and mutagenesis in Drosophila using
piggyBac
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 12677)
AUTHORS Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE Direct Submission
JOURNAL Submitted (13-DEC-2002) Invertebrate Targets, Syngenta
Biotechnology, Inc., 3054 Cornwallis Rd, Research Triangle Park, NC
27709, USA
FEATURES
source
1..12677
/organism="piggyBac transformation vector pB-UGIR w+"
/mol_type="genomic DNA"
/db_xref="taxon:221642"
complement(11..>620)
/transposon="piggyBac transposable element"
632..998
/note="5x UAS hsp70 TATA signal"
1003..2713
/note="Gateway recombination cassette A; attR1 Cmr codb
attR2"
2726..3040
/note="RpS5"
/number=3
complement(3076..4788)
/note="Gateway recombination cassette B; attR1 Cmr codb
attR2"
4789..5246
/note="SV40"
5247..9369
/gene="w"
/note="mini-white; derived from Drosophila"
repeat_region complement(<9370..9819)
/transposon="piggyBac transposable element"
BASE COUNT 3423 a 2924 c 2833 g 3497 t
ORIGIN
Query Match 100.0%; Score 25; DB 12; Length 12677;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 1030 GTTCAGCTTTTGTACAAACTTGT 1006

RESULT 16
AX590202
LOCUS AX590202 12789 bp DNA linear PAT 24-JAN-2003
DEFINITION Sequence 9 from Patent WO02083888.
ACCESSION AX590202
VERSION AX590202.1 GI:27901286
KEYWORDS
```

```
synthetic construct
synthetic construct
artificial sequences.
1
Goossens,A. and Inz,D.
The use of genes encoding membrane transporter pumps to stimulate
the production of secondary metabolites in biological cells
Patent: WO 02083888-A 9 24-OCT-2002;
Vlaams Interuniversitair Instituut voor Biotechnologie vzw. (BE)
FEATURES
source
1..12789
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="vector pK7WG2D"
BASE COUNT 3050 a 3326 c 3397 g 3015 t
ORIGIN
1 others
Query Match 100.0%; Score 25; DB 6; Length 12789;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 3701 GTTCAGCTTTTGTACAAACTTGT 3725

RESULT 17
AX356862
LOCUS AX356862 13274 bp DNA linear PAT 13-FEB-2002
DEFINITION Sequence 20 from Patent WO0206490.
ACCESSION AX356862
VERSION AX356862.1 GI:18674110
KEYWORDS
SOURCE synthetic construct
synthetic construct
artificial sequences.
1
Dudler,R., Schaffrath,U. and Lawton,K.A.
Lipoxygenase genes, promoters, transit peptides and proteins
thereof
Patent: WO 0206490-A 20 24-JAN-2002;
Syngenta Participations AG (CH); Universitaet Zuerich (CH)
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source
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
BASE COUNT 3343 a 3271 c 3178 g 3482 t
ORIGIN
Query Match 100.0%; Score 25; DB 6; Length 13274;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 4026 GTTCAGCTTTTGTACAAACTTGT 4050

RESULT 18
AF541939/c
LOCUS AF541939 13990 bp DNA linear SYN 01-DEC-2002
DEFINITION His-3 integration vector pJHAM007, complete sequence.
ACCESSION AF541939
VERSION AF541939.1 GI:25988997
KEYWORDS
SOURCE his-3 integration vector pJHAM007
ORGANISM his-3 integration vector pJHAM007
artificial sequences; vectors.
REFERENCE 1 (bases 1 to 13990)
AUTHORS Haag,J.R., Lee,D.W. and Aramayo,R.
TITLE Description of a GATEWAY Destination Vector For High-Throughput
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JOURNAL Unpublished
REFERENCE 2 (bases 1 to 11005)
AUTHORS Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE Direct Submission
JOURNAL Submitted (13-DEC-2002) Invertebrate Targets, Syngenta
Biotechnology, Inc., 3054 Cornwallis Rd, Research Triangle Park, NC
27709, USA

FEATURES
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        /db_xref="taxon:221641"
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        643..999
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        1003..2713
    misc_feature      /note="Gateway recombination cassette A; attr1 CmR ccdB
        attR2"
    intron            2726..3040
        /note="RpS5"
        /number=3
    polyA_signal      3072..3573
        /note="SV40"
    gene              3574..7697
        /gene="w"
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        Best Local Similarity 100.0%; Pred. No. 2.3;
        Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

    QY 1 GTTCAGCTTTTGTACAACTTGT 25
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    Db 3089 GTTCAGCTTTTGTACAACTTGT 3113

RESULT 13
AY196824/c
LOCUS AY196824 piggyBac transformation vector pB-UGateway w+ 11005 bp DNA circular SYN 26-FEB-2003
DEFINITION PiggyBac transformation vector pB-UGateway w+, complete sequence.
ACCESSION AY196824
VERSION AY196824.1 GI:28565716
KEYWORDS
SOURCE piggyBac transformation vector pB-UGateway w+
ORGANISM artificial sequences; vectors.
REFERENCE 1 (bases 1 to 11005)
AUTHORS Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE A toolkit for transformation and mutagenesis in Drosophila using
piggyBac
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 11005)
AUTHORS Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE Direct Submission
JOURNAL Submitted (13-DEC-2002) Invertebrate Targets, Syngenta
Biotechnology, Inc., 3054 Cornwallis Rd, Research Triangle Park, NC
27709, USA

FEATURES
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        /db_xref="taxon:221641"
        complement(11..>620)
    repeat_region     /transposon="piggyBac transposable element"
        643..999
    TATA_signal       /note="5x UAS hsp70 TATA signal"
        1003..2713
    misc_feature      /note="Gateway recombination cassette A; attr1 CmR ccdB
        attR2"
    intron            2726..3040
        /note="RpS5"
        /number=3
    polyA_signal      3072..3573
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        complement(<7698..8147)
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        Best Local Similarity 100.0%; Pred. No. 2.3;
        Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

    QY 1 GTTCAGCTTTTGTACAACTTGT 25
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    Db 3089 GTTCAGCTTTTGTACAACTTGT 3113

RESULT 14
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LOCUS AY196825 piggyBac transformation vector pB-UGIR w+ 12677 bp DNA circular SYN 26-FEB-2003
DEFINITION PiggyBac transformation vector pB-UGIR w+, complete sequence.
ACCESSION AY196825
VERSION AY196825.1 GI:28565731
KEYWORDS
SOURCE piggyBac transformation vector pB-UGIR w+
ORGANISM artificial sequences; vectors.
REFERENCE 1 (bases 1 to 12677)
AUTHORS Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE A toolkit for transformation and mutagenesis in Drosophila using
piggyBac
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 12677)
AUTHORS Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE Direct Submission
JOURNAL Submitted (13-DEC-2002) Invertebrate Targets, Syngenta
Biotechnology, Inc., 3054 Cornwallis Rd, Research Triangle Park, NC
27709, USA

FEATURES
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        /db_xref="taxon:221642"
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        1003..2713
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        attR2"
    intron            2726..3040
        /note="RpS5"
        /number=3
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        attR2"
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        /note="SV40"
    gene              5247..9369
        /gene="w"
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KVSRELYPVVHIGDESRRMTDMASVPVSVIGEEVADLSHRENDIKNAINLFWGI"
1610..1736
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1762..2048
/notes="contains intron 1 of Arabidopsis thaliana WRKY
transcription factor 33"
complement(2073..3783)
/notes="antisense orientation of Gateway conversion
cassette frame A containing attR1-R2 repeats, Cmr gene and
ccdB gene"
complement(2073..2199)
/notes="attR2 of Gateway conversion cassette frame A"
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complement(2241..2546)
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of DNA gyrase"
of DNA gyrase"
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/protein_id="AAM62303.1"
/db_xref="GI:21552740"
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chloramphenicol"
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/product="Cmr"
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/db_xref="GI:21552739"
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complement(3657..3783)
/notes="attR1 of Gateway conversion cassette frame A"
BASE COUNT      2337 a 2150 c 2185 g 2347 t
ORIGIN

Query Match      100.0%; Score 25; DB 12; Length 9019;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAACTTGT 25
|||||
Db 3756 GTTCAGCTTTTGTACAAACTTGT 3780

RESULT 11
AF408413/c
LOCUS      AF408413      9019 bp      DNA      circular SYN 25-JUN-2002
DEFINITION Binary vector pJawohl8-RNAi, complete sequence.
ACCESSION  AF408413
VERSION     AF408413.1 GI:21552736
KEYWORDS   Binary vector pJawohl8-RNAi
SOURCE     Binary vector pJawohl8-RNAi
ORGANISM   Binary vector pJawohl8-RNAi
artificial sequences; vectors.
REFERENCE  1 (bases 1 to 9019)
AUTHORS   Ulker,B., Lipka,V., Rademacher,T.R. and Somssich,I.E.
TITLE     pJawohl8-RNAi a binary vector for gene silencing in plants
JOURNAL   Unpublished
REFERENCE  2 (bases 1 to 9019)
AUTHORS   Ulker,B., Lipka,V., Rademacher,T.R. and Somssich,I.E.
TITLE     Direct Submission
JOURNAL   Submitted (08-AUG-2001) Biochemistry, Max-Planck-Institut
f. Zuechtungsforshung, Carl-von-Linne Weg 10, Koeln, NRW D-50829,
Germany
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:188084"
                     /focus
     note="binary plant gene silencing vector for one-step
cloning of inverted sequences"
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     /mol_type="genomic DNA"
     /db_xref="taxon:176105"
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frame A containing attR1-R2 repeats, Cmr gene and ccdB
gene"
     26..152
     /note="attR1 of Gateway conversion cassette frame A"
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     /function="confers resistance to antibiotic
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     /protein_id="AAM62300.1"
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A"
     1263..1568
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     /gene="ccdB"
     /note="encodes a cytotoxic protein that is a potent poison
of DNA gyrase"
of DNA gyrase"
/codon_start=1
/product="CcdB"
/protein_id="AAM62301.1"
/db_xref="GI:21552738"
/translation="MOKKYTYTKRSRYRLFDVQSDIIDTPGRRWVPIASARLLSD
KVSRELYPVVHIGDESRRMTDMASVPVSVIGEEVADLSHRENDIKNAINLFWGI"
1610..1736
/notes="attR2 of Gateway conversion cassette frame A"
1762..2048
/notes="contains intron 1 of Arabidopsis thaliana WRKY
transcription factor 33"
complement(2073..3783)
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/notes="attR2 of Gateway conversion cassette frame A"
complement(2241..2546)
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of DNA gyrase"
of DNA gyrase"
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/db_xref="GI:21552739"
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A"
complement(3657..3783)
/notes="attR1 of Gateway conversion cassette frame A"
BASE COUNT      2337 a 2150 c 2185 g 2347 t
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Query Match      100.0%; Score 25; DB 12; Length 9019;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAACTTGT 25
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Db 53 GTTCAGCTTTTGTACAAACTTGT 29

RESULT 12
AF196824
LOCUS      AF196824      11005 bp      DNA      circular SYN 26-FEB-2003
DEFINITION piggyBac transformation vector pB-UGateway w+, complete sequence.
ACCESSION  AF196824
VERSION     AF196824.1 GI:28565716
KEYWORDS   piggyBac transformation vector pB-UGateway w+
SOURCE     piggyBac transformation vector pB-UGateway w+
ORGANISM   piggyBac transformation vector pB-UGateway w+
artificial sequences; vectors.
REFERENCE  1 (bases 1 to 11005)
AUTHORS   Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE     A toolkit for transformation and mutagenesis in Drosophila using
piggyBac

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ORIGIN

Query Match 100.0%; Score 25; DB 12; Length 4462;
 Best Local Similarity 100.0%; Pred. No. 2.7; 0; Gaps 0;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTGT 25
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 Db 480 GTTCAGCTTTTGTACAACTTGT 456

RESULT 9

AX306327/c
 LOCUS AX306327 5148 bp DNA linear PAT 11-DEC-2001
 DEFINITION Sequence 10 from Patent WO0188121.
 ACCESSION AX306327
 VERSION AX306327.1 GI:17645566

KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.

REFERENCE 1
 AUTHORS Plaetinck, G., Renard, J.P. and Bogaert, T.
 TITLE Vector constructs
 JOURNAL Patent: WO 0188121-A 10 22-NOV-2001;
 Devgen NV (BE)

FEATURES

Location/Qualifiers
 source
 1..5148
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 /note="Plasmid pGN39"

BASE COUNT 1359 a 1199 c 1279 g 1311 t

ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 5148;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTGT 25
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 Db 171 GTTCAGCTTTTGTACAACTTGT 147

RESULT 10

AF408413
 LOCUS AF408413 9019 bp DNA circular SYN 25-JUN-2002
 DEFINITION Binary vector pJawohl8-RNAi, complete sequence.
 ACCESSION AF408413
 VERSION AF408413.1 GI:21552736

KEYWORDS Binary vector pJawohl8-RNAi
 SOURCE Binary vector pJawohl8-RNAi
 ORGANISM artificial sequences; vectors.

REFERENCE 1 (bases 1 to 9019)
 AUTHORS Ulker, B., Lipka, V., Rademacher, T.R. and Somssich, I.E.
 TITLE pJawohl8-RNAi a binary vector for gene silencing in plants
 JOURNAL Unpublished

REFERENCE 2 (bases 1 to 9019)
 AUTHORS Ulker, B., Lipka, V., Rademacher, T.R. and Somssich, I.E.
 TITLE Direct Submission

Submitted (08-AUG-2001) Biochemistry, Max-Planck-Institut
 f. Zuechtungsforchung, Carl-von-Linne Weg 10, Koeln, NRW D-50829,
 Germany

FEATURES

Location/Qualifiers
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 cloning of inverted sequences"

BASE COUNT 3803. .9019

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 /gene="ccdB"
 1263..1568
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 /product="CcdB"
 /protein_id="AA062301.1"
 /db_xref="GI:21552738"
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 KVSRELYPVVHIGDESWMRTDMASVPVSVIGEEVADLSHRENDIKNAINLMFWGI"
 1510..1736
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 1762..2048
 /note="contains intron 1 of Arabidopsis thaliana WRKY
 transcription factor 33"
 complement(2073..3783)
 /note="antisense orientation of Gateway conversion
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 complement(2073..2199)
 /note="attR2 of Gateway conversion cassette frame A"
 complement(2241..2546)
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 /note="encodes a cytotoxic protein that is a potent poison
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 /db_xref="GI:21552740"
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 SSLWSEYHDDFRQFLHYSDVACYGELAYFPKGFENMFVSNPWSFTSFDLNV
 ANMDFEAPVFTMGKYITQGDVKVLMPLAIQVHHAVCDFHVGRLNELQQYCDWQGG
 A"

Qy 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 6
AX684690/c
LOCUS AX684690 35 bp DNA linear PAT 29-MAR-2003
DEFINITION Sequence 9 from Patent WO0224865.
ACCESSION AX684690
VERSION AX684690.1 GI:29371240
KEYWORDS
SOURCE Escherichia coli
ORGANISM Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.

REFERENCE 1
AUTHORS Holtzman,D., Madden,K., Maxon,M. and Sherman,A.
TITLE Modulation of secondary metabolite production by zinc binuclear cluster proteins
JOURNAL Patent: WO 0224865-A 9 28-MAR-2002;
Microbia, INC. (US)

FEATURES
source
1. .35
/organism="Escherichia coli"
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/db_xref="taxon:562"
14 a 7 c 7 g 7 t

BASE COUNT 14 a 7 c 7 g 7 t
ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 35;
Best Local Similarity 100.0%; Pred.No. 6.7;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 35 GTTCAGCTTTTGTACAAACTTGT 11

RESULT 7
AX703501/c
LOCUS AX703501 1846 bp DNA linear PAT 03-APR-2003
DEFINITION Sequence 63 from Patent WO02066653.
ACCESSION AX703501
VERSION AX703501.1 GI:29538461
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Li,M. and Liu,Y.C.
TITLE Procarvotic libraries and uses
JOURNAL Patent: WO 02066653-A 63 29-AUG-2002;
Xencor (US)

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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
527 a 381 c 434 g 504 t

BASE COUNT 527 a 381 c 434 g 504 t
ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 1846;
Best Local Similarity 100.0%; Pred.No. 3.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 25 GTTCAGCTTTTGTACAAACTTGT 1

RESULT 8
VF0551314/c

LOCUS VF0551314
DEFINITION Transfection vector pBTdest.
ACCESSION AJ551314
VERSION AJ551314.1 GI:29335742
KEYWORDS amp gene; beta lactamase; cat gene; ccdB gene; chloramphenicol acetyl transferase; control of cell death B protein.
SOURCE Transfection vector pBTdest
ORGANISM artificial sequences; vectors.
REFERENCE 1
AUTHORS Jakoby,M.J., Heim,M.A. and Weishaar,B.
TITLE Use of a gateway compatible vector for transient plant transfection
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 4462)
AUTHORS Jakoby,M.J.
TITLE Direct Submission
JOURNAL Submitted (26-MAR-2003) Jakoby M.J., Salamini, MPI for Plant Breeding Research, Carl-von-Linne Weg 10, 50829 Koeln, GERMANY

FEATURES
source
1. .4462
/organism="Transfection vector pBTdest"
/mol_type="genomic DNA"
/db_xref="taxon:225975"
31. .443
/notes="35S"
421. .424
/notes="35S"
456. .580
/notes="attR1"
689. .1348
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/product="chloramphenicol acetyl transferase"
/protein_id="CAD83080.1"
/db_xref="GI:29335743"
/translation="MEKKTIGYTTVDISQWHRKEHFEAFQSAQCTYNQTVQLDITAF LKTVKKNKHFYPAFIHILARLNAHPEPRMAMKDGELVIWDSVHPCTYVHQTETFSLSWEVHDDFROFLHYSDVACYGENLAYFPKGIENMFVSNPVSFTSFDLNV ANMDFAPVFTMGKYTTQGDKVLMLAIQVHHAVCDGFHVGRLNELQYCDQWQGG A"
1690. .1995
/genes="ccdB"
1690. .1995
/genes="ccdB"
/codon_start=1
/product="control of cell death B protein"
/protein_id="CAD83081.1"
/db_xref="GI:29335744"
/translation="MQFKVITYKRESRYRLFDVQSDIIDTPGRMWIPLASRLSD KVSRELYPVVHIGDESWMRTTDMASVPVSVIGEEVADLSHRENDIKNALNLPWGI"
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2168. .2463
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2606. .3466
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2606. .3466
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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTGT 25
Db 1 GTTCAGCTTTTGTACAACTTGT 25

RESULT 2
LOCUS AR163180 25 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 9 from patent US 6270969.
ACCESSION AR163180
VERSION AR163180.1 GI:16233689
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6270969-A 9 07-AUG-2001;
FEATURES Location/Qualifiers
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Query Match
Best Local Similarity 100.0%; Score 25; DB 6; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTGT 25
Db 1 GTTCAGCTTTTGTACAACTTGT 25

RESULT 3
LOCUS AX491648 25 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 9 from Patent EP1227147.
ACCESSION AX491648
VERSION AX491648.1 GI:22324156
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: EP 1227147-A 9 31-JUL-2002;
FEATURES Location/Qualifiers
source
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BASE COUNT 5 a 4 c 4 g 12 t
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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GTTCAGCTTTTGTACAACTTGT 25

RESULT 4
LOCUS AX498619 25 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 9 from Patent EP1229113.
ACCESSION AX498619
VERSION AX498619.1 GI:23343416
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: EP 1229113-A 9 07-AUG-2002;
FEATURES Location/Qualifiers
source
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Query Match
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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTGT 25
Db 1 GTTCAGCTTTTGTACAACTTGT 25

RESULT 5
LOCUS BD131335 25 bp DNA linear PAT 18-SEP-2002
DEFINITION Recombinational cloning using nucleic acids having recombination sites.
ACCESSION BD131335
VERSION BD131335.1 GI:23226280
KEYWORDS JP 2002500861-A/9.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.
TITLE Recombinational cloning using nucleic acids having recombination sites
JOURNAL Patent: JP 2002500861-A 9 15-JAN-2002;
COMMENT LIFE TECHNOLOGIES INC
OS Unknown
PN JP 2002500861-A/9
PD 15-JAN-2002
PR 26-OCT-1998 JP 2000518069
PR 24-OCT-1997 US 60/065930,23-OCT-1998 US 09/177387 PI
C12N15/09,C12Q1/68,C12N15/00
CC Description of Unknown Organism: recombination products FH
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BASE COUNT 5 a 4 c 4 g 12 t
ORIGIN

Query Match
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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTGT 25
Db 1 GTTCAGCTTTTGTACAACTTGT 25

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 6, 2003, 21:07:03 ; Search time 601 Seconds
(without alignments)
1701.732 Million cell updates/sec

Title: US-10-055-001A-4

Perfect score: 25

Sequence: 1 gttcagctttttgtacaaactgt 25

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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3: gb.in.*

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40: em.htgo.mus.*

41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	25	100.0	25	6	ARI24529 Sequence
3	25	100.0	25	6	ARI24529 Sequence
4	25	100.0	25	6	AX491648 Sequence
5	25	100.0	25	6	AX498619 Sequence
6	25	100.0	25	6	BD131335 Recombina
7	25	100.0	35	6	AX684690 Sequence
8	25	100.0	1846	6	AX703501 Sequence
9	25	100.0	4462	12	VFO551314 Transfect
10	25	100.0	5148	6	AX306327 Sequence
11	25	100.0	9019	12	AF408413 Binary ve
12	25	100.0	9019	12	AF408413 Binary ve
13	25	100.0	11005	12	AX196824 PiggyBac
14	25	100.0	11005	12	AX196824 PiggyBac
15	25	100.0	12677	12	AX196825 PiggyBac
16	25	100.0	12677	12	AX196825 PiggyBac
17	25	100.0	12789	6	AX590202 Sequence
18	25	100.0	13274	6	AX356862 Sequence
19	23.4	93.6	13990	12	AF541939 His-3 int
20	23.4	93.6	25	6	ARI24530 Sequence
21	23.4	93.6	25	6	ARI24530 Sequence
22	23.4	93.6	25	6	AX491649 Sequence
23	23.4	93.6	25	6	AX498620 Sequence
24	22.6	90.4	25	6	BD131336 Recombina
25	22.4	89.6	25	6	BD131368 Recombina
26	22.4	89.6	25	6	ARI24535 Sequence
27	22.4	89.6	25	6	ARI24535 Sequence
28	22.4	89.6	25	6	AX491654 Sequence
29	22.4	89.6	25	6	AX498625 Sequence
30	22.4	89.6	18691	12	BD131341 Recombina
31	22.4	89.6	18691	12	BD131341 Recombina
32	21.8	87.2	25	6	AX269136 Cloning v
33	21.8	87.2	51	6	AX525413 Sequence
34	21.8	87.2	51	6	AX525421 Sequence
35	21.8	87.2	51	6	AX525429 Sequence
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37	21.8	87.2	145569	5	AL935194 Zebrafish
38	21.2	84.8	25	6	BD131369 Recombina
39	20.8	83.2	25	6	ARI24531 Sequence
40	20.8	83.2	25	6	ARI24536 Sequence
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44	20.8	83.2	25	6	AX491650 Sequence
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ALIGNMENTS

RESULT 1
ARI24529
LOCUS ARI24529 25 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 9 from patent US 6171861.
ACCESSION ARI24529
VERSION ARI24529.1 GI:14109890
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley, J.L. and Brasch, M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6171861-A 9 09-JAN-2001;
FEATURES Location/Qualifiers